

CORRECTED VERSION

(19) World Intellectual Property Organization
International Bureau



(43) International Publication Date
19 July 2007 (19.07.2007)

PCT

(10) International Publication Number
WO 2007/080126 A3

(51) International Patent Classification:

C12N 15/82 (2006.01) C12N 15/12 (2006.01)
A01H 5/00 (2006.01) C12N 15/11 (2006.01)
C12N 5/10 (2006.01)

(21) International Application Number:

PCT/EP2007/000286

(22) International Filing Date: 12 January 2007 (12.01.2007)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:

60/758,191	12 January 2006 (12.01.2006)	US
06447008.1	12 January 2006 (12.01.2006)	EP
60/771,160	7 February 2006 (07.02.2006)	US
60/837,910	16 August 2006 (16.08.2006)	US
60/875,356	18 December 2006 (18.12.2006)	US

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(81) Designated States (unless otherwise indicated, for every
kind of national protection available): AE, AG, AL, AM,
AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN,
CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI,
GB, GD, GE, GH, GM, GT, HN, HR, HU, ID, IL, IN, IS,
JP, KE, KG, KM, KN, KP, KR, KZ, LA, LC, LK, LR, LS,
LT, LU, LV, LY, MA, MD, MG, MK, MN, MW, MX, MY,
MZ, NA, NG, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RS,
RU, SC, SD, SE, SG, SK, SL, SM, SV, SY, TJ, TM, TN,
TR, TT, TZ, UA, UG, US, UZ, VC, VN, ZA, ZM, ZW.

(84) Designated States (unless otherwise indicated, for every
kind of regional protection available): ARIPO (BW, GH,

[Continued on next page]

(54) Title: DSRNA AS INSECT CONTROL AGENT

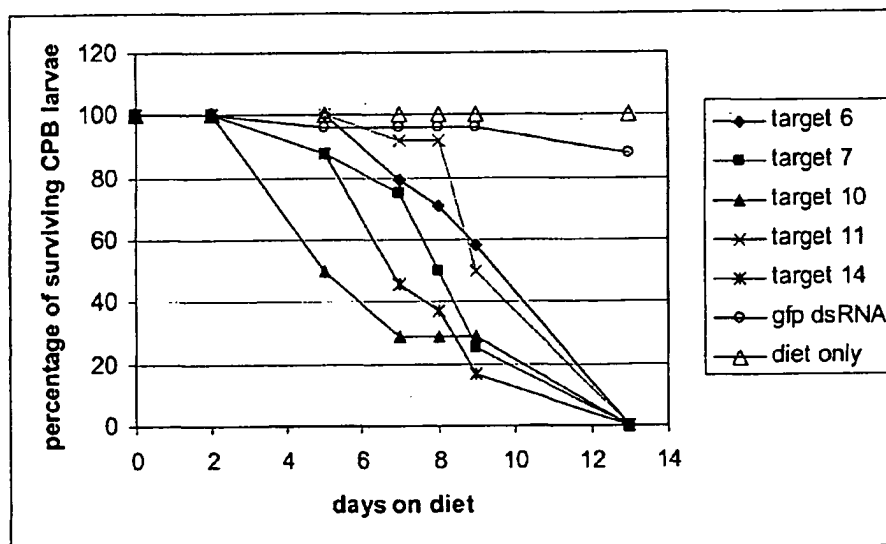


FIGURE 1-LD

(57) Abstract: The present invention relates to methods for controlling pest infestation using double stranded RNA molecules. The invention provides methods for making transgenic plants that express the double stranded RNA molecules, as well as pesticidal agents and commodity products produced by the inventive plants.

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GM, KE, LS, MW, MZ, NA, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European (AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IS, IT, LT, LU, LV, MC, NL, PL, PT, RO, SE, SI, SK, TR), OAPI (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

Published:

— *with international search report*

(88) Date of publication of the international search report:
27 March 2008

(48) Date of publication of this corrected version:
14 August 2008

Declaration under Rule 4.17:

— *of inventorship (Rule 4.17(iv))*

(15) Information about Correction:

see Notice of 14 August 2008

DSRNA AS INSECT CONTROL AGENT

Field of the invention

The present invention relates to the field of double-stranded RNA (dsRNA)-mediated gene silencing in insect species. More particularly, the present invention relates to genetic constructs designed for the expression of dsRNA corresponding to novel target genes. These constructs are particularly useful in RNAi-mediated plant pest control. The invention further relates to methods for controlling insects, methods for preventing insect infestation and methods for down-regulating gene expression in insects using RNAi. The invention also relates to transgenic plants resistant to insect infestation.

Background to the invention

The environment is replete with pests and numerous methods have attempted to control pests infestations of plants. Commercial crops are often the targets of insect attack. Substantial progress has been made in the last few decades towards developing more efficient methods and compositions for controlling insect infestation in plants.

Chemical pesticides have been very effective in eradicating pest infestation. However, there are several disadvantages to using chemical pesticidal agents. Not only are they potentially detrimental to the environment, but they are not selective and are harmful to various crops and non-target fauna. Chemical pesticides persist in the environment and generally are slow to be metabolized, if at all. They accumulate in the food chain, and particularly in the higher predator species where they can act as mutagens and/or carcinogens to cause irreversible and deleterious genetic modifications. There has thus been continued controversy in the use of chemical insecticides to combat crop pests. They can rapidly develop resistance against these insecticides because of repetitive usage of the same insecticide or of insecticides having the same mode of action, and because accumulation also results in the development of resistance to the agents in species higher up the evolutionary ladder.

Control of insect pests on agronomically important crops is important, particularly insect pests which damage plants belonging to the Solanaceae family, especially potato (*Solanum tuberosum*), but also tomato (*Solanum lycopersicum*), eggplant (*Solanum melongena*), capsicums (*Solanum capsicum*), and nightshade (for example, *Solanum aculeastrum*, *S. bulbocastanum*, *S. cardiophyllum*, *S. douglasii*, *S. dulcamara*, *S. lanceolatum*, *S. robustum*, and *S. triquetrum*), particularly the control of coleopteran pests.

Biological control using extract from neem seed has been shown to work against coleopteran pests of vegetables. Commercially available neem-based insecticides have azadirachtin as the primary active ingredient. These insecticides are applicable to a broad spectrum of insects. They act as insect growth regulator; azadirachtin prevents insects from molting by inhibiting production of an insect hormone, ecdysone.

Biological control using protein Cry3A from *Bacillus thuringiensis* varieties tenebrionis and san diego, and derived insecticidal proteins are alternatives to chemical control. The Bt toxin

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protein is effective in controlling Colorado potato beetle larvae either as formulations sprayed onto the foliage or expressed in the leaves of potatoes.

5 An alternative biological agent is dsRNA. Over the last few years, down-regulation of genes (also referred to as "gene silencing") in multicellular organisms by means of RNA interference or "RNAi" has become a well-established technique.

10 RNA interference or "RNAi" is a process of sequence-specific down-regulation of gene expression (also referred to as "gene silencing" or "RNA-mediated gene silencing") initiated by double-stranded RNA (dsRNA) that is complementary in sequence to a region of the target gene to be down-regulated (Fire, A. Trends Genet. Vol. 15, 358-363, 1999; Sharp, P.A. Genes Dev. Vol. 15, 485-490, 2001).

Over the last few years, down-regulation of target genes in multicellular organisms by means of RNA interference (RNAi) has become a well established technique. Reference may be made to International Applications WO 99/32619 (Carnegie Institution) and WO 00/01846 (by Applicant).

15 DsRNA gene silencing finds application in many different areas, such as for example dsRNA mediated gene silencing in clinical applications (WO2004/001013) and in plants. In plants, dsRNA constructs useful for gene silencing have also been designed to be cleaved and to be processed into short interfering RNAs (siRNAs).

20 RNAi has also been proposed as a means of protecting plants against plant parasitic nematodes, i.e. by expressing in the plant (e.g. in the entire plant, or in a part, tissue or cell of a plant) one or more nucleotide sequences that form a dsRNA fragment that corresponds to a target gene in the plant parasitic nematode that is essential for its growth, reproduction and/or survival. Reference may be made to the International Application WO 00/01846 (by Applicant) and US patent 6,506,559 (based on WO 99/32619).

25 Although the technique of RNAi has been generally known in the art in plants, *C. elegans* and mammalian cells for some years, to date little is known about the use of RNAi to down-regulate gene expression in insects. Since the filing and publication of the WO 00/01846 and WO 99/32619 applications, only few other applications have been published that relate to the use of RNAi to protect plants against insects. These include the International Applications WO 01/37654 (DNA Plant Technologies), WO 2005/019408 (Bar Ilan University), WO 2005/049841 (CSIRO, Bayer Cropscience), WO 05/047300 (University of Utah Research foundation), and the US application 30 2003/00150017 (Mesa et al.).

The present invention provides target genes and constructs useful in the RNAi-mediated insect pest control, especially the control of insect plant pathogens. The present invention also provides methods for controlling insect pest infestation by repressing, delaying, or otherwise 35 reducing target gene expression within a particular insect pest.

Description of the invention:

40 The present invention describes a novel non-compound, non-protein based approach for the control of insect crop pests. The active ingredient is a nucleic acid, a double-stranded RNA

(dsRNA), which can be used as an insecticidal formulation. In another embodiment, the dsRNA can be expressed constitutively in the host plant, plant part, plant cell or seed to protect the plant against chewing insects especially coleopterans such as beetles. The sequence of the dsRNA corresponds to part or whole of an essential insect gene and causes downregulation of the insect target via RNA interference (RNAi). As a result of the downregulation of mRNA, the dsRNA prevents expression of the target insect protein and hence causes death, growth arrest or sterility of the insect.

The methods of the invention can find practical application in any area of technology where it is desirable to inhibit viability, growth, development or reproduction of the insect, or to decrease pathogenicity or infectivity of the insect. The methods of the invention further find practical application where it is desirable to specifically down-regulate expression of one or more target genes in an insect. Particularly useful practical applications include, but are not limited to, protecting plants against insect pest infestation.

In accordance with one embodiment the invention relates to a method for controlling insect growth on a cell or an organism, or for preventing insect infestation of a cell or an organism susceptible to insect infection, comprising contacting insects with a double-stranded RNA, wherein the double-stranded RNA comprises annealed complementary strands, one of which has a nucleotide sequence which is complementary to at least part of the nucleotide sequence of an insect target gene, whereby the double-stranded RNA is taken up by the insect and thereby controls growth or prevents infestation.

The present invention therefore provides isolated novel nucleotide sequences of insect target genes, said isolated nucleotide sequences comprising at least one nucleic acid sequence selected from the group comprising:

(i) sequences represented by any of SEQ ID NOs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 49 to 158, 159, 160-163, 168, 173, 178, 183, 188, 193, 198, 203, 208, 215, 220, 225, 230, 240 to 247, 249, 251, 253, 255, 257, 259, 275 to 472, 473, 478, 483, 488, 493, 498, 503, 508 to 513, 515, 517, 519, 521, 533 to 575, 576, 581, 586, 591, 596, 601, 603, 605, 607, 609, 621 to 767, 768, 773, 778, 783, 788, 793, 795, 797, 799, 801, 813 to 862, 863, 868, 873, 878, 883, 888, 890, 892, 894, 896, 908 to 1040, 1041, 1046, 1051, 1056, 1061, 1066 to 1071, 1073, 1075, 1077, 1079, 1081, 1083, 1085, 1087, 1089, 1091, 1093, 1095, 1097, 1099, 1101, 1103, 1105, 1107, 1109, 1111, 1113, 1161 to 1571, 1572, 1577, 1582, 1587, 1592, 1597, 1602, 1607, 1612, 1617, 1622, 1627, 1632, 1637, 1642, 1647, 1652, 1657, 1662, 1667, 1672, 1677, 1682, 1684, 1686, 1688, 1690, 1692, 1694, 1696, 1698, 1700, 1702, 1704, 1730 to 2039, 2040, 2045, 2050, 2055, 2060, 2065, 2070, 2075, 2080, 2085, 2090, 2095, 2100, 2102, 2104, 2106, 2108, 2120 to 2338, 2339, 2344, 2349, 2354, 2359, 2364, 2366, 2368, 2370, 2372, 2384 to 2460, 2461, 2466, 2471, 2476, 2481 or 2486, or the complement thereof,

(ii) sequences which are at least 70 %, preferably at least 75%, 80%, 85%, 90%, more preferably at least 95%, 96%, 97%, 98% or 99% identical to a sequence represented by any of SEQ ID NOs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 49 to 158, 159, 160-163, 168, 173, 178, 183, 188, 193, 198, 203, 208, 215, 220, 225, 230, 240 to 247, 249, 251, 253, 255, 257, 259, 275 to 472,

473, 478, 483, 488, 493, 498, 503, 508 to 513, 515, 517, 519, 521, 533 to 575, 576, 581, 586, 591, 596, 601, 603, 605, 607, 609, 621 to 767, 768, 773, 778, 783, 788, 793, 795, 797, 799, 801, 813 to 862, 863, 868, 873, 878, 883, 888, 890, 892, 894, 896, 908 to 1040, 1041, 1046, 1051, 1056, 1061, 1066 to 1071, 1073, 1075, 1077, 1079, 1081, 1083, 1085, 1087, 1089, 1091, 1093, 1095, 1097, 1099, 1101, 1103, 1105, 1107, 1109, 1111, 1113, 1161 to 1571, 1572, 1577, 1582, 1587, 1592, 1597, 1602, 1607, 1612, 1617, 1622, 1627, 1632, 1637, 1642, 1647, 1652, 1657, 1662, 1667, 1672, 1677, 1682, 1684, 1686, 1688, 1690, 1692, 1694, 1696, 1698, 1700, 1702, 1704, 1730 to 2039, 2040, 2045, 2050, 2055, 2060, 2065, 2070, 2075, 2080, 2085, 2090, 2095, 2100, 2102, 2104, 2106, 2108, 2120 to 2338, 2339, 2344, 2349, 2354, 2359, 2364, 2366, 2368, 2370, 2372, 2384 to 2460, 2461, 2466, 2471, 2476, 2481 or 2486, or the complement thereof, and

(iii) sequences comprising at least 17 contiguous nucleotides of any of the sequences represented by SEQ ID NOs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 49 to 158, 159, 160-163, 168, 173, 178, 183, 188, 193, 198, 203, 208, 215, 220, 225, 230, 240 to 247, 249, 251, 253, 255, 257, 259, 275 to 472, 473, 478, 483, 488, 493, 498, 503, 508 to 513, 515, 517, 519, 521, 533 to 575, 576, 581, 586, 591, 596, 601, 603, 605, 607, 609, 621 to 767, 768, 773, 778, 783, 788, 793, 795, 797, 799, 801, 813 to 862, 863, 868, 873, 878, 883, 888, 890, 892, 894, 896, 908 to 1040, 1041, 1046, 1051, 1056, 1061, 1066 to 1071, 1073, 1075, 1077, 1079, 1081, 1083, 1085, 1087, 1089, 1091, 1093, 1095, 1097, 1099, 1101, 1103, 1105, 1107, 1109, 1111, 1113, 1161 to 1571, 1572, 1577, 1582, 1587, 1592, 1597, 1602, 1607, 1612, 1617, 1622, 1627, 1632, 1637, 1642, 1647, 1652, 1657, 1662, 1667, 1672, 1677, 1682, 1684, 1686, 1688, 1690, 1692, 1694, 1696, 1698, 1700, 1702, 1704, 1730 to 2039, 2040, 2045, 2050, 2055, 2060, 2065, 2070, 2075, 2080, 2085, 2090, 2095, 2100, 2102, 2104, 2106, 2108, 2120 to 2338, 2339, 2344, 2349, 2354, 2359, 2364, 2366, 2368, 2370, 2372, 2384 to 2460, 2461, 2466, 2471, 2476, 2481 or 2486, or the complement thereof,

or wherein said nucleic acid sequence is an orthologue of a gene comprising at least 17 contiguous nucleotides of any of SEQ ID NOs 49 to 158, 275 to 472, 533 to 575, 621 to 767, 813 to 862, 908 to 1040, 1161 to 1571, 1730 to 2039, 2120 to 2338, 2384 to 2460, or a complement thereof,

said nucleic acid sequences being useful for preparing the double stranded RNAs of the invention for controlling insect growth.

"Controlling pests" as used in the present invention means killing pests, or preventing pests to develop, or to grow or preventing pests to infect or infest. Controlling pests as used herein also encompasses controlling pest progeny (development of eggs). Controlling pests as used herein also encompasses inhibiting viability, growth, development or reproduction of the pest, or to decrease pathogenicity or infectivity of the pest. The compounds and/or compositions described herein, may be used to keep an organism healthy and may be used curatively, preventively or systematically to control pests or to avoid pest growth or development or infection or infestation. Particular pests envisaged in the present invention are plant pathogenic insect pests. "Controlling insects" as used herein thus also encompasses controlling insect progeny (such as development of eggs). Controlling insects as used herein also encompasses inhibiting viability, growth,

development or reproduction of the insect, or decreasing pathogenicity or infectivity of the insect. In the present invention, controlling insects may inhibit a biological activity in a insect, resulting in one or more of the following attributes: reduction in feeding by the insect, reduction in viability of the insect, death of the insect, inhibition of differentiation and development of the insect, absence of or
5 reduced capacity for sexual reproduction by the insect, muscle formation, juvenile hormone formation, juvenile hormone regulation, ion regulation and transport, maintenance of cell membrane potential, amino acid biosynthesis, amino acid degradation, sperm formation, pheromone synthesis, pheromone sensing, antennae formation, wing formation, leg formation, development and differentiation, egg formation, larval maturation, digestive enzyme formation, haemolymph
10 synthesis, haemolymph maintenance, neurotransmission, cell division, energy metabolism, respiration, apoptosis, and any component of a eukaryotic cells' cytoskeletal structure, such as, for example, actins and tubulins. The compounds and/or compositions described herein, may be used to keep an organism healthy and may be used curatively, preventively or systematically to control a insect or to avoid insect growth or development or infection or infestation. Thus, the invention may
15 allow previously susceptible organisms to develop resistance against infestation by the insect organism.

The expression "complementary to at least part of" as used herein means that the nucleotide sequence is fully complementary to the nucleotide sequence of the target over more than two nucleotides, for instance over at least 15, 16, 17, 18, 19, 20, 21, 22, 23, 24 or more contiguous
20 nucleotides.

According to a further embodiment, the invention relates to a method method for down-regulating expression of a target gene in an insect, comprising contacting said insect with a double-stranded RNA, wherein the double-stranded RNA comprises annealed complementary strands, one of which has a nucleotide sequence which is complementary to at least part of the nucleotide
25 sequence of the insect target gene to be down-regulated, whereby the double-stranded RNA is taken up into the insect and thereby down-regulates expression of the insect target gene.

Whenever the term "a" is used within the context of "a target gene", this means "at least one" target gene. The same applies for "a" target organism meaning "at least one" target organism, and "a" RNA molecule or host cell meaning "at least one" RNA molecule or host cell. This is also
30 detailed further below.

According to one embodiment, the methods of the invention rely on uptake by the insect of double-stranded RNA present outside of the insect (e. g. by feeding) and does not require expression of double-stranded RNA within cells of the insect. In addition, the present invention also encompasses methods as described above wherein the insect is contacted with a composition
35 comprising the double-stranded RNA.

The invention further provides a method for down-regulating expression of at least one target gene in a target organism (which is capable of ingesting a plant, plant part, plant cell or seeds) comprising feeding a plant, plant part, plant cell or seed to the target organism which plant, plant part, plant cell or seed expresses double-stranded RNA.

In a more preferred aspect, the invention provides a method for down-regulating expression of at least one target gene in a target organism (which is capable of ingesting a host cell, or extracts thereof) comprising feeding a hostplant, plant part, plant cell or seed to the target organism which hostplant, plant part, plant cell or seed expresses a double-stranded RNA molecule comprising a nucleotide sequence complementary to or representing the RNA equivalent of at least part of the nucleotide sequence of the at least one target gene, whereby the ingestion of the host cell, host plant, plant part, plant cell or seed by the target organism causes and/or leads to down-regulation of expression of the at least one target gene.

The invention provides for use of a plant, plant part, plant cell or seed as defined herein for down regulation of expression of an insect target gene. In more detailed terms, the invention provides for use of a host cell as defined herein and/or an RNA molecule comprising a nucleotide sequence that is the RNA complement of or that represents the RNA equivalent of at least part of the nucleotide sequence of a target gene from a target organism, as produced by transcription of a nucleic acid molecule in a plant, plant part, plant cell or seed, for instance in the manufacture of a commodity product, for down regulation of expression of a target gene. Suitable target genes and target organisms in respect of the invention are discussed below in further detail.

According to one embodiment, the methods of the invention rely on a GMO approach wherein the double-stranded RNA is expressed by a cell or an organism infested with or susceptible to infestation by insects. Preferably, said cell is a plant cell or said organism is a plant.

The present invention thus also relates to a method for producing a plant resistant to a plant pathogenic insect, comprising:

- transforming a plant cell with a recombinant construct comprising at least one regulatory sequence operably linked to a sequence complementary to at least part of (a) a nucleotide sequence of a target insect gene selected from the group consisting of:
 - (i) sequences which are at least 75% identical to a sequence represented by any of SEQ ID NOs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 49 to 158, 159, 160-163, 168, 173, 178, 183, 188, 193, 198, 203, 208, 215, 220, 225, 230, 247, 249, 251, 253, 255, 257, 259, 275 to 472, 473, 478, 483, 488, 493, 498, 503, 513, 515, 517, 519, 521, 533 to 575, 576, 581, 586, 591, 596, 601, 603, 605, 607, 609, 621 to 767, 768, 773, 778, 783, 788, 793, 795, 797, 799, 801, 813 to 862, 863, 868, 873, 878, 883, 888, 890, 892, 894, 896, 908 to 1040, 1041, 1046, 1051, 1056, 1061, 1071, 1073, 1075, 1077, 1079, 1081, 1083, 1085, 1087, 1089, 1091, 1093, 1095, 1097, 1099, 1101, 1103, 1105, 1107, 1109, 1111, 1113, 1161 to 1571, 1572, 1577, 1582, 1587, 1592, 1597, 1602, 1607, 1612, 1617, 1622, 1627, 1632, 1637, 1642, 1647, 1652, 1657, 1662, 1667, 1672, 1677, 1682, 1684, 1686, 1688, 1690, 1692, 1694, 1696, 1698, 1700, 1702, 1704, 1730 to 2039, 2040, 2045, 2050, 2055, 2060, 2065, 2070, 2075, 2080, 2085, 2090, 2095, 2100, 2102, 2104, 2106, 2108, 2120 to 2338, 2339, 2344, 2349, 2354, 2359, 2364, 2366, 2368, 2370, 2372, 2384 to 2460, 2461, 2466, 2471, 2476 or 2481, or the complement thereof,

- (ii) sequences comprising at least 17 contiguous nucleotides of any of SEQ ID Nos 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 49 to 158, 159, 160-163, 168, 173, 178, 183, 188, 193, 198, 203, 208, 215, 220, 225, 230, 247, 249, 251, 253, 255, 257, 259, 275 to 472, 473, 478, 483, 488, 493, 498, 503, 513, 515, 517, 519, 521, 533 to 575, 576, 581, 586, 591, 596, 601, 603, 605, 607, 609, 621 to 767, 768, 773, 778, 783, 788, 793, 795, 797, 799, 801, 813 to 862, 863, 868, 873, 878, 883, 888, 890, 892, 894, 896, 908 to 1040, 1041, 1046, 1051, 1056, 1061, 1071, 1073, 1075, 1077, 1079, 1081, 1083, 1085, 1087, 1089, 1091, 1093, 1095, 1097, 1099, 1101, 1103, 1105, 1107, 1109, 1111, 1113, 1161 to 1571, 1572, 1577, 1582, 1587, 1592, 1597, 1602, 1607, 1612, 1617, 1622, 1627, 1632, 1637, 1642, 1647, 1652, 1657, 1662, 1667, 1672, 1677, 1682, 1684, 1686, 1688, 1690, 1692, 1694, 1696, 1698, 1700, 1702, 1704, 1730 to 2039, 2040, 2045, 2050, 2055, 2060, 2065, 2070, 2075, 2080, 2085, 2090, 2095, 2100, 2102, 2104, 2106, 2108, 2120 to 2338, 2339, 2344, 2349, 2354, 2359, 2364, 2366, 2368, 2370, 2372, 2384 to 2460, 2461, 2466, 2471, 2476 or 2481, or the complement thereof, and
- (iii) sequences comprising a sense strand comprising a nucleotide sequence of (i) and an antisense strand comprising the complement of said nucleotide sequence of (i), wherein the transcript encoded by said nucleotide sequence is capable of forming a double-stranded RNA,
- or (b) a nucleotide sequence which is an insect orthologue of a gene comprising at least 17 contiguous nucleotides of any of SEQ ID Nos 49 to 158, 275 to 472, 533 to 575, 621 to 767, 813 to 862, 908 to 1040, 1161 to 1571, 1730 to 2039, 2120 to 2338, 2384 to 2460, or the complement thereof;
- regenerating a plant from the transformed plant cell; and
 - growing the transformed plant under conditions suitable for the expression of the recombinant construct, said grown transformed plant resistant to plant pathogenic insects compared to an untransformed plant.

The insect can be any insect, meaning any organism belonging to the Kingdom Animals, more specific to the Phylum Arthropoda, and to the Class Insecta or the Class Arachnida. The methods of the invention are applicable to all insects and that are susceptible to gene silencing by RNA interference and that are capable of internalising double-stranded RNA from their immediate environment. The invention is also applicable to the insect at any stage in its development. Because insects have a non-living exoskeleton, they cannot grow at a uniform rate and rather grow in stages by periodically shedding their exoskeleton. This process is referred to as moulting or ecdysis. The stages between moults are referred to as "instars" and these stages may be targeted according to the invention. Also, insect eggs or live young may also be targeted according to the present invention. All stages in the developmental cycle, which includes metamorphosis in the pterygotes, may be targeted according to the present invention. Thus, individual stages such as larvae, pupae, nymph etc stages of development may all be targeted.

In one embodiment of the invention, the insect may belong to the following orders: Acari, Araneae, Anoplura, Coleoptera, Collembola, Dermaptera, Dictyoptera, Diplura, Diptera, Embioptera, Ephemeroptera, Grylloblatodea, Hemiptera, Homoptera, Hymenoptera, Isoptera, Lepidoptera, Mallophaga, Mecoptera, Neuroptera, Odonata, Orthoptera, Phasmida, Plecoptera, 5 Protura, Psocoptera, Siphonaptera, Siphunculata, Thysanura, Strepsiptera, Thysanoptera, Trichoptera, and Zoraptera.

In preferred, but non-limiting, embodiments and methods of the invention the insect is chosen from the group consisting of an insect which is a plant pest, such as but not limited to *Nilaparvata* spp. (e.g. *N. lugens* (brown planthopper)); *Laodelphax* spp. (e.g. *L. striatellus* (small 10 brown planthopper)); *Nephotettix* spp. (e.g. *N. virescens* or *N. cincticeps* (green leafhopper), or *N. nigropictus* (rice leafhopper)); *Sogatella* spp. (e.g. *S. furcifera* (white-backed planthopper)); *Blissus* spp. (e.g. *B. leucopterus leucopterus* (chinch bug)); *Scotinophora* spp. (e.g. *S. vermidulata* (rice blackbug)); *Acrosternum* spp. (e.g. *A. hilare* (green stink bug)); *Pamara* spp. (e.g. *P. guttata* (rice skipper)); *Chilo* spp. (e.g. *C. suppressalis* (rice striped stem borer), *C. auricilius* (gold-fringed 15 stem borer), or *C. polychrysus* (dark-headed stem borer)); *Chilotraea* spp. (e.g. *C. polychrysa* (rice stalk borer)); *Sesamia* spp. (e.g. *S. inferens* (pink rice borer)); *Tryporyza* spp. (e.g. *T. innotata* (white rice borer), or *T. incertulas* (yellow rice borer)); *Cnaphalocrocis* spp. (e.g. *C. medinalis* (rice leafroller)); *Agromyza* spp. (e.g. *A. oryzae* (leafminer), or *A. parvicornis* (corn blot leafminer)); *Diatraea* spp. (e.g. *D. saccharalis* (sugarcane borer), or *D. grandiosella* (southwestern corn borer)); 20 *Namaga* spp. (e.g. *N. aenescens* (green rice caterpillar)); *Xanthodes* spp. (e.g. *X. transversa* (green caterpillar)); *Spodoptera* spp. (e.g. *S. frugiperda* (fall armyworm), *S. exigua* (beet armyworm), *S. littoralis* (climbing cutworm) or *S. praefica* (western yellowstriped armyworm)); *Mythimna* spp. (e.g. *Mythimna (Pseudaletia) separata* (armyworm)); *Helicoverpa* spp. (e.g. *H. zea* (corn earworm)); *Colaspis* spp. (e.g. *C. brunnea* (grape colaspis)); *Lissorhoptus* spp. (e.g. *L. oryzophilus* (rice water weevil)); 25 *Echinocnemus* spp. (e.g. *E. squamos* (rice plant weevil)); *Dictiodispa* spp. (e.g. *D. armigera* (rice hispa)); *Oulema* spp. (e.g. *O. oryzae* (leaf beetle); *Sitophilus* spp. (e.g. *S. oryzae* (rice weevil)); *Pachydiplosis* spp. (e.g. *P. oryzae* (rice gall midge)); *Hydrellia* spp. (e.g. *H. griseola* (small rice leafminer), or *H. sasakii* (rice stem maggot)); *Chlorops* spp. (e.g. *C. oryzae* (stem maggot)); *Diabrotica* spp. (e.g. *D. virgifera virgifera* (western corn rootworm), *D. barberi* (northern corn rootworm), *D. undecimpunctata howardi* (southern corn rootworm), *D. virgifera zea* (Mexican corn rootworm); *D. balteata* (banded cucumber beetle)); *Ostrinia* spp. (e.g. *O. nubilalis* (European corn borer)); *Agrotis* spp. (e.g. *A. ipsilon* (black cutworm)); *Elasmopalpus* spp. (e.g. *E. lignosellus* (lesser cornstalk borer)); *Melanotus* spp. (wireworms); *Cyclocephala* spp. (e.g. *C. borealis* (northern masked chafer), or *C. immaculata* (southern masked chafer)); *Popillia* 35 spp. (e.g. *P. japonica* (Japanese beetle)); *Chaetocnema* spp. (e.g. *C. pulicaria* (corn flea beetle)); *Sphenophorus* spp. (e.g. *S. maidis* (maize billbug)); *Rhopalosiphum* spp. (e.g. *R. maidis* (corn leaf aphid)); *Anuraphis* spp. (e.g. *A. maidiradicis* (corn root aphid)); *Melanoplus* spp. (e.g. *M. femurrubrum* (redlegged grasshopper) *M. differentialis* (differential grasshopper) or *M. sanguinipes* (migratory grasshopper)); *Hylemya* spp. (e.g. *H. platura* (seedcorn maggot)); *Anaphothrips* spp. 40 (e.g. *A. obscurus* (grass thrips)); *Solenopsis* spp. (e.g. *S. milesta* (thief ant)); or spp. (e.g. *T.*

urticae (twospotted spider mite), *T. cinnabarinus* (carmine spider mite); *Helicoverpa* spp. (e.g. *H. zea* (cotton bollworm), or *H. armigera* (American bollworm)); *Pectinophora* spp. (e.g. *P. gossypiella* (pink bollworm)); *Earias* spp. (e.g. *E. vittella* (spotted bollworm)); *Heliothis* spp. (e.g. *H. virescens* (tobacco budworm)); *Anthonomus* spp. (e.g. *A. grandis* (boll weevil)); *Pseudatomoscelis* spp. (e.g. *P. seriatus* (cotton fleahopper)); *Trialeurodes* spp. (e.g. *T. abutiloneus* (banded-winged whitefly) *T. vaporariorum* (greenhouse whitefly)); *Bemisia* spp. (e.g. *B. argentifolii* (silverleaf whitefly)); *Aphis* spp. (e.g. *A. gossypii* (cotton aphid)); *Lygus* spp. (e.g. *L. lineolaris* (tarnished plant bug) or *L. hesperus* (western tarnished plant bug)); *Euschistus* spp. (e.g. *E. conspersus* (conspersed stink bug)); *Chlorochroa* spp. (e.g. *C. sayi* (Say stinkbug)); *Nezara* spp. (e.g. *N. viridula* (southern green stinkbug)); *Thrips* spp. (e.g. *T. tabaci* (onion thrips)); *Frankliniella* spp. (e.g. *F. fusca* (tobacco thrips), or *F. occidentalis* (western flower thrips)); *Leptinotarsa* spp. (e.g. *L. decemlineata* (Colorado potato beetle), *L. juncta* (false potato beetle), or *L. texana* (Texan false potato beetle)); *Lema* spp. (e.g. *L. trilineata* (three-lined potato beetle)); *Epitrix* spp. (e.g. *E. cucumeris* (potato flea beetle), *E. hirtipennis* (flea beetle), or *E. tuberis* (tuber flea beetle)); *Epicauta* spp. (e.g. *E. vittata* (striped blister beetle)); *Phaedon* spp. (e.g. *P. cochleariae* (mustard leaf beetle)); *Epilachna* spp. (e.g. *E. varivertis* (mexican bean beetle)); *Acheta* spp. (e.g. *A. domesticus* (house cricket)); *Empoasca* spp. (e.g. *E. fabae* (potato leafhopper)); *Myzus* spp. (e.g. *M. persicae* (green peach aphid)); *Paratrioza* spp. (e.g. *P. cockerelli* (psyllid)); *Conoderus* spp. (e.g. *C. falli* (southern potato wireworm), or *C. vespertinus* (tobacco wireworm)); *Phthorimaea* spp. (e.g. *P. operculella* (potato tuberworm)); *Macrosiphum* spp. (e.g. *M. euphorbiae* (potato aphid)); *Thyanta* spp. (e.g. *T. pallidovirens* (redshouldered stinkbug)); *Phthorimaea* spp. (e.g. *P. operculella* (potato tuberworm)); *Helicoverpa* spp. (e.g. *H. zea* (tomato fruitworm); *Keiferia* spp. (e.g. *K. lycopersicella* (tomato pinworm)); *Limonius* spp. (wireworms); *Manduca* spp. (e.g. *M. sexta* (tobacco hornworm), or *M. quinquemaculata* (tomato hornworm)); *Liriomyza* spp. (e.g. *L. sativae*, *L. trifolii* or *L. huidobrensis* (leafminer)); *Drosophila* spp. (e.g. *D. melanogaster*, *D. yakuba*, *D. pseudoobscura* or *D. simulans*); *Carabus* spp. (e.g. *C. granulatus*); *Chironomus* spp. (e.g. *C. tentanus*); *Ctenocephalides* spp. (e.g. *C. felis* (cat flea)); *Diaprepes* spp. (e.g. *D. abbreviatus* (root weevil)); *Ips* spp. (e.g. *I. pini* (pine engraver)); *Tribolium* spp. (e.g. *T. castaneum* (red floor beetle)); *Glossina* spp. (e.g. *G. morsitans* (tsetse fly)); *Anopheles* spp. (e.g. *A. gambiae* (malaria mosquito)); *Helicoverpa* spp. (e.g. *H. armigera* (African Bollworm)); *Acyrtosiphon* spp. (e.g. *A. pisum* (pea aphid)); *Apis* spp. (e.g. *A. mellifera* (honey bee)); *Homalodisca* spp. (e.g. *H. coagulata* (glassy-winged sharpshooter)); *Aedes* spp. (e.g. *Ae. aegypti* (yellow fever mosquito)); *Bombyx* spp. (e.g. *B. mori* (silkworm)); *Locusta* spp. (e.g. *L. migratoria* (migratory locust)); *Boophilus* spp. (e.g. *B. microplus* (cattle tick)); *Acanthoscurria* spp. (e.g. *A. gomesiana* (red-haired chocolate bird eater)); *Diploptera* spp. (e.g. *D. punctata* (pacific beetle cockroach)); *Heliconius* spp. (e.g. *H. erato* (red passion flower butterfly) or *H. melpomene* (postman butterfly)); *Curculio* spp. (e.g. *C. glandium* (acorn weevil)); *Plutella* spp. (e.g. *P. xylostella* (diamondback moth)); *Amblyomma* spp. (e.g. *A. variegatum* (cattle tick)); *Anteraea* spp. (e.g. *A. yamamai* (silkmoth)); and *Armigeres* spp. (e.g. *A. subalbatus*);

Preferred plant pathogenic insects according to the invention are plant pest are selected from the group consisting of *Leptinotarsa* spp. (e.g. *L. decemlineata* (Colorado potato beetle), *L.*

juncta (false potato beetle), or *L. texana* (Texan false potato beetle)); *Nilaparvata* spp. (e.g. *N. lugens* (brown planthopper)); *Laodelphax* spp. (e.g. *L. striatellus* (small brown planthopper)); *Nephotettix* spp. (e.g. *N. virescens* or *N. cincticeps* (green leafhopper), or *N. nigropictus* (rice leafhopper)); *Sogatella* spp. (e.g. *S. furcifera* (white-backed planthopper)); *Chilo* spp. (e.g. *C. suppressalis* (rice striped stem borer), *C. auricilius* (gold-fringed stem borer), or *C. polychrysus* (dark-headed stem borer)); *Sesamia* spp. (e.g. *S. inferens* (pink rice borer)); *Tryporyza* spp. (e.g. *T. innotata* (white rice borer), or *T. incertulas* (yellow rice borer)); *Anthonomus* spp. (e.g. *A. grandis* (boll weevil)); *Phaedon* spp. (e.g. *P. cochleariae* (mustard leaf beetle)); *Epilachna* spp. (e.g. *E. varivetis* (mexican bean beetle)); *Tribolium* spp. (e.g. *T. castaneum* (red floor beetle)); *Diabrotica* spp. (e.g. *D. virgifera virgifera* (western corn rootworm), *D. barberi* (northern corn rootworm), *D. undecimpunctata howardi* (southern corn rootworm), *D. virgifera zea* (Mexican corn rootworm)); *Ostrinia* spp. (e.g. *O. nubilalis* (European corn borer)); *Anaphothrips* spp. (e.g. *A. obscurus* (grass thrips)); *Pectinophora* spp. (e.g. *P. gossypiella* (pink bollworm)); *Heliothis* spp. (e.g. *H. virescens* (tobacco budworm)); *Trialeurodes* spp. (e.g. *T. abutiloneus* (banded-winged whitefly) *T. vaporariorum* (greenhouse whitefly)); *Bemisia* spp. (e.g. *B. argentifolii* (silverleaf whitefly)); *Aphis* spp. (e.g. *A. gossypii* (cotton aphid)); *Lygus* spp. (e.g. *L. lineolaris* (tarnished plant bug) or *L. hesperus* (western tarnished plant bug)); *Euschistus* spp. (e.g. *E. conspersus* (conspere stink bug)); *Chlorochroa* spp. (e.g. *C. sayi* (Say stinkbug)); *Nezara* spp. (e.g. *N. viridula* (southern green stinkbug)); *Thrips* spp. (e.g. *T. tabaci* (onion thrips)); *Frankliniella* spp. (e.g. *F. fusca* (tobacco thrips), or *F. occidentalis* (western flower thrips)); *Acheta* spp. (e.g. *A. domesticus* (house cricket)); *Myzus* spp. (e.g. *M. persicae* (green peach aphid)); *Macrosiphum* spp. (e.g. *M. euphorbiae* (potato aphid)); *Blissus* spp. (e.g. *B. leucopterus leucopterus* (chinch bug)); *Acrosternum* spp. (e.g. *A. hilare* (green stink bug)); *Chilotraea* spp. (e.g. *C. polychrysa* (rice stalk borer)); *Lissorhoptrus* spp. (e.g. *L. oryzophilus* (rice water weevil)); *Rhopalosiphum* spp. (e.g. *R. maidis* (corn leaf aphid)); and *Anuraphis* spp. (e.g. *A. maidiradicis* (corn root aphid)).

According to a more specific embodiment, the methods of the invention are applicable for Leptinotarsa species. Leptinotarsa belong to the family of Chrysomelidae or leaf beetles. Chrysomelid beetles such as Flea Beetles and Corn Rootworms and Curculionids such as Alfalfa Weevils are particularly important pests. Flea Beetles include a large number of small leaf feeding beetles that feed on the leaves of a number of grasses, cereals and herbs. Flea Beetles include a large number of genera (e.g., Attica, Apphthona, Argopistes, Disonycha, Epitrix, Longitarsus, Prodagricomela, Systema, and Phyllotreta). The Flea Beetle, Phyllotreta cruciferae, also known as the Rape Flea Beetle, is a particularly important pest. Corn rootworms include species found in the genus Diabrotica (e.g., D. undecimpunctata undecimpunctata, D. undecimpunctata howardii, D. longicornis, D. virgifera and D. balteata). Corn rootworms cause extensive damage to corn and cucurbits. The Western Spotted Cucumber Beetle, D. undecimpunctata undecimpunctata, is a pest of cucurbits in the western U.S. Alfalfa weevils (also known as clover weevils) belong to the genus, Hypera (H. postica, H. brunneipennis, H. nigrostris, H. punctata and H. meles), and are considered an important pest of legumes. The Egyptian alfalfa weevil, H. brunneipennis, is an important pest of alfalfa in the western U.S.

There are more than 30 *Leptinotarsa* species. The present invention thus encompasses methods for controlling *Leptinotarsa* species, more specific methods for killing insects, or preventing *Leptinotarsa* insects to develop or to grow, or preventing insects to infect or infest. Specific *Leptinotarsa* species to control according to the invention include Colorado Potato Beetle
 5 (*Leptinotarsa decemlineata* (Say) and False Potato Beetle (*Leptinotarsa juncta* (Say)).

CPB is a (serious) pest on our domestic potato (*Solanum tuberosum*), other cultivated and wild tuber bearing and non-tuber bearing potato species (e.g. *S. demissum*, *S. phureja* a.o.) and other Solanaceous (nightshades) plant species including:

(a) the crop species tomato (several *Lycopersicon* species), eggplant (*Solanum melongena*), peppers (several *Capsicum* species), tobacco (several *Nicotiana* species including
 10 ornamentals) and ground cherry (*Physalis* species);

(b) the weed/herb species, horse nettle (*S. carolinense*), common nightshade (*S. dulcamara*), belladonna (*Atropa* species), thorn apple (*datura* species), henbane (*Hyoscyamus* species) and buffalo burr (*S. rostratum*).

15 FPB is primarily found on horse nettle, but also occurs on common nightshade, ground cherry, and husk tomato (*Physalis* species).

The term "insect" encompasses insects of all types and at all stages of development, including egg, larval or nymphal, pupal and adult stages.

The present invention extends to methods as described herein, wherein the insect is
 20 *Leptinotarsa decemlineata* (Colorado potato beetle) and the plant is potato, eggplant, tomato, pepper, tobacco, ground cherry or rice, corn or cotton.

The present invention extends to methods as described herein, wherein the insect is *Phaedon cochleariae* (mustard leaf beetle) and the plant is mustard, chinese cabbage, turnip greens, collard greens or bok choy.

25 The present invention extends to methods as described herein, wherein the insect is *Epilachna varivetis* (Mexican bean beetle) and the plants are beans, field beans, garden beans, snap beans, lima beans, mung beans, string beans, black-eyed beans, velvet beans, soybeans, cowpeas, pigeon peas, clover or alfalfa.

The present invention extends to methods as described herein, wherein the insect is
 30 *Anthonomus grandis* (cotton boll weevil) and the plant is cotton.

The present invention extends to methods as described herein, wherein the insect is *Tribolium castaneum* (red flour beetle) and the plant is in the form of stored grain products such as flour, cereals, meal, crackers, beans, spices, pasta, cake mix, dried pet food, dried flowers, chocolate, nuts, seeds, and even dried museum specimens.

35 The present invention extends to methods as described herein, wherein the insect is *Myzus persicae* (green peach aphid) and the plant is a tree such as *Prunus*, particularly peach, apricot and plum; a vegetable crop of the families *Solanaceae*, *Chenopodiaceae*, *Compositae*, *Cruciferae*, and *Cucurbitaceae*, including but not limited to, artichoke, asparagus, bean, beets, broccoli, Brussels sprouts, cabbage, carrot, cauliflower, cantaloupe, celery, corn, cucumber, fennel,
 40 kale, kohlrabi, turnip, eggplant, lettuce, mustard, okra, parsley, parsnip, pea, pepper, potato, radish,

spinach, squash, tomato, turnip, watercress, and watermelon; a field crops such as, but not limited to, tobacco, sugar beet, and sunflower; a flower crop or other ornamental plant.

The present invention extends to methods as described herein, wherein the insect is *Nilaparvata lugens* and the plant is a rice plant.

5 The present invention extends to methods as described herein, wherein the insect is *Chilo suppressalis* (rice striped stem borer) and the plant is a rice plant, bareley, sorghum, maize, wheat or a grass.

10 The present invention extends to methods as described herein, wherein the insect is *Plutella xylostella* (Diamondback moth) and the plant is a *Brassica* species such as, but not limited to cabbage, chinese cabbage, Brussels sprouts, kale, rapeseed, broccoli, cauliflower, turnip, mustard or radish.

 The present invention extends to methods as described herein, wherein the insect is *Acheta domesticus* (house cricket) and the plant is any plant as described herein or any organic matter.

15 In terms of "susceptible organisms", which benefit from the present invention, any organism which is susceptible to pest infestation is included. Preferably plants may benefit from the present invention by protection from infestation by plant pest organisms.

20 In a preferred embodiment the susceptible organism is a plant and the pest is a plant pathogenic insect. In this embodiment the insect is contacted with the RNA molecule by expressing the dsRNA molecule in a plant, plant part, plant cell or plant seed that is infested with or susceptible to infestation with the plant pathogenic pest.

25 In this context the term "plant" encompasses any plant material that it is desired to treat to prevent or reduce insect growth and/or insect infestation. This includes, *inter alia*, whole plants, seedlings, propagation or reproductive material such as seeds, cuttings, grafts, explants, etc. and also plant cell and tissue cultures. The plant material should express, or have the capability to express, the RNA molecule comprising at least one nucleotide sequence that is the RNA complement of or that represents the RNA equivalent of at least part of the nucleotide sequence of the sense strand of at least one target gene of the pest organism, such that the RNA molecule is taken up by a pest upon plant-pest interaction, said RNA molecule being capable of inhibiting the target gene or down-regulating expression of the target gene by RNA interference.

30 The target gene may be any of the target genes herein described, for instance a target gene that is essential for the viability, growth, development or reproduction of the pest. The present invention relates to any gene of interest in the insect (which may be referred to herein as the "target gene") that can be down-regulated.

35 The terms "down-regulation of gene expression" and "inhibition of gene expression" are used interchangeably and refer to a measurable or observable reduction in gene expression or a complete abolition of detectable gene expression, at the level of protein product and/or mRNA product from the target gene. Preferably the down-regulation does not substantially directly inhibit the expression of other genes of the insect. The down-regulation effect of the dsRNA on gene expression may be calculated as being at least 30%, 40%, 50%, 60%, preferably 70%, 80% or

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even more preferably 90% or 95% when compared with normal gene expression. Depending on the nature of the target gene, down-regulation or inhibition of gene expression in cells of an insect can be confirmed by phenotypic analysis of the cell or the whole insect or by measurement of mRNA or protein expression using molecular techniques such as RNA solution hybridization, PCR, nuclease protection, Northern hybridization, reverse transcription, gene expression monitoring with a microarray, antibody binding, enzyme-linked immunosorbent assay (ELISA), Western blotting, radioimmunoassay (RIA), other immunoassays, or fluorescence-activated cell analysis (FACS).

The "target gene" may be essentially any gene that is desirable to be inhibited because it interferes with growth or pathogenicity or infectivity of the insect. For instance, if the method of the invention is to be used to prevent insect growth and/or infestation then it is preferred to select a target gene which is essential for viability, growth, development or reproduction of the insect, or any gene that is involved with pathogenicity or infectivity of the insect, such that specific inhibition of the target gene leads to a lethal phenotype or decreases or stops insect infestation.

According to one non-limiting embodiment, the target gene is such that when its expression is down-regulated or inhibited using the method of the invention, the insect is killed, or the reproduction or growth of the insect is stopped or retarded. This type of target genes is considered to be essential for the viability of the insect and is referred to as essential genes. Therefore, the present invention encompasses a method as described herein, wherein the target gene is an essential gene.

According to a further non-limiting embodiment, the target gene is such that when it is down-regulated using the method of the invention, the infestation or infection by the insect, the damage caused by the insect, and/or the ability of the insect to infest or infect host organisms and/or cause such damage, is reduced. The terms "infest" and "infect" or "infestation" and "infection" are generally used interchangeably throughout. This type of target genes is considered to be involved in the pathogenicity or infectivity of the insect. Therefore, the present invention extends to methods as described herein, wherein the target gene is involved in the pathogenicity or infectivity of the insect. The advantage of choosing the latter type of target gene is that the insect is blocked to infect further plants or plant parts and is inhibited to form further generations.

According to one embodiment, target genes are conserved genes or insect-specific genes.

In addition, any suitable double-stranded RNA fragment capable of directing RNAi or RNA-mediated gene silencing or inhibition of an insect target gene may be used in the methods of the invention.

In another embodiment, a gene is selected that is essentially involved in the growth, development, and reproduction of a pest, (such as an insect). Exemplary genes include but are not limited to the structural subunits of ribosomal proteins and a beta-coatamer gene, such as the CHD3 gene. Ribosomal proteins such as S4 (RpS4) and S9(RpS9) are structural constituents of the ribosome involved in protein biosynthesis and which are components of the cytosolic small ribosomal subunit, the ribosomal proteins such as L9 and L19 are structural constituent of ribosome involved in protein biosynthesis which is localised to the ribosome. The beta coatamer gene in *C. elegans* encodes a protein which is a subunit of a multimeric complex that forms a membrane

vesicle coat. Similar sequences have been found in diverse organisms such as *Arabidopsis thaliana*, *Drosophila melanogaster*, and *Saccharomyces cerevisiae*. Related sequences are found in diverse organisms such as *Leptinotarsa decemlineata*, *Phaedon cochleariae*, *Epilachna varivestis*, *Anthonomus grandis*, *Tribolium castaneum*, *Myzus persicae*, *Nilaparvata lugens*, *Chilo suppressalis*, *Plutella xylostella* and *Acheta domesticus*.

Other target genes for use in the present invention may include, for example, those that play important roles in viability, growth, development, reproduction, and infectivity. These target genes include, for example, house keeping genes, transcription factors, and pest specific genes or lethal knockout mutations in *Caenorhabditis* or *Drosophila*. The target genes for use in the present invention may also be those that are from other organisms, e.g., from insects or arachnidae (e.g. *Leptinotarsa* spp., *Phaedon* spp., *Epilachna* spp., *Anthonomus* spp., *Tribolium* spp., *Myzus* spp., *Nilaparvata* spp., *Chilo* spp., *Plutella* spp., or *Acheta* spp.).

Preferred target genes include those specified in Table 1A and orthologous genes from other target organisms, such as from other pest organisms.

In the methods of the present invention, dsRNA is used to inhibit growth or to interfere with the pathogenicity or infectivity of the insect.

The invention thus relates to isolated double-stranded RNA comprising annealed complementary strands, one of which has a nucleotide sequence which is complementary to at least part of a target nucleotide sequence of a target gene of an insect. The target gene may be any of the target genes described herein, or a part thereof that exerts the same function.

According to one embodiment of the present invention, an isolated double-stranded RNA is provided comprising annealed complementary strands, one of which has a nucleotide sequence which is complementary to at least part of a nucleotide sequence of an insect target gene, wherein said target gene comprises a sequence which is selected from the group comprising:

(i) sequences which are at least 75% identical to a sequence represented by any of SEQ ID NOs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 49 to 158, 159, 160-163, 168, 173, 178, 183, 188, 193, 198, 203, 208, 215, 220, 225, 230, 247, 249, 251, 253, 255, 257, 259, 275 to 472, 473, 478, 483, 488, 493, 498, 503, 513, 515, 517, 519, 521, 533 to 575, 576, 581, 586, 591, 596, 601, 603, 605, 607, 609, 621 to 767, 768, 773, 778, 783, 788, 793, 795, 797, 799, 801, 813 to 862, 863, 868, 873, 878, 883, 888, 890, 892, 894, 896, 908 to 1040, 1041, 1046, 1051, 1056, 1061, 1071, 1073, 1075, 1077, 1079, 1081, 1083, 1085, 1087, 1089, 1091, 1093, 1095, 1097, 1099, 1101, 1103, 1105, 1107, 1109, 1111, 1113, 1161 to 1571, 1572, 1577, 1582, 1587, 1592, 1597, 1602, 1607, 1612, 1617, 1622, 1627, 1632, 1637, 1642, 1647, 1652, 1657, 1662, 1667, 1672, 1677, 1682, 1684, 1686, 1688, 1690, 1692, 1694, 1696, 1698, 1700, 1702, 1704, 1730 to 2039, 2040, 2045, 2050, 2055, 2060, 2065, 2070, 2075, 2080, 2085, 2090, 2095, 2100, 2102, 2104, 2106, 2108, 2120 to 2338, 2339, 2344, 2349, 2354, 2359, 2364, 2366, 2368, 2370, 2372, 2384 to 2460, 2461, 2466, 2471, 2476 or 2481, or the complement thereof, and

(ii) sequences comprising at least 17 contiguous nucleotides of any of SEQ ID NOs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 49 to 158, 159, 160-163, 168, 173, 178, 183, 188, 193, 198, 203,

208, 215, 220, 225, 230, 247, 249, 251, 253, 255, 257, 259, 275 to 472, 473, 478, 483, 488, 493, 498, 503, 513, 515, 517, 519, 521, 533 to 575, 576, 581, 586, 591, 596, 601, 603, 605, 607, 609, 621 to 767, 768, 773, 778, 783, 788, 793, 795, 797, 799, 801, 813 to 862, 863, 868, 873, 878, 883, 888, 890, 892, 894, 896, 908 to 1040, 1041, 1046, 1051, 1056, 1061, 1071, 1073, 1075, 1077, 1079, 1081, 1083, 1085, 1087, 1089, 1091, 1093, 1095, 1097, 1099, 1101, 1103, 1105, 1107, 1109, 1111, 1113, 1161 to 1571, 1572, 1577, 1582, 1587, 1592, 1597, 1602, 1607, 1612, 1617, 1622, 1627, 1632, 1637, 1642, 1647, 1652, 1657, 1662, 1667, 1672, 1677, 1682, 1684, 1686, 1688, 1690, 1692, 1694, 1696, 1698, 1700, 1702, 1704, 1730 to 2039, 2040, 2045, 2050, 2055, 2060, 2065, 2070, 2075, 2080, 2085, 2090, 2095, 2100, 2102, 2104, 2106, 2108, 2120 to 2338, 2339, 2344, 2349, 2354, 2359, 2364, 2366, 2368, 2370, 2372, 2384 to 2460, 2461, 2466, 2471, 2476 or 2481, or the complement thereof;

or wherein said insect target gene is an insect orthologue of a gene comprising at least 17 contiguous nucleotides of any of SEQ ID NOs 49 to 158, 275 to 472, 533 to 575, 621 to 767, 813 to 862, 908 to 1040, 1161 to 1571, 1730 to 2039, 2120 to 2338, 2384 to 2460, or the complement thereof.

Depending on the assay used to measure gene silencing, the growth inhibition can be quantified as being greater than about 5%, 10%, more preferably about 20%, 25%, 33%, 50%, 60%, 75%, 80%, most preferably about 90%, 95%, or about 99% as compared to a pest organism that has been treated with control dsRNA.

According to another embodiment of the present invention, an isolated double-stranded RNA is provided, wherein at least one of said annealed complementary strands comprises the RNA equivalent of at least one of the nucleotide sequences represented by any of SEQ ID NOs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 49 to 158, 159, 160-163, 168, 173, 178, 183, 188, 193, 198, 203, 208, 215, 220, 225, 230, 247, 249, 251, 253, 255, 257, 259, 275 to 472, 473, 478, 483, 488, 493, 498, 503, 513, 515, 517, 519, 521, 533 to 575, 576, 581, 586, 591, 596, 601, 603, 605, 607, 609, 621 to 767, 768, 773, 778, 783, 788, 793, 795, 797, 799, 801, 813 to 862, 863, 868, 873, 878, 883, 888, 890, 892, 894, 896, 908 to 1040, 1041, 1046, 1051, 1056, 1061, 1071, 1073, 1075, 1077, 1079, 1081, 1083, 1085, 1087, 1089, 1091, 1093, 1095, 1097, 1099, 1101, 1103, 1105, 1107, 1109, 1111, 1113, 1161 to 1571, 1572, 1577, 1582, 1587, 1592, 1597, 1602, 1607, 1612, 1617, 1622, 1627, 1632, 1637, 1642, 1647, 1652, 1657, 1662, 1667, 1672, 1677, 1682, 1684, 1686, 1688, 1690, 1692, 1694, 1696, 1698, 1700, 1702, 1704, 1730 to 2039, 2040, 2045, 2050, 2055, 2060, 2065, 2070, 2075, 2080, 2085, 2090, 2095, 2100, 2102, 2104, 2106, 2108, 2120 to 2338, 2339, 2344, 2349, 2354, 2359, 2364, 2366, 2368, 2370, 2372, 2384 to 2460, 2461, 2466, 2471, 2476 or 2481, or wherein at least one of said annealed complementary strands comprises the RNA equivalent of a fragment of at least 17 basepairs in length thereof, preferably at least 18, 19, 20 or 21, more preferably at least 22, 23 or 24 basepairs in length thereof.

If the method of the invention is used for specifically controlling growth or infestation of a specific insect in or on a host cell or host organism, it is preferred that the double-stranded RNA does not share any significant homology with any host gene, or at least not with any essential gene of the host. In this context, it is preferred that the double-stranded RNA shows less than 30%, more

preferably less than 20%, more preferably less than 10%, and even more preferably less than 5% nucleic acid sequence identity with any gene of the host cell. % sequence identity should be calculated across the full length of the double-stranded RNA region. If genomic sequence data is available for the host organism one may cross-check sequence identity with the double-stranded RNA using standard bioinformatics tools. In one embodiment, there is no sequence identity between the dsRNA and a host sequences over 21 contiguous nucleotides, meaning that in this context, it is preferred that 21 contiguous base pairs of the dsRNA do not occur in the genome of the host organism. In another embodiment, there is less than about 10% or less than about 12.5 % sequence identity over 24 contiguous nucleotides of the dsRNA with any nucleotide sequence from a host species.

The double-stranded RNA comprises annealed complementary strands, one of which has a nucleotide sequence which corresponds to a target nucleotide sequence of the target gene to be down-regulated. The other strand of the double-stranded RNA is able to base-pair with the first strand.

The expression "target region" or "target nucleotide sequence" of the target insect gene may be any suitable region or nucleotide sequence of the gene. The target region should comprise at least 17, at least 18 or at least 19 consecutive nucleotides of the target gene, more preferably at least 20 or at least 21 nucleotide and still more preferably at least 22, 23 or 24 nucleotides of the target gene.

It is preferred that (at least part of) the double-stranded RNA will share 100% sequence identity with the target region of the insect target gene. However, it will be appreciated that 100% sequence identity over the whole length of the double stranded region is not essential for functional RNA inhibition. RNA sequences with insertions, deletions, and single point mutations relative to the target sequence have also been found to be effective for RNA inhibition. The terms "corresponding to" or "complementary to" are used herein interchangeable, and when these terms are used to refer to sequence correspondence between the double-stranded RNA and the target region of the target gene, they are to be interpreted accordingly, i.e. as not absolutely requiring 100% sequence identity. However, the % sequence identity between the double-stranded RNA and the target region will generally be at least 80% or 85% identical, preferably at least 90%, 95%, 96%, or more preferably at least 97%, 98% and still more preferably at least 99%. Two nucleic acid strands are "substantially complementary" when at least 85% of their bases pair.

The term "complementary" as used herein relates to both DNA-DNA complementarity as to DNA-RNA complementarity. In analogy herewith, the term "RNA equivalent" substantially means that in the DNA sequence(s), the base "T" may be replaced by the corresponding base "U" normally present in ribonucleic acids.

Although the dsRNA contains a sequence which corresponds to the target region of the target gene it is not absolutely essential for the whole of the dsRNA to correspond to the sequence of the target region. For example, the dsRNA may contain short non-target regions flanking the target-specific sequence, provided that such sequences do not affect performance of the dsRNA in RNA inhibition to a material extent.

The dsRNA may contain one or more substitute bases in order to optimise performance in RNAi. It will be apparent to the skilled reader how to vary each of the bases of the dsRNA in turn and test the activity of the resulting dsRNAs (e.g. in a suitable *in vitro* test system) in order to optimise the performance of a given dsRNA.

5 The dsRNA may further contain DNA bases, non-natural bases or non-natural backbone linkages or modifications of the sugar-phosphate backbone, for example to enhance stability during storage or enhance resistance to degradation by nucleases.

10 It has been previously reported that the formation of short interfering RNAs (siRNAs) of about 21 bp is desirable for effective gene silencing. However, in applications of applicant it has been shown that the minimum length of dsRNA preferably is at least about 80-100 bp in order to be efficiently taken up by certain pest organisms. There are indications that in invertebrates such as the free living nematode *C. elegans* or the plant parasitic nematode *Meloidogyne incognita*, these longer fragments are more effective in gene silencing, possibly due to a more efficient uptake of these long dsRNA by the invertebrate.

15 It has also recently been suggested that synthetic RNA duplexes consisting of either 27-mer blunt or short hairpin (sh) RNAs with 29 bp stems and 2-nt 3' overhangs are more potent inducers of RNA interference than conventional 21-mer siRNAs. Thus, molecules based upon the targets identified above and being either 27-mer blunt or short hairpin (sh) RNA's with 29-bp stems and 2-nt 3'overhangs are also included within the scope of the invention.

20 Therefore, in one embodiment, the double-stranded RNA fragment (or region) will itself preferably be at least 17 bp in length, preferably 18 or 19bp in length, more preferably at least 20bp, more preferably at least 21 bp, or at least 22 bp, or at least 23 bp, or at least 24 bp, 25 bp, 26 bp or at least 27 bp in length. The expressions "double-stranded RNA fragment" or "double-stranded RNA region" refer to a small entity of the double-stranded RNA corresponding with (part
25 of) the target gene.

30 Generally, the double stranded RNA is preferably between about 17-1500 bp, even more preferably between about 80 - 1000 bp and most preferably between about 17-27 bp or between about 80-250 bp; such as double stranded RNA regions of about 17 bp, 18 bp, 19 bp, 20 bp, 21 bp, 22 bp, 23 bp, 24 bp, 25 bp, 27 bp, 50 bp, 80 bp, 100 bp, 150 bp, 200 bp, 250 bp, 300 bp, 350 bp, 400 bp, 450 bp, 500 bp, 550 bp, 600 bp, 650 bp, 700 bp, 900 bp, 100 bp, 1100 bp, 1200 bp, 1300 bp, 1400 bp or 1500 bp.

35 The upper limit on the length of the double-stranded RNA may be dependent on i) the requirement for the dsRNA to be taken up by the insect and ii) the requirement for the dsRNA to be processed within the cell into fragments that direct RNAi. The chosen length may also be influenced by the method of synthesis of the RNA and the mode of delivery of the RNA to the cell. Preferably the double-stranded RNA to be used in the methods of the invention will be less than 10,000 bp in length, more preferably 1000 bp or less, more preferably 500 bp or less, more preferably 300 bp or less, more preferably 100 bp or less. For any given target gene and insect, the optimum length of the dsRNA for effective inhibition may be determined by experiment.

The double-stranded RNA may be fully or partially double-stranded. Partially double-stranded RNAs may include short single-stranded overhangs at one or both ends of the double-stranded portion, provided that the RNA is still capable of being taken up by insects and directing RNAi. The double-stranded RNA may also contain internal non-complementary regions.

5 The methods of the invention encompass the simultaneous or sequential provision of two or more different double-stranded RNAs or RNA constructs to the same insect, so as to achieve down-regulation or inhibition of multiple target genes or to achieve a more potent inhibition of a single target gene.

10 Alternatively, multiple targets are hit by the provision of one double-stranded RNA that hits multiple target sequences, and a single target is more efficiently inhibited by the presence of more than one copy of the double stranded RNA fragment corresponding to the target gene. Thus, in one embodiment of the invention, the double-stranded RNA construct comprises multiple dsRNA regions, at least one strand of each dsRNA region comprising a nucleotide sequence that is complementary to at least part of a target nucleotide sequence of an insect target gene. According to the invention, the dsRNA regions in the RNA construct may be complementary to the same or to different target genes and/or the dsRNA regions may be complementary to targets from the same or from different insect species.

20 The terms "hit", "hits" and "hitting" are alternative wordings to indicate that at least one of the strands of the dsRNA is complementary to, and as such may bind to, the target gene or nucleotide sequence.

In one embodiment, the double stranded RNA region comprises multiple copies of the nucleotide sequence that is complementary to the target gene. Alternatively, the dsRNA hits more than one target sequence of the same target gene. The invention thus encompasses isolated double stranded RNA constructs comprising at least two copies of said nucleotide sequence complementary to at least part of a nucleotide sequence of an insect target.

25 The term "multiple" in the context of the present invention means at least two, at least three, at least four, at least five, at least six, etc.

The expressions "a further target gene" or "at least one other target gene" mean for instance a second, a third or a fourth, etc. target gene.

30 DsRNA that hits more than one of the above-mentioned targets, or a combination of different dsRNA against different of the above mentioned targets are developed and used in the methods of the present invention.

Accordingly the invention relates to an isolated double stranded RNA construct comprising at least two copies of the RNA equivalent of at least one of the nucleotide sequences represented by any of SEQ ID NOs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 49 to 158, 159, 160-163, 168, 173, 178, 183, 188, 193, 198, 203, 208, 215, 220, 225, 230, 247, 249, 251, 253, 255, 257, 259, 275 to 472, 473, 478, 483, 488, 493, 498, 503, 513, 515, 517, 519, 521, 533 to 575, 576, 581, 586, 591, 596, 601, 603, 605, 607, 609, 621 to 767, 768, 773, 778, 783, 788, 793, 795, 797, 799, 801, 813 to 862, 863, 868, 873, 878, 883, 888, 890, 892, 894, 896, 908 to 1040, 1041, 1046, 1051, 1056, 1061, 40 1071, 1073, 1075, 1077, 1079, 1081, 1083, 1085, 1087, 1089, 1091, 1093, 1095, 1097, 1099,

1101, 1103, 1105, 1107, 1109, 1111, 1113, 1161 to 1571, 1572, 1577, 1582, 1587, 1592, 1597, 1602, 1607, 1612, 1617, 1622, 1627, 1632, 1637, 1642, 1647, 1652, 1657, 1662, 1667, 1672, 1677, 1682, 1684, 1686, 1688, 1690, 1692, 1694, 1696, 1698, 1700, 1702, 1704, 1730 to 2039, 2040, 2045, 2050, 2055, 2060, 2065, 2070, 2075, 2080, 2085, 2090, 2095, 2100, 2102, 2104, 2106, 2108, 2120 to 2338, 2339, 2344, 2349, 2354, 2359, 2364, 2366, 2368, 2370, 2372, 2384 to 2460, 2461, 2466, 2471, 2476 or 2481, or at least two copies of the RNA equivalent of a fragment of at least 17 basepairs in length thereof, preferably at least 18, 19, 20 or 21, more preferably at least 22, 23 or 24 basepairs in length thereof. Preferably, said double-stranded RNA comprises the RNA equivalent of the nucleotide sequence as represented in SEQ ID NO 159 or 160, or a fragment of at least 17, preferably at least 18, 19, 20 or 21, more preferably at least 22, 23 or 24 basepairs in length thereof. In a further embodiment, the invention relates to an an isolated double stranded RNA construct comprising at least two copies of the RNA equivalent of the nucleotide sequence as represented by SEQ ID NO 159 or 160.

Accordingly, the present invention extends to methods as described herein, wherein the dsRNA comprises annealed complementary strands, one of which has a nucleotide sequence which is complementary to at least part of a target nucleotide sequence of an insect target gene, and which comprises the RNA equivalents of at least two nucleotide sequences independently chosen from each other. In one embodiment, the dsRNA comprises the RNA equivalents of at least two, preferably at least three, four or five, nucleotide sequences indepently chosen from the sequences represented by any of SEQ ID NOs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 49 to 158, 159, 160-163, 168, 173, 178, 183, 188, 193, 198, 203, 208, 215, 220, 225, 230, 247, 249, 251, 253, 255, 257, 259, 275 to 472, 473, 478, 483, 488, 493, 498, 503, 513, 515, 517, 519, 521, 533 to 575, 576, 581, 586, 591, 596, 601, 603, 605, 607, 609, 621 to 767, 768, 773, 778, 783, 788, 793, 795, 797, 799, 801, 813 to 862, 863, 868, 873, 878, 883, 888, 890, 892, 894, 896, 908 to 1040, 1041, 1046, 1051, 1056, 1061, 1071, 1073, 1075, 1077, 1079, 1081, 1083, 1085, 1087, 1089, 1091, 1093, 1095, 1097, 1099, 1101, 1103, 1105, 1107, 1109, 1111, 1113, 1161 to 1571, 1572, 1577, 1582, 1587, 1592, 1597, 1602, 1607, 1612, 1617, 1622, 1627, 1632, 1637, 1642, 1647, 1652, 1657, 1662, 1667, 1672, 1677, 1682, 1684, 1686, 1688, 1690, 1692, 1694, 1696, 1698, 1700, 1702, 1704, 1730 to 2039, 2040, 2045, 2050, 2055, 2060, 2065, 2070, 2075, 2080, 2085, 2090, 2095, 2100, 2102, 2104, 2106, 2108, 2120 to 2338, 2339, 2344, 2349, 2354, 2359, 2364, 2366, 2368, 2370, 2372, 2384 to 2460, 2461, 2466, 2471, 2476 or 2481, or fragments thereof of at least 17 basepairs in length, preferably at least 18, 19, 20 or 21, more preferably at least 22, 23 or 24 basepairs in length thereof.

The at least two nucleotide sequences may be derived from the target genes herein described. According to one preferred embodiment the dsRNA hits at least one target gene that is essential for viability, growth, development or reproduction of the insect and hits at least one gene involved in pathogenicity or infectivity as described hereinabove. Alternatively, the dsRNA hits multiple genes of the same category, for example, the dsRNA hits at least 2 essential genes or at least 2 genes involved in the same cellular function. According to a further embodiment, the dsRNA hits at least 2 target genes, which target genes are involved in a different cellular function. For

example the dsRNA hits two or more genes involved in protein synthesis (e.g. ribosome subunits), intracellular protein transport, nuclear mRNA splicing, or involved in one of the functions described in Table 1A.

- Preferably, the present invention extends to methods as described herein, wherein said
- 5 insect target gene comprises a sequence which is which is selected from the group comprising:
- (i) sequences which are at least 75% identical to a sequence represented by any of SEQ ID NOs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 49 to 158, 159, 160-163, 168, 173, 178, 183, 188, 193, 198, 203, 208, 215, 220, 225, 230, 247, 249, 251, 253, 255, 257, 259, 275 to 472, 473, 478, 483, 488, 493, 498, 503, 513, 515, 517, 519, 521, 533 to 575, 576, 581, 586, 591, 596,
- 10 601, 603, 605, 607, 609, 621 to 767, 768, 773, 778, 783, 788, 793, 795, 797, 799, 801, 813 to 862, 863, 868, 873, 878, 883, 888, 890, 892, 894, 896, 908 to 1040, 1041, 1046, 1051, 1056, 1061, 1071, 1073, 1075, 1077, 1079, 1081, 1083, 1085, 1087, 1089, 1091, 1093, 1095, 1097, 1099, 1101, 1103, 1105, 1107, 1109, 1111, 1113, 1161 to 1571, 1572, 1577, 1582, 1587, 1592, 1597, 1602, 1607, 1612, 1617, 1622, 1627, 1632, 1637, 1642, 1647, 1652, 1657, 1662,
- 15 1667, 1672, 1677, 1682, 1684, 1686, 1688, 1690, 1692, 1694, 1696, 1698, 1700, 1702, 1704, 1730 to 2039, 2040, 2045, 2050, 2055, 2060, 2065, 2070, 2075, 2080, 2085, 2090, 2095, 2100, 2102, 2104, 2106, 2108, 2120 to 2338, 2339, 2344, 2349, 2354, 2359, 2364, 2366, 2368, 2370, 2372, 2384 to 2460, 2461, 2466, 2471, 2476 or 2481, or the complement thereof, and
- 20 (ii) sequences comprising at least 17 contiguous nucleotides of any of SEQ ID NOs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 49 to 158, 159, 160-163, 168, 173, 178, 183, 188, 193, 198, 203, 208, 215, 220, 225, 230, 247, 249, 251, 253, 255, 257, 259, 275 to 472, 473, 478, 483, 488, 493, 498, 503, 513, 515, 517, 519, 521, 533 to 575, 576, 581, 586, 591, 596, 601, 603, 605, 607, 609, 621 to 767, 768, 773, 778, 783, 788, 793, 795, 797, 799, 801, 813 to 862, 863, 868,
- 25 873, 878, 883, 888, 890, 892, 894, 896, 908 to 1040, 1041, 1046, 1051, 1056, 1061, 1071, 1073, 1075, 1077, 1079, 1081, 1083, 1085, 1087, 1089, 1091, 1093, 1095, 1097, 1099, 1101, 1103, 1105, 1107, 1109, 1111, 1113, 1161 to 1571, 1572, 1577, 1582, 1587, 1592, 1597, 1602, 1607, 1612, 1617, 1622, 1627, 1632, 1637, 1642, 1647, 1652, 1657, 1662, 1667, 1672, 1677, 1682, 1684, 1686, 1688, 1690, 1692, 1694, 1696, 1698, 1700, 1702, 1704, 1730 to
- 30 2039, 2040, 2045, 2050, 2055, 2060, 2065, 2070, 2075, 2080, 2085, 2090, 2095, 2100, 2102, 2104, 2106, 2108, 2120 to 2338, 2339, 2344, 2349, 2354, 2359, 2364, 2366, 2368, 2370, 2372, 2384 to 2460, 2461, 2466, 2471, 2476 or 2481, or the complement thereof,
- or wherein said insect target gene is an insect orthologue of a gene comprising at least 17 contiguous nucleotides of any of SEQ ID NOs 49 to 158, 275 to 472, 533 to 575, 621 to 767, 813 to
- 35 862, 908 to 1040, 1161 to 1571, 1730 to 2039, 2120 to 2338, 2384 to 2460, or the complement thereof.

The dsRNA regions (or fragments) in the double stranded RNA may be combined as follows:

- a) when multiple dsRNA regions targeting a single target gene are combined, they may be combined in the original order (ie the order in which the regions appear in the target gene) in the RNA construct,
- 5 b) alternatively, the original order of the fragments may be ignored so that they are scrambled and combined randomly or deliberately in any order into the double stranded RNA construct,
- c) alternatively, one single fragment may be repeated several times, for example from 1 to 10 times, e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10 times, in the ds RNA construct, or
- 10 d) the dsRNA regions (targeting a single or different target genes) may be combined in the sense or antisense orientation.

In addition, the target gene(s) to be combined may be chosen from one or more of the following categories of genes:

- e) "essential" genes or "pathogenicity genes" as described above encompass genes that are vital for one or more target insects and result in a lethal or severe (e.g. feeding, reproduction, growth) phenotype when silenced. The choice of a strong lethal target gene results in a potent RNAi effect. In the RNA constructs of the invention, multiple dsRNA regions targeting the same or different (very effective) lethal genes can be combined to further increase the potency, efficacy or speed of the RNAi effect in insect control.
- 15 f) "weak" genes encompass target genes with a particularly interesting function in one of the cellular pathways described herein, but which result in a weak phenotypic effect when silenced independently. In the RNA constructs of the invention, multiple dsRNA regions targeting a single or different weak gene(s) may be combined to obtain a stronger RNAi effect.
- 20 g) "insect specific" genes encompass genes that have no substantial homologous counterpart in non-insect organisms as can be determined by bioinformatics homology searches, for example by BLAST searches. The choice of an insect specific target gene results in a species specific RNAi effect, with no effect or no substantial (adverse) effect in non-target organisms.
- 25 h) "conserved genes" encompass genes that are conserved (at the amino acid level) between the target organism and non-target organism(s). To reduce possible effects on non-target species, such effective but conserved genes are analysed and target sequences from the variable regions of these conserved genes are chosen to be targeted by the dsRNA regions in the RNA construct. Here, conservation is assessed at the level of the nucleic acid sequence. Such variable regions thus encompass the least conserved sections, at the level of the nucleic acid sequence, of the conserved target gene(s).
- 30 i) "conserved pathway" genes encompass genes that are involved in the same biological pathway or cellular process, or encompass genes that have the same functionality in different insect species resulting in a specific and potent RNAi effect and more efficient insect control;
- 35

j) alternatively, the RNA constructs according to the present invention target multiple genes from different biological pathways, resulting in a broad cellular RNAi effect and more efficient insect control.

According to the invention, all double stranded RNA regions comprise at least one strand that is complementary to at least part or a portion of the nucleotide sequence of any of the target genes herein described. However, provided one of the double stranded RNA regions comprises at least one strand that is complementary to a portion of the nucleotide sequence of any one of the target genes herein described, the other double stranded RNA regions may comprise at least one strand that is complementary to a portion of any other insect target gene (including known target genes).

According to yet another embodiment of the present invention there is provided an isolated double stranded RNA or RNA construct as herein described, further comprising at least one additional sequence and optionally a linker. In one embodiment, the additional sequence is chosen from the group comprising (i) a sequence facilitating large-scale production of the dsRNA construct; (ii) a sequence effecting an increase or decrease in the stability of the dsRNA; (iii) a sequence allowing the binding of proteins or other molecules to facilitate uptake of the RNA construct by insects; (iv) a sequence which is an aptamer that binds to a receptor or to a molecule on the surface or in the cytoplasm of an insect to facilitate uptake, endocytosis and/or transcytosis by the insect; or (v) additional sequences to catalyze processing of dsRNA regions. In one embodiment, the linker is a conditionally self-cleaving RNA sequence, preferably a pH sensitive linker or a hydrophobic sensitive linker. In one embodiment, the linker is an intron.

In one embodiment, the multiple dsRNA regions of the double-stranded RNA construct are connected by one or more linkers. In another embodiment, the linker is present at a site in the RNA construct, separating the dsRNA regions from another region of interest. Different linker types for the dsRNA constructs are provided by the present invention.

In another embodiment, the multiple dsRNA regions of the double-stranded RNA construct are connected without linkers.

In a particular embodiment of the invention, the linkers may be used to disconnect smaller dsRNA regions in the pest organism. Advantageously, in this situation the linker sequence may promote division of a long dsRNA into smaller dsRNA regions under particular circumstances, resulting in the release of separate dsRNA regions under these circumstances and leading to more efficient gene silencing by these smaller dsRNA regions. Examples of suitable conditionally self-cleaving linkers are RNA sequences that are self-cleaving at high pH conditions. Suitable examples of such RNA sequences are described by Borda et al. (Nucleic Acids Res. 2003 May 15;31(10):2595-600), which document is incorporated herein by reference. This sequence originates from the catalytic core of the hammerhead ribozyme HH16.

In another aspect of the invention, a linker is located at a site in the RNA construct, separating the dsRNA regions from another, e.g. the additional, sequence of interest, which preferably provides some additional function to the RNA construct.

In one particular embodiment of the invention, the dsRNA constructs of the present invention are provided with an aptamer to facilitate uptake of the dsRNA by the insect. The aptamer is designed to bind a substance which is taken up by the insect. Such substances may be from an insect or plant origin. One specific example of an aptamer, is an aptamer that binds to a transmembrane protein, for example a transmembrane protein of an insect. Alternatively, the aptamer may bind a (plant) metabolite or nutrient which is taken up by the insect.

Alternatively, the linkers are self-cleaving in the endosomes. This may be advantageous when the constructs of the present invention are taken up by the insect via endocytosis or transcytosis, and are therefore compartmentalized in the endosomes of the insect species. The endosomes may have a low pH environment, leading to cleavage of the linker.

The above mentioned linkers that are self-cleaving in hydrophobic conditions are particularly useful in dsRNA constructs of the present invention when used to be transferred from one cell to another via the transit in a cell wall, for example when crossing the cell wall of an insect pest organism.

An intron may also be used as a linker. An "intron" as used herein may be any non-coding RNA sequence of a messenger RNA. Particular suitable intron sequences for the constructs of the present invention are (1) U-rich (35-45%); (2) have an average length of 100 bp (varying between about 50 and about 500 bp) which base pairs may be randomly chosen or may be based on known intron sequences; (3) start at the 5' end with -AG:GT- or -CG:GT- and/or (4) have at their 3' end -AG:GC- or -AG:AA.

A non-complementary RNA sequence, ranging from about 1 base pair to about 10,000 base pairs, may also be used as a linker.

Without wishing to be bound by any particular theory or mechanism, it is thought that long double-stranded RNAs are taken up by the insect from their immediate environment. Double-stranded RNAs taken up into the gut and transferred to the gut epithelial cells are then processed within the cell into short double-stranded RNAs, called small interfering RNAs (siRNAs), by the action of an endogenous endonuclease. The resulting siRNAs then mediate RNAi via formation of a multi-component RNase complex termed the RISC or RNA interfering silencing complex.

In order to achieve down-regulation of a target gene within an insect cell the double-stranded RNA added to the exterior of the cell wall may be any dsRNA or dsRNA construct that can be taken up into the cell and then processed within the cell into siRNAs, which then mediate RNAi, or the RNA added to the exterior of the cell could itself be an siRNA that can be taken up into the cell and thereby direct RNAi.

siRNAs are generally short double-stranded RNAs having a length in the range of from 19 to 25 base pairs, or from 20 to 24 base pairs. In preferred embodiments siRNAs having 19, 20, 21, 22, 23, 24 or 25 base pairs, and in particular 21 or 22 base pairs, corresponding to the target gene to be down-regulated may be used. However, the invention is not intended to be limited to the use of such siRNAs.

siRNAs may include single-stranded overhangs at one or both ends, flanking the double-stranded portion. In a particularly preferred embodiment the siRNA may contain 3' overhanging

nucleotides, preferably two 3' overhanging thymidines (dTdT) or uridines (UU). 3' TT or UU overhangs may be included in the siRNA if the sequence of the target gene immediately upstream of the sequence included in double-stranded part of the dsRNA is AA. This allows the TT or UU overhang in the siRNA to hybridise to the target gene. Although a 3' TT or UU overhang may also be included at the other end of the siRNA it is not essential for the target sequence downstream of the sequence included in double-stranded part of the siRNA to have AA. In this context, siRNAs which are RNA/DNA chimeras are also contemplated. These chimeras include, for example, the siRNAs comprising a double-stranded RNA with 3' overhangs of DNA bases (e.g. dTdT), as discussed above, and also double-stranded RNAs which are polynucleotides in which one or more of the RNA bases or ribonucleotides, or even all of the ribonucleotides on an entire strand, are replaced with DNA bases or deoxynucleotides.

The dsRNA may be formed from two separate (sense and antisense) RNA strands that are annealed together by (non-covalent) basepairing. Alternatively, the dsRNA may have a foldback stem-loop or hairpin structure, wherein the two annealed strands of the dsRNA are covalently linked. In this embodiment the sense and antisense strands of the dsRNA are formed from different regions of single polynucleotide molecule that is partially self-complementary. RNAs having this structure are convenient if the dsRNA is to be synthesised by expression *in vivo*, for example in a host cell or organism as discussed below, or by *in vitro* transcription. The precise nature and sequence of the "loop" linking the two RNA strands is generally not material to the invention, except that it should not impair the ability of the double-stranded part of the molecule to mediate RNAi. The features of "hairpin" or "stem-loop" RNAs for use in RNAi are generally known in the art (see for example WO 99/53050, in the name of CSIRO, the contents of which are incorporated herein by reference). In other embodiments of the invention, the loop structure may comprise linker sequences or additional sequences as described above.

Another aspect of the present invention are target nucleotide sequences of the insect target genes herein disclosed. Such target nucleotide sequences are particularly important to design the dsRNA constructs according to the present invention. Such target nucleotide sequences are preferably at least 17, preferably at least 18, 19, 20 or 21, more preferably at least 22, 23 or 24 nucleotides in length. Non-limiting examples of preferred target nucleotide sequences are given in the examples.

According to one embodiment, the present invention provides an isolated nucleotide sequence encoding a double stranded RNA or double stranded RNA construct as described herein.

According to a more specific embodiment, the present invention relates to an isolated nucleic acid sequence consisting of a sequence represented by any of SEQ ID NOs 49 to 158, 275 to 472, 533 to 575, 621 to 767, 813 to 862, 908 to 1040, 1161 to 1571, 1730 to 2039, 2120 to 2338, 2384 to 2460, or a fragment of at least 17 preferably at least 18, 19, 20 or 21, more preferably at least 22, 23 or 24 nucleotides thereof.

A person skilled in the art will recognize that homologues of these target genes can be found and that these homologues are also useful in the methods of the present invention.

Protein, or nucleotide sequences are likely to be homologous if they show a "significant" level of sequence similarity or more preferably sequence identity. Truly homologous sequences are related by divergence from a common ancestor gene. Sequence homologues can be of two types: (i) where homologues exist in different species they are known as orthologues. e.g. the α -globin genes in mouse and human are orthologues. (ii) paralogues are homologous genes in within a single species. e.g. the α - and β - globin genes in mouse are paralogues

Preferred homologues are genes comprising a sequence which is at least about 85% or 87.5%, still more preferably about 90%, still more preferably at least about 95% and most preferably at least about 99% identical to a sequence selected from the group of sequences represented by SEQ ID NOs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 49 to 158, 159, 160-163, 168, 173, 178, 183, 188, 193, 198, 203, 208, 215, 220, 225, 230, 247, 249, 251, 253, 255, 257, 259, 275 to 472, 473, 478, 483, 488, 493, 498, 503, 513, 515, 517, 519, 521, 533 to 575, 576, 581, 586, 591, 596, 601, 603, 605, 607, 609, 621 to 767, 768, 773, 778, 783, 788, 793, 795, 797, 799, 801, 813 to 862, 863, 868, 873, 878, 883, 888, 890, 892, 894, 896, 908 to 1040, 1041, 1046, 1051, 1056, 1061, 1071, 1073, 1075, 1077, 1079, 1081, 1083, 1085, 1087, 1089, 1091, 1093, 1095, 1097, 1099, 1101, 1103, 1105, 1107, 1109, 1111, 1113, 1161 to 1571, 1572, 1577, 1582, 1587, 1592, 1597, 1602, 1607, 1612, 1617, 1622, 1627, 1632, 1637, 1642, 1647, 1652, 1657, 1662, 1667, 1672, 1677, 1682, 1684, 1686, 1688, 1690, 1692, 1694, 1696, 1698, 1700, 1702, 1704, 1730 to 2039, 2040, 2045, 2050, 2055, 2060, 2065, 2070, 2075, 2080, 2085, 2090, 2095, 2100, 2102, 2104, 2106, 2108, 2120 to 2338, 2339, 2344, 2349, 2354, 2359, 2364, 2366, 2368, 2370, 2372, 2384 to 2460, 2461, 2466, 2471, 2476 or 2481, or the complement thereof. Methods for determining sequence identity are routine in the art and include use of the Blast software and *EMBOSS software* (*The European Molecular Biology Open Software Suite* (2000), Rice, P. Longden, I. and Bleasby, A. Trends in Genetics 16, (6) pp276—277). The term "identity" as used herein refers to the relationship between sequences at the nucleotide level. The expression "% identical" is determined by comparing optimally aligned sequences, e.g. two or more, over a comparison window wherein the portion of the sequence in the comparison window may comprise insertions or deletions as compared to the reference sequence for optimal alignment of the sequences. The reference sequence does not comprise insertions or deletions. The reference window is chosen from between at least 10 contiguous nucleotides to about 50, about 100 or to about 150 nucleotides, preferably between about 50 and 150 nucleotides. "% identity" is then calculated by determining the number of nucleotides that are identical between the sequences in the window, dividing the number of identical nucleotides by the number of nucleotides in the window and multiplying by 100.

Other homologues are genes which are alleles of a gene comprising a sequence as represented by any of SEQ ID NOs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 49 to 158, 159, 160-163, 168, 173, 178, 183, 188, 193, 198, 203, 208, 215, 220, 225, 230, 247, 249, 251, 253, 255, 257, 259, 275 to 472, 473, 478, 483, 488, 493, 498, 503, 513, 515, 517, 519, 521, 533 to 575, 576, 581, 586, 591, 596, 601, 603, 605, 607, 609, 621 to 767, 768, 773, 778, 783, 788, 793, 795, 797, 799, 801, 813 to 862, 863, 868, 873, 878, 883, 888, 890, 892, 894, 896, 908 to 1040, 1041, 1046,

1051, 1056, 1061, 1071, 1073, 1075, 1077, 1079, 1081, 1083, 1085, 1087, 1089, 1091, 1093, 1095, 1097, 1099, 1101, 1103, 1105, 1107, 1109, 1111, 1113, 1161 to 1571, 1572, 1577, 1582, 1587, 1592, 1597, 1602, 1607, 1612, 1617, 1622, 1627, 1632, 1637, 1642, 1647, 1652, 1657, 1662, 1667, 1672, 1677, 1682, 1684, 1686, 1688, 1690, 1692, 1694, 1696, 1698, 1700, 1702, 5 1704, 1730 to 2039, 2040, 2045, 2050, 2055, 2060, 2065, 2070, 2075, 2080, 2085, 2090, 2095, 2100, 2102, 2104, 2106, 2108, 2120 to 2338, 2339, 2344, 2349, 2354, 2359, 2364, 2366, 2368, 2370, 2372, 2384 to 2460, 2461, 2466, 2471, 2476 or 2481. Further preferred homologues are genes comprising at least one single nucleotide polymorphism (SNIP) compared to a gene comprising a sequence as represented by any of SEQ ID NO 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 10 23, 49 to 158, 159, 160-163, 168, 173, 178, 183, 188, 193, 198, 203, 208, 215, 220, 225, 230, 247, 249, 251, 253, 255, 257, 259, 275 to 472, 473, 478, 483, 488, 493, 498, 503, 513, 515, 517, 519, 521, 533 to 575, 576, 581, 586, 591, 596, 601, 603, 605, 607, 609, 621 to 767, 768, 773, 778, 783, 788, 793, 795, 797, 799, 801, 813 to 862, 863, 868, 873, 878, 883, 888, 890, 892, 894, 896, 908 to 1040, 1041, 1046, 1051, 1056, 1061, 1071, 1073, 1075, 1077, 1079, 1081, 1083, 1085, 1087, 15 1089, 1091, 1093, 1095, 1097, 1099, 1101, 1103, 1105, 1107, 1109, 1111, 1113, 1161 to 1571, 1572, 1577, 1582, 1587, 1592, 1597, 1602, 1607, 1612, 1617, 1622, 1627, 1632, 1637, 1642, 1647, 1652, 1657, 1662, 1667, 1672, 1677, 1682, 1684, 1686, 1688, 1690, 1692, 1694, 1696, 1698, 1700, 1702, 1704, 1730 to 2039, 2040, 2045, 2050, 2055, 2060, 2065, 2070, 2075, 2080, 2085, 2090, 2095, 2100, 2102, 2104, 2106, 2108, 2120 to 2338, 2339, 2344, 2349, 2354, 2359, 20 2364, 2366, 2368, 2370, 2372, 2384 to 2460, 2461, 2466, 2471, 2476 or 2481.

According to another embodiment, the invention encompasses target genes which are insect orthologues of a gene comprising a nucleotide sequence as represented in any of SEQ ID NOs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 49 to 158, 159, 160-163, 168, 173, 178, 183, 188, 193, 198, 203, 208, 215, 220, 225, 230, 247, 249, 251, 253, 255, 257, 259, 275 to 472, 473, 478, 483, 25 488, 493, 498, 503, 513, 515, 517, 519, 521, 533 to 575, 576, 581, 586, 591, 596, 601, 603, 605, 607, 609, 621 to 767, 768, 773, 778, 783, 788, 793, 795, 797, 799, 801, 813 to 862, 863, 868, 873, 878, 883, 888, 890, 892, 894, 896, 908 to 1040, 1041, 1046, 1051, 1056, 1061, 1071, 1073, 1075, 1077, 1079, 1081, 1083, 1085, 1087, 1089, 1091, 1093, 1095, 1097, 1099, 1101, 1103, 1105, 1107, 1109, 1111, 1113, 1161 to 1571, 1572, 1577, 1582, 1587, 1592, 1597, 1602, 1607, 1612, 30 1617, 1622, 1627, 1632, 1637, 1642, 1647, 1652, 1657, 1662, 1667, 1672, 1677, 1682, 1684, 1686, 1688, 1690, 1692, 1694, 1696, 1698, 1700, 1702, 1704, 1730 to 2039, 2040, 2045, 2050, 2055, 2060, 2065, 2070, 2075, 2080, 2085, 2090, 2095, 2100, 2102, 2104, 2106, 2108, 2120 to 2338, 2339, 2344, 2349, 2354, 2359, 2364, 2366, 2368, 2370, 2372, 2384 to 2460, 2461, 2466, 2471, 2476 or 2481. By way of example, orthologues may comprise a nucleotide sequence as represented in any of SEQ ID NOs 49 to 123, 275 to 434, 533 to 562, 621 to 738, 813 to 852, 908 35 to 1010, 1161 to 1437, 1730 to 1987, 2120 to 2290, and 2384 to 2438, or a fragment thereof of at least 17, 18, 19, 20, 21, 22, 23, 24, 25, 26 or 27 nucleotides. A non-limiting list of insect or arachnida orthologues genes or sequences comprising at least a fragment of 17 bp of one of the sequences of the invention, is given in Tables 4.

According to another embodiment, the invention encompasses target genes which are nematode orthologues of a gene comprising a nucleotide sequence as represented in any of 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 49 to 158, 159, 160-163, 168, 173, 178, 183, 188, 193, 198, 203, 208, 215, 220, 225, 230, 247, 249, 251, 253, 255, 257, 259, 275 to 472, 473, 478, 483, 488, 493, 498, 503, 513, 515, 517, 519, 521, 533 to 575, 576, 581, 586, 591, 596, 601, 603, 605, 607, 609, 621 to 767, 768, 773, 778, 783, 788, 793, 795, 797, 799, 801, 813 to 862, 863, 868, 873, 878, 883, 888, 890, 892, 894, 896, 908 to 1040, 1041, 1046, 1051, 1056, 1061, 1071, 1073, 1075, 1077, 1079, 1081, 1083, 1085, 1087, 1089, 1091, 1093, 1095, 1097, 1099, 1101, 1103, 1105, 1107, 1109, 1111, 1113, 1161 to 1571, 1572, 1577, 1582, 1587, 1592, 1597, 1602, 1607, 1612, 1617, 1622, 1627, 1632, 1637, 1642, 1647, 1652, 1657, 1662, 1667, 1672, 1677, 1682, 1684, 1686, 1688, 1690, 1692, 1694, 1696, 1698, 1700, 1702, 1704, 1730 to 2039, 2040, 2045, 2050, 2055, 2060, 2065, 2070, 2075, 2080, 2085, 2090, 2095, 2100, 2102, 2104, 2106, 2108, 2120 to 2338, 2339, 2344, 2349, 2354, 2359, 2364, 2366, 2368, 2370, 2372, 2384 to 2460, 2461, 2466, 2471, 2476 or 248. By way of example, nematode orthologues may comprise a nucleotide sequence as represented in any of SEQ ID NOs 124 to 135, 435 to 446, 563 to 564, 739 to 751, 853, 854, 1011 to 1025, 1438 to 1473, 1988 to 2001, 2291 to 2298, 2439 or 2440, or a fragment of at least 17, 18, 19, 20 or 21 nucleotides thereof. According to another aspect, the invention thus encompasses any of the methods described herein for controlling nematode growth in an organism, or for preventing nematode infestation of an organism susceptible to nematode infection, comprising contacting nematode cells with a double-stranded RNA, wherein the double-stranded RNA comprises annealed complementary strands, one of which has a nucleotide sequence which is complementary to at least part of the nucleotide sequence of a target gene comprising a fragment of at least 17, 18, 19, 20 or 21 nucleotides of any of the sequences as represented in SEQ ID NOs 124 to 135, 435 to 446, 563 to 564, 739 to 751, 853, 854, 1011 to 1025, 1438 to 1473, 1988 to 2001, 2291 to 2298, 2439 or 2440, whereby the double-stranded RNA is taken up by the nematode and thereby controls growth or prevents infestation. The invention also relates to nematode-resistant transgenic plants comprising a fragment of at least 17, 18, 19, 20 or 21 nucleotides of any of the sequences as represented in SEQ ID NOs 124 to 135, 435 to 446, 563 to 564, 739 to 751, 853, 854, 1011 to 1025, 1438 to 1473, 1988 to 2001, 2291 to 2298, 2439 or 2440. A non-limiting list of nematode orthologues genes or sequences comprising at least a fragment of 17 bp of one of the sequences of the invention, is given in Tables 5.

According to another embodiment, the invention encompasses target genes which are fungal orthologues of a gene comprising a nucleotide sequence as represented in any of 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 49 to 158, 159, 160-163, 168, 173, 178, 183, 188, 193, 198, 203, 208, 215, 220, 225, 230, 247, 249, 251, 253, 255, 257, 259, 275 to 472, 473, 478, 483, 488, 493, 498, 503, 513, 515, 517, 519, 521, 533 to 575, 576, 581, 586, 591, 596, 601, 603, 605, 607, 609, 621 to 767, 768, 773, 778, 783, 788, 793, 795, 797, 799, 801, 813 to 862, 863, 868, 873, 878, 883, 888, 890, 892, 894, 896, 908 to 1040, 1041, 1046, 1051, 1056, 1061, 1071, 1073, 1075, 1077, 1079, 1081, 1083, 1085, 1087, 1089, 1091, 1093, 1095, 1097, 1099, 1101, 1103, 1105, 1107, 1109, 1111, 1113, 1161 to 1571, 1572, 1577, 1582, 1587, 1592, 1597, 1602, 1607, 1612, 1617, 1622,

1627, 1632, 1637, 1642, 1647, 1652, 1657, 1662, 1667, 1672, 1677, 1682, 1684, 1686, 1688, 1690, 1692, 1694, 1696, 1698, 1700, 1702, 1704, 1730 to 2039, 2040, 2045, 2050, 2055, 2060, 2065, 2070, 2075, 2080, 2085, 2090, 2095, 2100, 2102, 2104, 2106, 2108, 2120 to 2338, 2339, 2344, 2349, 2354, 2359, 2364, 2366, 2368, 2370, 2372, 2384 to 2460, 2461, 2466, 2471, 2476 or
5 2481. By way of example, fungal orthologues may comprise a nucleotide sequence as represented in any of SEQ ID NOs 136 to 158, 447 to 472, 565 to 575, 752 to 767, 855 to 862, 1026 to 1040, 1475 to 1571, 2002 to 2039, 2299 to 2338, 2441 to 2460, or a fragment of at least 17, 18, 19, 20, 21, 22, 23, 24, 25, 26 or 27 nucleotides thereof. According to another aspect, the invention thus encompasses any of the methods described herein for controlling fungal growth on a cell or an
10 organism, or for preventing fungal infestation of a cell or an organism susceptible to fungal infection, comprising contacting fungal cells with a double-stranded RNA, wherein the double-stranded RNA comprises annealed complementary strands, one of which has a nucleotide sequence which is complementary to at least part of the nucleotide sequence of a target gene comprising a fragment of at least 17, 18, 19, 20 or 21 nucleotides of any of the sequences as
15 represented in SEQ ID NOs 136 to 158, 447 to 472, 565 to 575, 752 to 767, 855 to 862, 1026 to 1040, 1475 to 1571, 2002 to 2039, 2299 to 2338, 2441 to 2460, whereby the double-stranded RNA is taken up by the fungus and thereby controls growth or prevents infestation. The invention also relates to fungal-resistant transgenic plants comprising a fragment of at least 17, 18, 19, 20 or 21 of any of the sequences as represented in SEQ ID NOs 136 to 158, 447 to 472, 565 to 575, 752 to
20 767, 855 to 862, 1026 to 1040, 1475 to 1571, 2002 to 2039, 2299 to 2338, 2441 to 2460. A non-limiting list of fungal orthologues genes or sequences comprising at least a fragment of 17 bp of one of the sequences of the invention, is given in Tables 6.

In one preferred embodiment of the invention the dsRNA may be expressed by (e.g. transcribed within) a host cell or host organism, the host cell or organism being an organism
25 susceptible or vulnerable to infestation by an insect. In this embodiment RNAi-mediated gene silencing of one or more target genes in the insect may be used as a mechanism to control growth of the insect in or on the host organism and/or to prevent or reduce insect infestation of the host organism. Thus, expression of the double-stranded RNA within cells of the host organism may confer resistance to a particular insect or to a class of insects. In case the dsRNA hits more than
30 one insect target gene, expression of the double-stranded RNA within cells of the host organism may confer resistance to more than one insect or more than one class of insects.

In a preferred embodiment the host organism is a plant and the insect is a plant pathogenic insect. In this embodiment the insect is contacted with the double-stranded RNA by expressing the double-stranded RNA in a plant or plant cell that is infested with or susceptible to infestation with
35 the plant pathogenic insect.

In this context the term "plant" encompasses any plant material that it is desired to treat to prevent or reduce insect growth and/or insect infestation. This includes, *inter alia*, whole plants, seedlings, propagation or reproductive material such as seeds, cuttings, grafts, explants, etc. and also plant cell and tissue cultures. The plant material should express, or have the capability to
40 express, dsRNA corresponding to one or more target genes of the insect.

Therefore, in a further aspect the invention provides a plant, preferably a transgenic plant, or propagation or reproductive material for a (transgenic) plant, or a plant cell culture expressing or capable of expressing at least one double-stranded RNA, wherein the double-stranded RNA comprises annealed complementary strands, one of which has a nucleotide sequence which is complementary to at least part of a target nucleotide sequence of a target gene of an insect, such that the double-stranded RNA is taken up by an insect upon plant-insect interaction, said double stranded RNA being capable of inhibiting the target gene or down-regulating expression of the target gene by RNA interference. The target gene may be any of the target genes herein described, for instance a target gene that is essential for the viability, growth, development or reproduction of the insect.

In this embodiment the insect can be any insect, but is preferably plant pathogenic insect. Preferred plant pathogenic insects include, but are not limited to, those listed above.

A plant to be used in the methods of the invention, or a transgenic plant according to the invention encompasses any plant, but is preferably a plant that is susceptible to infestation by a plant pathogenic insect.

Accordingly, the present invention extends to methods as described herein wherein the plant is chosen from the following group of plants (or crops): alfalfa, apple, apricot, artichoke, asparagus, avocado, banana, barley, beans, beet, blackberry, blueberry, broccoli, brussel sprouts, cabbage, canola, carrot, cassava, cauliflower, a cereal, celery, cherry, citrus, clemintine, coffee, corn, cotton, cucumber, eggplant, endive, eucalyptus, figes, grape, grapefruit, groundnuts, ground cherry, kiwifruit, lettuce, leek, lemon, lime, pine, maize, mango, melon, millet, mushroom, nut aot, okra, onion, orange, an ornamental plant or flower or tree, papaya,, parsley, pea, peach, peanut, peat, pepper, persimmon, pineapple, plantain, plum, pomegranate, potato, pumpkin, radicchio, radish, rapeseed, raspberry, rice, rye, sorghum, soy, soybean, spinach, strawberry, sugarbeet, sugarcane, sunflower, sweet poatao, tangerine, tea, tobacco, tomato, a vine, waetermelon, wheat, yams and zucchini.

In one embodiment the present invention extends to methods as described herein, wherein the plant is potato and the target gene is a gene from an insect selected from the group consisting of *Leptinotarsa* spp. (e.g. *L. decemlineata* (Colorado potato beetle), *L. juncta* (false potato beetle), or *L. texana* (Texan false potato beetle)); *Lema* spp. (e.g. *L. trilineata* (three-lined potato beetle)); *Epitrix* spp. (e.g. *E. cucumeris* (potato flea beetle) or *E. tuberis* (tuber flea beetle)); *Epicauta* spp. (e.g. *E. vittata* (striped blister beetle)); *Phaedon* spp. (e.g. *P. cochleariae* (mustard leaf beetle)); *Empoasca* spp. (e.g. *E. fabae* (potato leafhopper)); *Myzus* spp. (e.g. *M. persicae* (green peach aphid)); *Paratrioza* spp. (e.g. *P. cockerelli* (potato psyllid)); *Ostrinia* spp. (e.g. *O. nubilalis* (European corn borer)); *Conoderus* spp. (e.g. *C. falli* (southern potato wireworm), or *C. vespertinus* (tobacco wireworm)); and *Phthorimaea* spp. (e.g. *P. operculella* (potato tuberworm)); in another embodiment the present invention extends to methods as described herein, wherein the plant is tomato and the target gene is a gene from an insect selected from the group consisting of: *Macrosiphum* spp. (e.g. *M. euphorbiae* (potato aphid)); *Myzus* spp. (e.g. *M. persicae* (green peach aphid)); *Trialeurodes* spp. (e.g. *T. vaporariorum* (greenhouse whitefly), or *T. abutilonia* (banded-

winged whitefly)); *Bemisia* spp. (e.g. *B. argentifolii* (silverleaf whitefly)); *Frankliniella* spp. (e.g. *F. occidentalis* (western flower thrips)); *Leptinotarsa* spp. (e.g. *L. decemlineata* (Colorado potato beetle), *L. juncta* (false potato beetle), or *L. texana* (Texan false potato beetle)); *Epitrix* spp. (e.g. *E. hirtipennis* (flea beetle)); *Lygus* spp. (e.g. *L. lineolaris* (tarnished plant bug), or *L. hesperus* (western tarnished plant bug)); *Euschistus* spp. (e.g. *E. conspersus* (conspersed stinkbug)); *Nezara* spp. (e.g. *N. viridula* (southern green stinkbug)); *Thyanta* spp. (e.g. *T. pallidovirens* (redshouldered stinkbug)); *Phthorimaea* spp. (e.g. *P. operculella* (potato tuberworm)); *Helicoverpa* spp. (e.g. *H. zea* (tomato fruitworm); *Keiferia* spp. (e.g. *K. lycopersicella* (tomato pinworm)); *Spodoptera* spp. (e.g. *S. exigua* (beet armyworm), or *S. praefica* (western yellowstriped armyworm)); *Limonius* spp. (wireworms); *Agrotis* spp. (e.g. *A. ipsilon* (black cutworm)); *Manduca* spp. (e.g. *M. sexta* (tobacco hornworm), or *M. quinquemaculata* (tomato hornworm)); *Liriomyza* spp. (e.g. *L. sativae*, *L. trifolii* or *L. huidobrensis* (leafminer)); and *Paratrioza* spp. (e.g. *P. cockerelli* (tomato psyllid)); In another embodiment the present invention extends to methods as described herein, wherein the plant is corn and the target gene is a gene from an insect selected from the group consisting of: *Diabrotica* spp. (e.g. *D. virgifera virgifera* (western corn rootworm), *D. barberi* (northern corn rootworm), *D. undecimpunctata howardi* (southern corn rootworm), *D. virgifera zea* (Mexican corn rootworm); *D. balteata* (banded cucumber beetle)); *Ostrinia* spp. (e.g. *O. nubilalis* (European corn borer)); *Agrotis* spp. (e.g. *A. ipsilon* (black cutworm)); *Helicoverpa* spp. (e.g. *H. zea* (corn earworm)); *Spodoptera* spp. (e.g. *S. frugiperda* (fall armyworm)); *Diatraea* spp. (e.g. *D. grandiosella* (southwestern corn borer), or *D. saccharalis* (sugarcane borer)); *Elasmopalpus* spp. (e.g. *E. lignosellus* (lesser cornstalk borer)); *Melanotus* spp. (wireworms); *Cyclocephala* spp. (e.g. *C. borealis* (northern masked chafer)); *Cyclocephala* spp. (e.g. *C. immaculata* (southern masked chafer)); *Popillia* spp. (e.g. *P. japonica* (Japanese beetle)); *Chaetocnema* spp. (e.g. *C. pulicaria* (corn flea beetle)); *Sphenophorus* spp. (e.g. *S. maidis* (maize billbug)); *Rhopalosiphum* spp. (e.g. *R. maidis* (corn leaf aphid)); *Anuraphis* spp. (e.g. *A. maidiradicis* (corn root aphid)); *Blissus* spp. (e.g. *B. leucopterus leucopterus* (chinch bug)); *Melanoplus* spp. (e.g. *M. femurrubrum* (redlegged grasshopper), *M. sanguinipes* (migratory grasshopper)); *Hylemya* spp. (e.g. *H. platura* (seedcorn maggot)); *Agromyza* spp. (e.g. *A. parvicornis* (corn blot leafminer)); *Anaphothrips* spp. (e.g. *A. obscurus* (grass thrips)); *Solenopsis* spp. (e.g. *S. milesta* (thief ant)); and *Tetranychus* spp. (e.g. *T. urticae* (twospotted spider mite)); in another embodiment the present invention extends to methods as described herein, wherein the plant is cotton and the target gene is a gene from an insect selected from the group consisting of: *Helicoverpa* spp. (e.g. *H. zea* (cotton bollworm)); *Pectinophora* spp. (e.g. *P. gossypiella* (pink bollworm)); *Helicoverpa* spp. (e.g. *H. armigera* (American bollworm)); *Earias* spp. (e.g. *E. vittella* (spotted bollworm)); *Heliothis* spp. (e.g. *H. virescens* (tobacco budworm)); *Spodoptera* spp. (e.g. *S. exigua* (beet armyworm)); *Anthonomus* spp. (e.g. *A. grandis* (boll weevil)); *Pseudatomoscelis* spp. (e.g. *P. seriatus* (cotton fleahopper)); *Trialeurodes* spp. (e.g. *T. abutiloneus* (banded-winged whitefly) *T. vaporariorum* (greenhouse whitefly)); *Bemisia* spp. (e.g. *B. argentifolii* (silverleaf whitefly)); *Aphis* spp. (e.g. *A. gossypii* (cotton aphid)); *Lygus* spp. (e.g. *L. lineolaris* (tarnished plant bug) or *L. hesperus* (western tarnished plant bug)); *Euschistus* spp. (e.g. *E. conspersus* (conspersed stink bug)); *Chlorochroa* spp. (e.g. *C. sayi* (Say stinkbug)); *Nezara* spp.

(e.g. *N. viridula* (green stinkbug)); *Thrips* spp. (e.g. *T. tabaci* (onion thrips)); *Frankliniella* spp. (e.g. *F. fusca* (tobacco thrips), or *F. occidentalis* (western flower thrips)); *Melanoplus* spp. (e.g. *M. femurrubrum* (redlegged grasshopper), or *M. differentialis* (differential grasshopper)); and *Tetranychus* spp. (e.g. *T. cinnabarinus* (carmine spider mite), or *T. urticae* (twospotted spider mite)); in another embodiment the present invention extends to methods as described herein, wherein the plant is rice and the target gene is a gene from an insect selected from the group consisting of: *Nilaparvata* spp. (e.g. *N. lugens* (brown planthopper)); *Laodelphax* spp. (e.g. *L. striatellus* (small brown planthopper)); *Nephotettix* spp. (e.g. *N. virescens* or *N. cincticeps* (green leafhopper), or *N. nigropictus* (rice leafhopper)); *Sogatella* spp. (e.g. *S. furcifera* (white-backed planthopper)); *Blissus* spp. (e.g. *B. leucopterus leucopterus* (chinch bug)); *Scotinophora* spp. (e.g. *S. vermidulate* (rice blackbug)); *Acrosternum* spp. (e.g. *A. hilare* (green stink bug)); *Pamara* spp. (e.g. *P. guttata* (rice skipper)); *Chilo* spp. (e.g. *C. suppressalis* (rice striped stem borer), *C. auricilius* (gold-fringed stem borer), or *C. polychrysus* (dark-headed stem borer)); *Chilotraea* spp. (e.g. *C. polychrysa* (rice stalk borer)); *Sesamia* spp. (e.g. *S. inferens* (pink rice borer)); *Tryporyza* spp. (e.g. *T. innotata* (white rice borer)); *Tryporyza* spp. (e.g. *T. incertulas* (yellow rice borer)); *Cnaphalocrocis* spp. (e.g. *C. medinalis* (rice leafroller)); *Agromyza* spp. (e.g. *A. oryzae* (leafminer)); *Diatraea* spp. (e.g. *D. saccharalis* (sugarcane borer)); *Namaga* spp. (e.g. *N. aenescens* (green rice caterpillar)); *Xanthodes* spp. (e.g. *X. transversa* (green caterpillar)); *Spodoptera* spp. (e.g. *S. frugiperda* (fall armyworm)); *Mythimna* spp. (e.g. *Mythimna (Pseudaletia) seperata* (armyworm)); *Helicoverpa* spp. (e.g. *H. zea* (corn earworm)); *Colaspis* spp. (e.g. *C. brunnea* (grape colaspis)); *Lissorhoptrus* spp. (e.g. *L. oryzophilus* (rice water weevil)); *Echinocnemus* spp. (e.g. *E. squamos* (rice plant weevil)); *Diclodispa* spp. (e.g. *D. armigera* (rice hispa)); *Oulema* spp. (e.g. *O. oryzae* (leaf beetle)); *Sitophilus* spp. (e.g. *S. oryzae* (rice weevil)); *Pachytiplosis* spp. (e.g. *P. oryzae* (rice gall midge)); *Hydrellia* spp. (e.g. *H. griseola* (small rice leafminer)); *Chlorops* spp. (e.g. *C. oryzae* (stem maggot)); and *Hydrellia* spp. (e.g. *H. sasakii* (rice stem maggot));

Transgenic plants according to the invention extend to all plant species specifically described above being resistant to the respective insect species as specifically described above. Preferred transgenic plants (or reproductive or propagation material for a transgenic plant, or a cultured transgenic plant cell) are plants (or reproductive or propagation material for a transgenic plant, or a cultured transgenic plant cell) wherein said plant comprises a nucleic acid sequence which is selected from the group comprising:

- (i) sequences which are at least 75% identical to a sequence represented by any of SEQ ID NOs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 49 to 158, 159, 160-163, 168, 173, 178, 183, 188, 193, 198, 203, 208, 215, 220, 225, 230, 247, 249, 251, 253, 255, 257, 259, 275 to 472, 473, 478, 483, 488, 493, 498, 503, 513, 515, 517, 519, 521, 533 to 575, 576, 581, 586, 591, 596, 601, 603, 605, 607, 609, 621 to 767, 768, 773, 778, 783, 788, 793, 795, 797, 799, 801, 813 to 862, 863, 868, 873, 878, 883, 888, 890, 892, 894, 896, 908 to 1040, 1041, 1046, 1051, 1056, 1061, 1071, 1073, 1075, 1077, 1079, 1081, 1083, 1085, 1087, 1089, 1091, 1093, 1095, 1097, 1099, 1101, 1103, 1105, 1107, 1109, 1111, 1113, 1161 to 1571, 1572, 1577, 1582, 1587, 1592, 1597, 1602, 1607, 1612, 1617, 1622, 1627, 1632, 1637, 1642, 1647, 1652, 1657, 1662,

1667, 1672, 1677, 1682, 1684, 1686, 1688, 1690, 1692, 1694, 1696, 1698, 1700, 1702, 1704, 1730 to 2039, 2040, 2045, 2050, 2055, 2060, 2065, 2070, 2075, 2080, 2085, 2090, 2095, 2100, 2102, 2104, 2106, 2108, 2120 to 2338, 2339, 2344, 2349, 2354, 2359, 2364, 2366, 2368, 2370, 2372, 2384 to 2460, 2461, 2466, 2471, 2476 or 2481, or the complement thereof, and

(ii) sequences comprising at least 17 contiguous nucleotides of any of SEQ ID NOs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 49 to 158, 159, 160-163, 168, 173, 178, 183, 188, 193, 198, 203, 208, 215, 220, 225, 230, 247, 249, 251, 253, 255, 257, 259, 275 to 472, 473, 478, 483, 488, 493, 498, 503, 513, 515, 517, 519, 521, 533 to 575, 576, 581, 586, 591, 596, 601, 603, 605, 607, 609, 621 to 767, 768, 773, 778, 783, 788, 793, 795, 797, 799, 801, 813 to 862, 863, 868, 873, 878, 883, 888, 890, 892, 894, 896, 908 to 1040, 1041, 1046, 1051, 1056, 1061, 1071, 1073, 1075, 1077, 1079, 1081, 1083, 1085, 1087, 1089, 1091, 1093, 1095, 1097, 1099, 1101, 1103, 1105, 1107, 1109, 1111, 1113, 1161 to 1571, 1572, 1577, 1582, 1587, 1592, 1597, 1602, 1607, 1612, 1617, 1622, 1627, 1632, 1637, 1642, 1647, 1652, 1657, 1662, 1667, 1672, 1677, 1682, 1684, 1686, 1688, 1690, 1692, 1694, 1696, 1698, 1700, 1702, 1704, 1730 to 2039, 2040, 2045, 2050, 2055, 2060, 2065, 2070, 2075, 2080, 2085, 2090, 2095, 2100, 2102, 2104, 2106, 2108, 2120 to 2338, 2339, 2344, 2349, 2354, 2359, 2364, 2366, 2368, 2370, 2372, 2384 to 2460, 2461, 2466, 2471, 2476 or 2481, or the complement thereof,

or wherein said nucleic acid is an insect orthologue of a gene comprising at least 17 contiguous nucleotides of any of SEQ ID NOs 49 to 158, 275 to 472, 533 to 575, 621 to 767, 813 to 862, 908 to 1040, 1161 to 1571, 1730 to 2039, 2120 to 2338, 2384 to 2460, or the complement thereof.

The present invention also encompasses plants (or reproductive or propagation material for a transgenic plant, or a cultured transgenic plant cell) which express or are capable of expressing at least one of the nucleotides of the invention, for instance at least one of the nucleotide sequences represented in any of SEQ ID NOs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 49 to 158, 159, 160-163, 168, 173, 178, 183, 188, 193, 198, 203, 208, 215, 220, 225, 230, 240 to 247, 249, 251, 253, 255, 257, 259, 275 to 472, 473, 478, 483, 488, 493, 498, 503, 508 to 513, 515, 517, 519, 521, 533 to 575, 576, 581, 586, 591, 596, 601, 603, 605, 607, 609, 621 to 767, 768, 773, 778, 783, 788, 793, 795, 797, 799, 801, 813 to 862, 863, 868, 873, 878, 883, 888, 890, 892, 894, 896, 908 to 1040, 1041, 1046, 1051, 1056, 1061, 1066 to 1071, 1073, 1075, 1077, 1079, 1081, 1083, 1085, 1087, 1089, 1091, 1093, 1095, 1097, 1099, 1101, 1103, 1105, 1107, 1109, 1111, 1113, 1161 to 1571, 1572, 1577, 1582, 1587, 1592, 1597, 1602, 1607, 1612, 1617, 1622, 1627, 1632, 1637, 1642, 1647, 1652, 1657, 1662, 1667, 1672, 1677, 1682, 1684, 1686, 1688, 1690, 1692, 1694, 1696, 1698, 1700, 1702, 1704, 1730 to 2039, 2040, 2045, 2050, 2055, 2060, 2065, 2070, 2075, 2080, 2085, 2090, 2095, 2100, 2102, 2104, 2106, 2108, 2120 to 2338, 2339, 2344, 2349, 2354, 2359, 2364, 2366, 2368, 2370, 2372, 2384 to 2460, 2461, 2466, 2471, 2476, 2481 or 2486, or the complement thereof, or comprising a fragment thereof comprising at least 17, preferably at least 18, 19, 20 or 21, more preferably at least 22, 23 or 24 nucleotides.

The plant may be provided in a form wherein it is actively expressing (transcribing) the double-stranded RNA in one or more cells, cell types or tissues. Alternatively, the plant may be "capable of expressing", meaning that it is transformed with a transgene which encodes the desired dsRNA but that the transgene is not active in the plant when (and in the form in which) the plant is supplied.

Therefore, according to another embodiment, a recombinant DNA construct is provided comprising the nucleotide sequence encoding the dsRNA or dsRNA construct according to the present invention operably linked to at least one regulatory sequence. Preferably, the regulatory sequence is selected from the group comprising constitutive promoters or tissue specific promoters as described below.

The target gene may be any target gene herein described. Preferably the regulatory element is a regulatory element that is active in a plant cell. More preferably, the regulatory element is originating from a plant. The term "regulatory sequence" is to be taken in a broad context and refers to a regulatory nucleic acid capable of effecting expression of the sequences to which it is operably linked.

Encompassed by the aforementioned term are promoters and nucleic acids or synthetic fusion molecules or derivatives thereof which activate or enhance expression of a nucleic acid, so called activators or enhancers. The term "operably linked" as used herein refers to a functional linkage between the promoter sequence and the gene of interest, such that the promoter sequence is able to initiate transcription of the gene of interest.

By way of example, the transgene nucleotide sequence encoding the double-stranded RNA could be placed under the control of an inducible or growth or developmental stage-specific promoter which permits transcription of the dsRNA to be turned on, by the addition of the inducer for an inducible promoter or when the particular stage of growth or development is reached.

Alternatively, the transgene encoding the double-stranded RNA is placed under the control of a strong constitutive promoter such as any selected from the group comprising the CaMV35S promoter, doubled CaMV35S promoter, ubiquitin promoter, actin promoter, rubisco promoter, GOS2 promoter, Figwort mosaic virus (FMV) 34S promoter, cassava vein mosaic virus (CsVMV) promoter (Verdaguer B. et al, Plant Mol Biol. 1998 37(6):1055-67).

Alternatively, the transgene encoding the double-stranded RNA is placed under the control of a tissue specific promoter such as any selected from the group comprising root specific promoters of genes encoding PsMTA Class III chitinase, photosynthetic tissue-specific promoters such as promoters of cab1 and cab2, rbcS, gapA, gapB and ST-LS1 proteins, JAS promoters, chalcone synthase promoter and promoter of RJ39 from strawberry.

In another embodiment, the transgene encoding the double-stranded RNA is placed under the control of an insect-induced promoter, for instance the potato proteinase inhibitor II (PinII) promoter (Duan X et al, Nat Biotechnol. 1996, 14(4):494-8); or a wounding-induced promoter, for instance the jasmonates and ethylene induced promoters, PDF1.2 promoter (Manners JM et al., Plant Mol Biol. 1998, 38(6):1071-80); or under a defense related promoter, for instance the salicylic acid induced promoters and plant-pathogenesis related protein (PR protein) promoters (PR1

promoter (Cornelissen BJ et al., Nucleic Acids Res. 1987, 15(17):6799-811 ; COMT promoter (Toquin V et al, Plant Mol Biol. 2003, 52(3):495-509).

Furthermore, when using the methods of the present invention for developing transgenic plants resistant against insects, it might be beneficial to place the nucleic acid encoding the double-stranded RNA according to the present invention under the control of a tissue-specific promoter. In order to improve the transfer of the dsRNA from the plant cell to the pest, the plants could preferably express the dsRNA in a plant part that is first accessed or damaged by the plant pest. In case of plant pathogenic insects, preferred tissues to express the dsRNA are the leaves, stems, roots, and seeds. Therefore, in the methods of the present invention, a plant tissue-preferred promoter may be used, such as a leaf-specific promoter, a stem-specific promoter, a phloem-specific promoter, a xylem-specific promoter, a root-specific promoter, or a seed-specific promoter (sucrose transporter gene AtSUC promoter (Baud S et al., Plant J. 2005, 43(6):824-36), wheat high molecular weight glutenin gene promoter (Robert LS et al., Plant Cell. 1989, 1(6):569-78.)). Suitable examples of a root specific promoter are PsMTA (Fordam-Skelton, A.P., et al., 1997 Plant Molecular Biology 34: 659-668.) and the Class III Chitinase promoter. Examples of leaf- and stem-specific or photosynthetic tissue-specific promoters that are also photoactivated are promoters of two chlorophyll binding proteins (cab1 and cab2) from sugar beet (Stahl D.J., et al., 2004 BMC Biotechnology 2004 4:31), ribulose-bisphosphate carboxylase (Rubisco), encoded by rbcS (Nomura M. et al., 2000 Plant Mol. Biol. 44: 99-106), A (gapA) and B (gapB) subunits of chloroplast glyceraldehyde-3-phosphate dehydrogenase (Conley T.R. et al. 1994 Mol. Cell Biol. 19: 2525-33; Kwon H.B. et al. 1994 Plant Physiol. 105: 357-67), promoter of the *Solanum tuberosum* gene encoding the leaf and stem specific (ST-LS1) protein (Zaidi M.A. et al., 2005 Transgenic Res. 14:289-98), stem-regulated, defense-inducible genes, such as JAS promoters (patent publication no. 20050034192/US-A1). An example of a flower-specific promoter is for instance, the chalcone synthase promoter (Faktor O. et al. 1996 Plant Mol. Biol. 32: 849) and an example of a fruit-specific promoter is for instance RJ39 from strawberry (WO 98 31812).

In yet other embodiments of the present invention, other promoters useful for the expression of dsRNA are used and include, but are not limited to, promoters from an RNA PolI, an RNA PolII, an RNA PolIII, T7 RNA polymerase or SP6 RNA polymerase. These promoters are typically used for *in vitro*-production of dsRNA, which dsRNA is then included in an antiinsecticidal agent, for example, in an anti-insecticidal liquid, spray or powder.

Therefore, the present invention also encompasses a method for generating any of the double-stranded RNA or RNA constructs of the invention. This method comprises the steps of

- a. contacting an isolated nucleic acid or a recombinant DNA construct of the invention with cell-free components; or
- b. introducing (e.g. by transformation, transfection or injection) an isolated nucleic acid or a recombinant DNA construct of the invention in a cell,

under conditions that allow transcription of said nucleic acid or recombinant DNA construct to produce the dsRNA or RNA construct.

Optionally, one or more transcription termination sequences may also be incorporated in the recombinant construct of the invention. The term "transcription termination sequence" encompasses a control sequence at the end of a transcriptional unit, which signals 3' processing and poly-adenylation of a primary transcript and termination of transcription. Additional regulatory elements, such as transcriptional or translational enhancers, may be incorporated in the expression construct.

The recombinant constructs of the invention may further include an origin of replication which is required for maintenance and/or replication in a specific cell type. One example is when an expression construct is required to be maintained in a bacterial cell as an episomal genetic element (e.g. plasmid or cosmid molecule) in a cell. Preferred origins of replication include, but are not limited to, f1-ori and colE1 ori.

The recombinant construct may optionally comprise a selectable marker gene. As used herein, the term "selectable marker gene" includes any gene, which confers a phenotype on a cell in which it is expressed to facilitate the identification and/or selection of cells, which are transfected or transformed, with an expression construct of the invention. Examples of suitable selectable markers include resistance genes against ampicillin (Ampr), tetracycline (Tcr), kanamycin (Kanr), phosphinothricin, and chloramphenicol (CAT) gene. Other suitable marker genes provide a metabolic trait, for example manA. Visual marker genes may also be used and include for example beta-glucuronidase (GUS), luciferase and Green Fluorescent Protein (GFP).

Plants that have been stably transformed with a transgene encoding the dsRNA may be supplied as seed, reproductive material, propagation material or cell culture material which does not actively express the dsRNA but has the capability to do so.

Accordingly, the present invention encompasses a plant (e.g. a rice plant), or a seed (e.g. a rice seed), or a cell (e.g. a bacterial or plant cell), comprising at least one double-stranded RNA or at least one double-stranded RNA construct as described herein; or at least one nucleotide sequence or at least one recombinant DNA construct as described herein; or at least one plant cell as described herein. The present invention also encompasses a plant (e.g. an alfalfa, apple, apricot, artichoke, asparagus, avocado, banana, barley, beans, beet, blackberry, blueberry, broccoli, brussel sprouts, cabbage, canola, carrot, cassava, cauliflower, a cereal, celery, cherry, citrus, clemintine, coffee, corn, cotton, cucumber, eggplant, endive, eucalyptus, figes, grape, grapefruit, groundnuts, ground cherry, kiwifruit, lettuce, leek, lemon, lime, pine, maize, mango, melon, millet, mushroom, nut aot, okra, onion, orange, an ornamental plant or flower or tree, papaya,, parsley, pea, peach, peanut, peat, pepper, persimmon, pineapple, plantain, plum, pomegranate, potato, pumpkin, radicchio, radish, rapeseed, raspberry, rice, rye, sorghum, soy, soybean, spinach, strawberry, sugarbeet, sugarcane, sunflower, sweet poatao, tangerine, tea, tobacco, tomato, a vine, waetermelon, wheat, yams or zucchiniplant; preferably a potato, eggplant, tomato, pepper, tobacco, ground cherry, rice corn or cotton plant), or a seed or tuber (e.g. an alfalfa, apple, apricot, artichoke, asparagus, avocado, banana, barley, beans, beet, blackberry, blueberry, broccoli, brussel sprouts, cabbage, canola, carrot, cassava, cauliflower, a cereal, celery, cherry, citrus, clemintine, coffee, corn, cotton, cucumber, eggplant, endive, eucalyptus, figes,

grape, grapefruit, groundnuts, ground cherry, kiwifruit, lettuce, leek, lemon, lime, pine, maize, mango, melon, millet, mushroom, nut aot, okra, onion, orange, an ornamental plant or flower or tree, papaya, parsley, pea, peach, peanut, peat, pepper, persimmon, pineapple, plantain, plum, pomegranate, potato, pumpkin, radicchio, radish, rapeseed, raspberry, rice, rye, sorghum, soy, soybean, spinach, strawberry, sugarbeet, sugarcane, sunflower, sweet potato, tangerine, tea, tobacco, tomato, a vine, waatermelon, wheat, yams or zucchini plant; preferably a potato, eggplant, tomato, pepper, tobacco, ground cherry, rice, corn or cotton seed or tuber), or a cell (e.g. a bacterial or plant cell), comprising at least one double-stranded RNA or at least one double-stranded RNA construct as described herein: or at least one nucleotide sequence or at least one recombinant DNA construct as described herein. Preferably, these plants or seeds or cells comprise a recombinant construct wherein the nucleotide sequence encoding the dsRNA or dsRNA construct according to the present invention is operably linked to at least one regulatory element as described above.

The plant may be provided in a form wherein it is actively expressing (transcribing) the RNA molecule in one or more cells, cell types or tissues. Alternatively, the plant may be "capable of expressing", meaning that it is transformed with a transgene which encodes the desired RNA molecule but that the transgene is not active in the plant when (and in the form in which) the plant is supplied.

In one particular embodiment, there is provided a recombinant (expression) construct for expression of an RNA molecule in a plant or in a plant cell comprising at least one regulatory sequence operably linked to a nucleic acid molecule comprising at least 14, 15, 16, 17, 18, 19, 20, 21, 22 etc. nucleotides, up to all of the nucleotides of the sequence set forth as SEQ ID NOs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 49 to 158, 159, 160-163, 168, 173, 178, 183, 188, 193, 198, 203, 208, 215, 220, 225, 230, 240 to 247, 249, 251, 253, 255, 257, 259, 275 to 472, 473, 478, 483, 488, 493, 498, 503, 508 to 513, 515, 517, 519, 521, 533 to 575, 576, 581, 586, 591, 596, 601, 603, 605, 607, 609, 621 to 767, 768, 773, 778, 783, 788, 793, 795, 797, 799, 801, 813 to 862, 863, 868, 873, 878, 883, 888, 890, 892, 894, 896, 908 to 1040, 1041, 1046, 1051, 1056, 1061, 1066 to 1071, 1073, 1075, 1077, 1079, 1081, 1083, 1085, 1087, 1089, 1091, 1093, 1095, 1097, 1099, 1101, 1103, 1105, 1107, 1109, 1111, 1113, 1161 to 1571, 1572, 1577, 1582, 1587, 1592, 1597, 1602, 1607, 1612, 1617, 1622, 1627, 1632, 1637, 1642, 1647, 1652, 1657, 1662, 1667, 1672, 1677, 1682, 1684, 1686, 1688, 1690, 1692, 1694, 1696, 1698, 1700, 1702, 1704, 1730 to 2039, 2040, 2045, 2050, 2055, 2060, 2065, 2070, 2075, 2080, 2085, 2090, 2095, 2100, 2102, 2104, 2106, 2108, 2120 to 2338, 2339, 2344, 2349, 2354, 2359, 2364, 2366, 2368, 2370, 2372, 2384 to 2460, 2461, 2466, 2471, 2476, 2481 or 2486, or comprising at least 14, 15, 16, 17, 18, 19, 20, 21, 22 etc. up to all nucleotides of the sequence of an orthologous nucleic acid molecule from a different target species. Many vectors are available for this purpose, and selection of the appropriate vector will depend mainly on the size of the nucleic acid to be inserted into the vector and the particular host cell to be transformed with the vector.

General techniques for expression of exogenous double-stranded RNA in plants for the purposes of RNAi are known in the art (see Baulcombe D, 2004, Nature. 431(7006):356-63. RNA

silencing in plants, the contents of which are incorporated herein by reference). More particularly, methods for expression of double-stranded RNA in plants for the purposes of down-regulating gene expression in plant pests such as nematodes or insects are also known in the art. Similar methods can be applied in an analogous manner in order to express double-stranded RNA in plants for the purposes of down-regulating expression of a target gene in a plant pathogenic insect. In order to achieve this effect it is necessary only for the plant to express (transcribe) the double-stranded RNA in a part of the plant which will come into direct contact with the insect, such that the double-stranded RNA can be taken up by the insect. Depending on the nature of the insect and its relationship with the host plant, expression of the dsRNA could occur within a cell or tissue of a plant within which the insect is also present during its life cycle, or the RNA may be secreted into a space between cells, such as the apoplast, that is occupied by the insect during its life cycle. Furthermore, the dsRNA may be located in the plant cell, for example in the cytosol, or in the plant cell organelles such as a chloroplast, mitochondrion, vacuole or endoplasmic reticulum.

Alternatively, the dsRNA may be secreted by the plant cell and by the plant to the exterior of the plant. As such, the dsRNA may form a protective layer on the surface of the plant.

In a further aspect, the invention also provides combinations of methods and compositions for preventing or protecting plants from pest infestation. For instance, one means provides using the plant transgenic approach combining methods using expression of dsRNA molecules and methods using expression of such Bt insecticidal proteins.

Therefore the invention also relates to a method or a plant cell or plant described herein, wherein said plant cell or plant expressing said RNA molecule comprises or expresses a pesticidal agent selected from the group consisting of a patatin, a *Bacillus thuringiensis* insecticidal protein, a *Xenorhabdus* insecticidal protein, a *Photorhabdus* insecticidal protein, a *Bacillus laterosporus* insecticidal protein, and a *Bacillus sphearicus* insecticidal protein. Preferably said *Bacillus thuringiensis* insecticidal protein is selected from the group consisting of a Cry1, a Cry3, a TIC851, a CryET170, a Cry22, a binary insecticidal protein CryET33 and CryET34, a binary insecticidal protein CryET80 and CryET76, a binary insecticidal protein TIC100 and TIC101, and a binary insecticidal protein PS149B1.

In a further embodiment, the invention relates to a composition for controlling insect growth and/or preventing or reducing insect infestation, comprising at least a plant part, plant cell, plant tissue or seed comprising at least one double-stranded RNA, wherein said double-stranded RNA comprises annealed complementary strands, one of which has a nucleotide sequence which is complementary to at least part of a nucleotide sequence of an insect target gene. Optionally, the composition further comprises at least one suitable carrier, excipient or diluent. The target gene may be any target gene described herein. Preferably the insect target gene is essential for the viability, growth, development or reproduction of the insect.

In another aspect the invention relates to a composition as described above, wherein the insect target gene comprises a sequence which is at least 75%, preferably at least 80%, 85%, 90%, more preferably at least 95%, 98% or 99% identical to a sequence selected from the group of sequences represented by any of SEQ ID NOs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 49 to 158,

159, 160-163, 168, 173, 178, 183, 188, 193, 198, 203, 208, 215, 220, 225, 230, 240 to 247, 249, 251, 253, 255, 257, 259, 275 to 472, 473, 478, 483, 488, 493, 498, 503, 508 to 513, 515, 517, 519, 521, 533 to 575, 576, 581, 586, 591, 596, 601, 603, 605, 607, 609, 621 to 767, 768, 773, 778, 783, 788, 793, 795, 797, 799, 801, 813 to 862, 863, 868, 873, 878, 883, 888, 890, 892, 894, 896, 908 to 1040, 1041, 1046, 1051, 1056, 1061, 1066 to 1071, 1073, 1075, 1077, 1079, 1081, 1083, 1085, 1087, 1089, 1091, 1093, 1095, 1097, 1099, 1101, 1103, 1105, 1107, 1109, 1111, 1113, 1161 to 1571, 1572, 1577, 1582, 1587, 1592, 1597, 1602, 1607, 1612, 1617, 1622, 1627, 1632, 1637, 1642, 1647, 1652, 1657, 1662, 1667, 1672, 1677, 1682, 1684, 1686, 1688, 1690, 1692, 1694, 1696, 1698, 1700, 1702, 1704, 1730 to 2039, 2040, 2045, 2050, 2055, 2060, 2065, 2070, 2075, 2080, 2085, 2090, 2095, 2100, 2102, 2104, 2106, 2108, 2120 to 2338, 2339, 2344, 2349, 2354, 2359, 2364, 2366, 2368, 2370, 2372, 2384 to 2460, 2461, 2466, 2471, 2476, 2481 or 2486, or the complement thereof, or wherein said insect target gene is an insect orthologue of a gene comprising at least 17 contiguous nucleotides of any of SEQ ID NOs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 49 to 158, 159, 160-163, 168, 173, 178, 183, 188, 193, 198, 203, 208, 215, 220, 225, 230, 240 to 247, 249, 251, 253, 255, 257, 259, 275 to 472, 473, 478, 483, 488, 493, 498, 503, 508 to 513, 515, 517, 519, 521, 533 to 575, 576, 581, 586, 591, 596, 601, 603, 605, 607, 609, 621 to 767, 768, 773, 778, 783, 788, 793, 795, 797, 799, 801, 813 to 862, 863, 868, 873, 878, 883, 888, 890, 892, 894, 896, 908 to 1040, 1041, 1046, 1051, 1056, 1061, 1066 to 1071, 1073, 1075, 1077, 1079, 1081, 1083, 1085, 1087, 1089, 1091, 1093, 1095, 1097, 1099, 1101, 1103, 1105, 1107, 1109, 1111, 1113, 1161 to 1571, 1572, 1577, 1582, 1587, 1592, 1597, 1602, 1607, 1612, 1617, 1622, 1627, 1632, 1637, 1642, 1647, 1652, 1657, 1662, 1667, 1672, 1677, 1682, 1684, 1686, 1688, 1690, 1692, 1694, 1696, 1698, 1700, 1702, 1704, 1730 to 2039, 2040, 2045, 2050, 2055, 2060, 2065, 2070, 2075, 2080, 2085, 2090, 2095, 2100, 2102, 2104, 2106, 2108, 2120 to 2338, 2339, 2344, 2349, 2354, 2359, 2364, 2366, 2368, 2370, 2372, 2384 to 2460, 2461, 2466, 2471, 2476, 2481 or 2486, or the complement thereof.

According to a still further embodiment, the present invention extends to a method for increasing plant yield comprising introducing in a plant any of the nucleotide sequences or recombinant DNA constructs as herein described in an expressible format. Plants encompassed by this method are as described earlier.

The invention will be further understood with reference to the following non-limiting examples.

Brief Description of Figures and Tables

Figure 1-LD: Survival of *L. decemlineata* on artificial diet treated with dsRNA. Insects of the second larval stage were fed diet treated with 50 µl of topically-applied solution of dsRNA (targets or gfp control). Diet was replaced with fresh diet containing topically-applied dsRNA after 7 days. The number of surviving insects were assessed at days 2, 5, 7, 8, 9, & 13. The percentage of surviving larvae was calculated relative to day 0 (start of assay). Target LD006: (SEQ ID NO 178);

Target LD007 (SEQ ID NO 183); Target LD010 (SEQ ID NO 188); Target LD011 (SEQ ID NO 193); Target LD014 (SEQ ID NO 198); gfp dsRNA (SEQ ID NO 235).

5 **Figure 2-LD:** Survival of *L. decemlineata* on artificial diet treated with dsRNA. Insects of the second larval stage were fed diet treated with 50 µl of topically-applied solution of dsRNA (targets or gfp control). Diet was replaced with fresh diet only after 7 days. The number of surviving insects was assessed at days 2, 5, 6, 7, 8, 9, 12, & 14. The percentage of surviving larvae was calculated relative to day 0 (start of assay). Target LD001 (SEQ ID NO 163); Target LD002 (SEQ ID NO 168); Target LD003 (SEQ ID NO 173); Target LD015 (SEQ ID NO 215); Target LD016 (SEQ ID NO 220); gfp dsRNA (SEQ ID NO 235).

10 **Figure 3-LD:** Average weight of *L. decemlineata* larvae on potato leaf discs treated with dsRNA. Insects of the second larval stage were fed leaf discs treated with 20 µl of a topically-applied solution (10 ng/µl) of dsRNA (target LD002 or gfp). After two days the insects were transferred on to untreated leaves every day.

15 **Figure 4-LD:** Survival of *L. decemlineata* on artificial diet treated with shorter versions of target LD014 dsRNA and concatemer dsRNA. Insects of the second larval stage were fed diet treated with 50 µl of topically-applied solution of dsRNA (gfp or targets). The number of surviving insects were assessed at days 3, 4, 5, 6, & 7. The percentage of surviving larvae were calculated relative to day 0 (start of assay).

20 **Figure 5-LD:** Survival of *L. decemlineata* larvae on artificial diet treated with different concentrations of dsRNA of target LD002 (a), target LD007 (b), target LD010 (c), target LD011 (d), target LD014 (e), target LD015 (f), LD016 (g) and target LD027 (h). Insects of the second larval stage were fed diet treated with 50 µl of topically-applied solution of dsRNA. Diet was replaced with fresh diet containing topically-applied dsRNA after 7 days. The number of surviving insects were assessed at regular intervals. The percentage of surviving larvae were calculated relative to day 0 (start of assay).

25 **Figure 6-LD.** Survival of *L. decemlineata* adults on potato leaf discs treated with dsRNA. Young adult insects were fed double-stranded-RNA-treated leaf discs for the first two days and were then placed on untreated potato foliage. The number of surviving insects were assessed regularly; mobile insects were recorded as insects which were alive and appeared to move normally; moribund insects were recorded as insects which were alive but appeared sick and slow moving – these insects were not able to right themselves once placed on their backs. Target LD002 (SEQ ID NO 168); Target LD010 (SEQ ID NO 188); Target LD014 (SEQ ID NO 198); Target LD016 (SEQ ID NO 220); gfp dsRNA (SEQ ID NO 235).

35 **Figure 7-LD.** Mortality and growth/developmental delay of larval survivors of the Colorado potato beetle, *Leptinotarsa decemlineata*, on transgenic potato plants. Seven CPB L1 larvae were fed on transgenic potato siblings harbouring LD002 construct (●), empty vector (▲), or wild type line V plants (■) for seven days. Mortality is expressed in percentage and average larval weight in mg.

Figure 1-PC: Effects of ingested target dsRNAs on survival and growth of *P. cochleariae* larvae. Neonate larvae were fed oilseed rape leaf discs treated with 25 µl of topically-applied solution of 0.1 µg/µl dsRNA (targets or gfp control). After 2 days, the insects were transferred onto fresh dsRNA-treated leaf discs. At day 4, larvae from one replicate for every treatment were collected and placed in a Petri dish containing fresh untreated oilseed rape foliage. The insects were assessed at days 2, 4, 7, 9 & 11. (a) Survival of *E. varivestis* larvae on oilseed rape leaf discs treated with dsRNA. The percentage of surviving larvae was calculated relative to day 0 (start of assay). (b) Average weights of *P. cochleariae* larvae on oilseed rape leaf discs treated with dsRNA. Insects from each replicate were weighed together and the average weight per larva determined. Error bars represent standard deviations. Target 1: SEQ ID NO 473; target 3: SEQ ID NO 478; target 5: SEQ ID NO 483 –; target 10: SEQ ID NO 488; target 14: SEQ ID NO 493; target 16: SEQ ID NO 498; target 27: SEQ ID NO 503; gfp dsRNA: SEQ ID NO 235.

Figure 2-PC: Survival of *P. cochleariae* on oilseed rape leaf discs treated with different concentrations of dsRNA of (a) target PC010 and (b) target PC027. Neonate larvae were placed on leaf discs treated with 25 µl of topically-applied solution of dsRNA. Insects were transferred to fresh treated leaf discs at day 2. At day 4 for target PC010 and day 5 for target PC027, the insects were transferred to untreated leaves. The number of surviving insects were assessed at days 2, 4, 7, 8, 9 & 11 for PC010 and 2, 5, 8, 9 & 12 for PC027. The percentage of surviving larvae was calculated relative to day 0 (start of assay).

Figure 1-EV: Survival of *E. varivestis* larvae on bean leaf discs treated with dsRNA. Neonate larvae were fed bean leaf discs treated with 25 µl of topically-applied solution of 1 µg/µl dsRNA (targets or gfp control). After 2 days, the insects were transferred onto fresh dsRNA-treated leaf discs. At day 4, larvae from one treatment were collected and placed in a plastic box containing fresh untreated bean foliage. The insects were assessed for mortality at days 2, 4, 6, 8 & 10. The percentage of surviving larvae was calculated relative to day 0 (start of assay). Target 5: SEQ ID NO 576; target 10: SEQ ID NO 586; target 15: SEQ ID NO 591; target 16: SEQ ID NO 596; gfp dsRNA: SEQ ID NO 235.

Figure 2-EV: Effects of ingested target dsRNAs on survival of *E. varivestis* adults and resistance to snap bean foliar insect damage. (a) Survival of *E. varivestis* adults on bean leaf treated with dsRNA. Adults were fed bean leaf discs treated with 75 µl of topically-applied solution of 0.1 µg/µl dsRNA (targets or gfp control). After 24 hours, the insects were transferred onto fresh dsRNA-treated leaf discs. After a further 24 hours, adults from one treatment were collected and placed in a plastic box containing potted fresh untreated whole bean plants. The insects were assessed for mortality at days 4, 5, 6, 7, 8, & 11. The percentage of surviving adults was calculated relative to day 0 (start of assay). Target 10: SEQ ID NO 586; target 15: SEQ ID NO 591; target 16: SEQ ID NO 596; gfp dsRNA: SEQ ID NO 235. (b) Resistance to bean foliar damage caused by adults of the *E. varivestis* by dsRNA. Whole plants containing insects from one treatment (see (a)) were checked visually for foliar damage on day 9. (i) target 10; (ii) target 15; (iii) target 16; (iv) gfp dsRNA; (v) untreated.

Figure 1-TC: Survival of *T. castaneum* larvae on artificial diet treated with dsRNA of target 14. Neonate larvae were fed diet based on a flour/milk mix with 1 mg dsRNA target 14. Control was water (without dsRNA) in diet. Four replicates of 10 first instar larvae per replicate were performed for each treatment. The insects were assessed for survival as average percentage means at days 6, 17, 31, 45 and 60. The percentage of surviving larvae was calculated relative to day 0 (start of assay). Error bars represent standard deviations. Target TC014: SEQ ID NO 878.

Figure 1-MP: Effect of ingested target 27 dsRNA on the survival of *Myzus persicae* nymphs. First instars were placed in feeding chambers containing 50 μ l of liquid diet with 2 μ g/ μ l dsRNA (target 27 or gfp dsRNA control). Per treatment, 5 feeding chambers were set up with 10 instars in each feeding chamber. Number of survivors were assessed at 8 days post start of bioassay. Error bars represent standard deviations. Target MP027: SEQ ID NO 1061; gfp dsRNA: SEQ ID NO 235.

Figure 1-NL: Survival of *Nilaparvata lugens* on liquid artificial diet treated with dsRNA. Nymphs of the first to second larval stage were fed diet supplemented with 2 mg/ml solution of dsRNA targets in separate bioassays: (a) NL002, NL003, NL005, NL010; (b) NL009, NL016; (c) NL014, NL018; (d) NL013, NL015, NL021. Insect survival on targets were compared to diet only and diet with gfp dsRNA control at same concentration. Diet was replaced with fresh diet containing dsRNA every two days. The number of surviving insects were assessed every day

Figure 2-NL: Survival of *Nilaparvata lugens* on liquid artificial diet treated with different concentrations of target dsRNA NL002. Nymphs of the first to second larval stage were fed diet supplemented with 1, 0.2, 0.08, and 0.04 mg/ml (final concentration) of NL002. Diet was replaced with fresh diet containing dsRNA every two days. The numbers of surviving insects were assessed every day.

25 Examples

Example 1: Silencing *C.elegans* target genes in *C. elegans* in High Throughput Screening

A *C. elegans* genome wide library was prepared in the pGN9A vector (WO 01/88121) between two identical T7-promoters and terminators, driving its expression in the sense and antisense direction upon expression of the T7 polymerase, which was induced by IPTG.

30 This library was transformed into the bacterial strain AB301-105 (DE3) in 96 well plate format. For the genome wide screening, these bacterial cells were fed to the nuclease deficient *C. elegans* *nuc-1(e1392)* strain.

Feeding the dsRNA produced in the bacterial strain AB301-105 (DE3), to *C. elegans* *nuc-1(e1392)* worms, was performed in a 96 well plate format as follows: *nuc-1* eggs were transferred to a separate plate and allowed to hatch simultaneously at 20 °C for synchronization of the L1 generation. 96 well plates were filled with 100 μ L liquid growth medium comprising IPTG and with 10 μ L bacterial cell culture of OD₆₀₀1 AB301-105 (DE3) of the *C. elegans* dsRNA library carrying each a vector with a *C. elegans* genomic fragment for expression of the dsRNA. To each well, 4 of

the synchronized L1 worms were added and were incubated at 25 °C for at least 4 to 5 days. These experiments were performed in quadruplicate. In the screen 6 controls were used:

- pGN29 = negative control, wild type
- pGZ1 = *unc-22* = twitcher phenotype
- 5 - pGZ18 = chitin synthase = embryonic lethal
- pGZ25 = *pos-1* = embryonic lethal
- pGZ59 = *bli-4D* = acute lethal
- ACC = acetyl co-enzyme A carboxylase = acute lethal

After 5 days, the phenotype of the *C. elegans nuc-1* (e1392) worms fed with the bacteria
 10 producing dsRNA were compared to the phenotype of worms fed with the empty vector (pGN29) and the other controls. The worms that were fed with the dsRNA were screened for lethality (acute or larval) lethality for the parent (Po) generation, (embryonic) lethality for the first filial (F1) generation, or for growth retardation of Po as follows: (i) Acute lethality of Po: L1's have not developed and are dead, this phenotype never gives progeny and the well looks quite empty; (ii)
 15 (Larval) lethality of Po: Po died in a later stage than L1, this phenotype also never gives progeny. Dead larvae or dead adult worms are found in the wells; (iii) Lethality for F1: L1's have developed until adult stage and are still alive. This phenotype has no progeny. This can be due to sterility, embryonic lethality (dead eggs on the bottom of well), embryonic arrest or larval arrest (eventually ends up being lethal); (iv) Arrested in growth and growth retardation/delay: Compared to a well
 20 with normal development and normal # of progeny.

For the target sequences presented in Table 1A, it was concluded that dsRNA mediated silencing of the *C. elegans* target gene in nematodes, such as *C. elegans*, had a fatal effect on the growth and viability of the worm.

Subsequent to the above dsRNA silencing experiment, a more detailed phenotyping
 25 experiment was conducted in *C. elegans* in a high throughput format on 24 well plates. The dsRNA library produced in bacterial strain AB301-105 (DE3), as described above, was fed to *C. elegans nuc-1* (e1392) worms on 24 well plates as follows: *nuc-1* eggs were transferred to a separate plate and allowed to hatch simultaneously at 20 C for synchronization of the L1 generation. Subsequently 100 of the synchronized L1 worms were soaked in a mixture of 500 µL S-complete
 30 fed medium, comprising 5 µg/mL cholesterol, 4 µL/mL PEG and 1mM IPTG, and 500 µL of bacterial cell culture of OD₆₀₀1 AB301-105 (DE3) of the *C. elegans* dsRNA library carrying each a vector with a *C. elegans* genomic fragment for expression of the dsRNA. The soaked L1 worms were rolled for 2 hours at 25 C.

After centrifugation and removal of 950 µL of the supernatant, 5 µL of the remaining and
 35 resuspended pellet (comprising about 10 to 15 worms) was transferred in the middle of each well of a 24 well plate, filled with a layer of agar LB broth. The inoculated plate was incubated at 25°C for 2 days. At the adult stage, 1 adult worm was singled and incubated at 25°C for 2 days for inspection of its progeny. The other adult worms are inspected *in situ* on the original 24 well plate. These experiments were performed in quadruplicate.

This detailed phenotypic screen was repeated with a second batch of worms, the only difference being that the worms of the second batch were incubated at 20 C for 3 days.

The phenotype of the worms fed with *C. elegans* dsRNA was compared to the phenotype of *C. elegans nuc-1* (e1392) worms fed with the empty vector.

5 Based on this experiment, it was concluded that silencing the *C. elegans* target genes as represented in **Table 1A** had a fatal effect on the growth and viability of the worm and that the target gene is essential to the viability of nematodes. Therefore these genes are good target genes to control (kill or prevent from growing) nematodes via dsRNA mediated gene silencing. Accordingly, the present invention encompasses the use of nematode orthologues of the above *C.*
10 *elegans* target gene, to control nematode infestation, such as nematode infestation of plants.

Example 2: Identification of *D. melanogaster* orthologues

As described above in Example 1, numerous *C. elegans* lethal sequences were identified and can be used for identifying orthologues in other species and genera. For example, the *C.*
15 *elegans* lethal sequences can be used to identify orthologous *D. melanogaster* sequences. That is, each *C. elegans* sequence can be queried against a public database, such as GenBank, for orthologous sequences in *D. melanogaster*. Potential *D. melanogaster* orthologues were selected that share a high degree of sequence homology (E value preferably less than or equal to 1E-30) and the sequences are blast reciprocal best hits, the latter means that the sequences from different
20 organisms (e.g. *C. elegans* and *D. melanogaster*) are each other's top blast hits. For example, sequence C from *C. elegans* is compared against sequences in *D. melanogaster* using BLAST. If sequence C has the *D. melanogaster* sequence D as best hit and when D is compared to all the sequences of *C. elegans*, also turns out to be sequence C, then D and C are reciprocal best hits. This criterium is often used to define orthology, meaning similar sequences of different species,
25 having similar function. The *D. melanogaster* sequence identifiers are represented in **Table 1A**.

Example 3: *Leptinotarsa decemlineata* (Colorado potato beetle)

A. Cloning partial gene sequences from *Leptinotarsa decemlineata*

High quality, intact RNA was isolated from 4 different larval stages of *Leptinotarsa*
30 *decemlineata* (Colorado potato beetle; source: Jeroen van Schaik, Entocare CV Biologische Gewasbescherming, Postbus 162, 6700 AD Wageningen, the Netherlands) using TRIzol Reagent (Cat. Nr. 15596-026/15596-018, Invitrogen, Rockville, Maryland, USA) following the manufacturer's instructions. Genomic DNA present in the RNA preparation was removed by DNase treatment following the manufacturer's instructions (Cat. Nr. 1700, Promega). cDNA was generated using a
35 commercially available kit (SuperScript™ III Reverse Transcriptase, Cat. Nr. 18080044, Invitrogen, Rockville, Maryland, USA) following the manufacturer's instructions.

To isolate cDNA sequences comprising a portion of the LD001, LD002, LD003, LD006, LD007, LD010, LD011, LD014, LD015, LD016, LC018 and LD027 genes, a series of PCR

reactions with degenerate primers were performed using Amplitaq Gold (Cat. Nr. N8080240, Applied Biosystems) following the manufacturer's instructions.

The sequences of the degenerate primers used for amplification of each of the genes are given in **Table 2-LD**, which displays *Leptintarsa decemlineata* target genes including primer sequences and cDNA sequences obtained. These primers were used in respective PCR reactions with the following conditions: 10 minutes at 95°C, followed by 40 cycles of 30 seconds at 95°C, 1 minute at 55°C and 1 minute at 72°C, followed by 10 minutes at 72°C. The resulting PCR fragments were analyzed on agarose gel, purified (QIAquick Gel Extraction kit, Cat. Nr. 28706, Qiagen), cloned into the pCR8/GW/topo vector (Cat. Nr. K2500 20, Invitrogen), and sequenced. The sequences of the resulting PCR products are represented by the respective SEQ ID NOs as given in **Table 2-LD** and are referred to as the partial sequences. The corresponding partial amino acid sequence are represented by the respective SEQ ID NOs as given in **Table 3-LD**, where the start of the reading frame is indicated in brackets.

B. dsRNA production of the *Leptinotarsa decemlineata* genes

dsRNA was synthesized in milligram amounts using the commercially available kit T7 RibomaxTM Express RNAi System (Cat. Nr. P1700, Promega). First two separate single 5' T7 RNA polymerase promoter templates were generated in two separate PCR reactions, each reaction containing the target sequence in a different orientation relative to the T7 promoter.

For each of the target genes, the sense T7 template was generated using specific T7 forward and specific reverse primers. The sequences of the respective primers for amplifying the sense template for each of the target genes are given in **Table 8-LD**. The conditions in the PCR reactions were as follows: 4 minutes at 95°C, followed by 35 cycles of 30 seconds at 95°C, 30 seconds at 55°C and 1 minute at 72°C, followed by 10 minutes at 72°C. The anti-sense T7 template was generated using specific forward and specific T7 reverse primers in a PCR reaction with the same conditions as described above. The sequences of the respective primers for amplifying the anti-sense template for each of the target genes are given in **Table 8-LD**. The resulting PCR products were analyzed on agarose gel and purified by PCR purification kit (Qiaquick PCR Purification Kit, Cat. Nr. 28106, Qiagen) and NaClO₄ precipitation. The generated T7 forward and reverse templates were mixed to be transcribed and the resulting RNA strands were annealed, DNase and RNase treated, and purified by sodium acetate, following the manufacturer's instructions. The sense strand of the resulting dsRNA for each of the target genes is given in **Table 8-LD**. **Table 8-LD** displays sequences for preparing ds RNA fragments of *Leptinotarsa decemlineata* target sequences and concatemer sequences, including primer sequences.

C. Cloning *Leptinotarsa decemlineata* genes into plant vector pK7GWIWG2D(II)

Since the mechanism of RNA interference operates through dsRNA fragments, the target nucleotide sequences of the target genes, as selected above, were cloned in anti-sense and sense orientation, separated by the intron - CmR - intron, whereby CmR is the chloramphenicol resistance marker, to form a dsRNA hairpin construct. These hairpin constructs were generated using the LR

recombination reaction between an attL- containing entry clone (see Example 1) and an attR- containing destination vector (= pK7GWIWG2D(II)). The plant vector pK7GWIWG2D(II) was obtained from the VIB/Plant Systems Biology with a Material Transfer Agreement. LR recombination reaction was performed by using LR Clonase™ II enzyme mix (Cat. Nr. 11791-020, Invitrogen) following the manufacturer's instructions. These cloning experiments resulted in a hairpin construct for each of the LD002, LD006, LD007, LD010, LD011, LD014 and LD016 genes, having either the promoter - sense - intron - CmR - intron - antisense orientation, or promoter - antisense - intron - CmR - intron - sense orientation, and wherein the promoter is the plant operable 35S promoter. The binary vector pK7GWIWG2D(II) with the 35S promoter is suitable for transformation into *A. tumefaciens*.

For LD002 and LD010, a double digest with restriction enzymes BsoBI & PvuI was done on LD002 cloned into pCR8/GW/topo (see Example 3A). For LD006, LD007, LD011, LD014, LD016 and LD027, a digest with restriction enzyme BsoBI was done on LD006 cloned into pCR8/GW/topo (see Example 3A). The band containing the gene of interest flanked by the attL sites using Qiaquick Gel Extraction Kit (Cat. Nr. 28706, Qiagen) was purified. An amount of 150 ng of purified fragment and 150 ng pK7GWIWG2D(II) was added together with the LR clonase II enzyme and incubated for at least 1h at 25°C. After proteinase K solution treatment (10 min at 37°C), the whole recombination mix was transformed into Top 10 chemically competent cells. Positive clones were selected by restriction digest analysis. The complete sequence of the hairpin construct for:

- LD002 (antisense - intron - CmR - intron - sense) is set forth in SEQ ID NO 240;
- LD006 (sense - intron - CmR - intron - antisense) is set forth in SEQ ID NO 241;
- LD007 (sense - intron - CmR - intron - antisense) is set forth in SEQ ID NO 242;
- LD010 (antisense - intron - CmR - intron - sense) is set forth in SEQ ID NO 243;
- LD011 (sense - intron - CmR - intron - antisense) is set forth in SEQ ID NO 244;
- LD014 (sense - intron - CmR - intron - antisense) is set forth in SEQ ID NO 245;
- LD016 (antisense - intron - CmR - intron - sense) is set forth in SEQ ID NO 246;
- LD027 (sense - intron - CmR - intron - antisense) is set forth in SEQ ID NO 2486.

Table 9-LD provides complete sequences for each hairpin construct.

D. Screening dsRNA targets using artificial diet for activity against *Leptinotarsa decemlineata*

Artificial diet for the Colorado potato beetle was prepared as follows (adapted from Gelman *et al.*, 2001, J. Ins. Sc., vol. 1, no. 7, 1-10): water and agar were autoclaved, and the remaining ingredients (shown in Table A below) were added when the temperature dropped to 55 °C. At this temperature, the ingredients were mixed well before the diet was aliquoted into 24-well plates (Nunc) with a quantity of 1ml of diet per well. The artificial diet was allowed to solidify by cooling at room temperature. Diet was stored at 4 °C for up to three weeks.

Table A: Ingredients for Artificial diet

Ingredients	Volume for 1 L
water	768ml
agar	14g
rolled oats	40g
Torula yeast	60g
lactalbumin hydrolysate	30g
casein	10g
fructose	20g
Wesson salt mixture	4g
tomato fruit powder	12.5g
potato leaf powder	25g
b-sitosterol	1g
sorbic acid	0.8g
methyl paraben	0.8g
Vanderzant vitamin mix	12g
neomycin sulfate	0.2g
aureomycin	0.130g
rifampicin	0.130g
chloramphenicol	0.130g
nystatin	0.050g
soybean oil	2ml
wheat germ oil	2ml

Fifty μ l of a solution of dsRNA at a concentration of 1 mg/ml was applied topically onto the solid artificial diet in the wells of the multiwell plate. The diet was dried in a laminar flow cabin. Per treatment, twenty-four Colorado potato beetle larvae (2nd stage), with two insects per well, were tested. The plates were stored in the insect rearing chamber at 25 ± 2 °C, 60 % relative humidity, with a 16:8 hours light:dark photoperiod. The beetles were assessed as live or dead every 1, 2 or 3 days. After seven days, for targets LD006, LD007, LD010, LD011, and LD014, the diet was replaced with fresh diet with topically applied dsRNA at the same concentration (1 mg/ml); for targets LD001, LD002, LD003, LD015, and LD016, the diet was replaced with fresh diet only. The dsRNA targets were compared to diet only or diet with topically applied dsRNA corresponding to a fragment of the GFP (green fluorescent protein) coding sequence (SEQ ID NO 235).

Feeding artificial diet containing intact naked dsRNAs to *L. decemlineata* larvae resulted in significant increases in larval mortalities as indicated in two separate bioassays (Figures 1LD-2LD).

All dsRNAs tested resulted ultimately in 100 % mortality after 7 to 14 days. Diet with or without GFP dsRNA sustained the insects throughout the bioassays with very little or no mortality.

Typically, in all assays observed, CPB second-stage larvae fed normally on diet with or without dsRNA for 2 days and molted to the third larval stage. At this new larval stage the CPB were observed to reduce significantly or stop altogether their feeding, with an increase in mortality as a result.

E. Bioassay of dsRNA targets using potato leaf discs for activity against the *Leptinotarsa decemlineata*

An alternative bioassay method was employed using potato leaf material rather than artificial diet as food source for CPB. Discs of approximately 1.1 cm in diameter (or 0.95 cm²) were cut out off leaves of 2 to 3-week old potato plants using a suitably-sized cork borer. Treated leaf discs were prepared by applying 20 µl of a 10 ng/µl solution of target LD002 dsRNA or control gfp dsRNA on the adaxial leaf surface. The leaf discs were allowed to dry and placed individually in 24 wells of a 24-well multiplate (Nunc). A single second-larval stage CPB was placed into each well, which was then covered with tissue paper and a multiwell plastic lid. The plate containing the insects and leaf discs were kept in an insect chamber at 28°C with a photoperiod of 16h light/8h dark. The insects were allowed to feed on the leaf discs for 2 days after which the insects were transferred to a new plate containing fresh treated leaf discs. Thereafter, the insects were transferred to a plate containing untreated leaf discs every day until day 7. Insect mortality and weight scores were recorded.

Feeding potato leaf discs with surface-applied intact naked dsRNA of target LD002 to *L. decemlineata* larvae resulted in a significant increase in larval mortalities (i.e. at day 7 all insects were dead; 100 % mortality) whereas control gfp dsRNA had no effect on CPB survival. Target LD002 dsRNA severely affected the growth of the larvae after 2 to 3 days whereas the larvae fed with gfp dsRNA at the same concentration developed as normal (Figure 3-LD).

F. Screening shorter versions of dsRNAs using artificial diet for activity against *Leptinotarsa decemlineata*

This example exemplifies the finding that shorter (60 or 100bp) dsRNA fragments on their own or as concatemer constructs are sufficient in causing toxicity towards the Colorado potato beetle.

LD014, a target known to induce lethality in Colorado potato beetle, was selected for this example. This gene encodes a V-ATPase subunit E (SEQ ID NO 15).

A 100 base pair fragment, LD014_F1, at position 195-294 on SEQ ID NO 15 (SEQ ID NO 159) and a 60 base pair fragment, LD014_F2, at position 235-294 on SEQ ID NO 15 (SEQ ID NO 160) were further selected. See also Table 7-LD.

Two concatemers of 300 base pairs, LD014_C1 and LD014_C2, were designed (SEQ ID NO 161 and SEQ ID NO 162). LD014_C1 contained 3 repeats of the 100 base pair fragment described above (SEQ ID NO 159) and LD014_C2 contained 5 repeats of the 60 base pair fragment described above (SEQ ID NO 160). See also Table 7-LD.

The fragments LD014_F1 and LD014_F2 were synthesized as sense and antisense primers. These primers were annealed to create the double strands DNA molecules prior to cloning. *Xba*I and *Xma*I restrictions sites were included at the 5' and 3' ends of the primers, respectively, to facilitate the cloning.

The concatemers were made as 300 base pairs synthetic genes. *Xba*I and *Xma*I restrictions sites were included at the 5' and 3' ends of the synthetic DNA fragments, respectively, to facilitate the cloning.

5 The 4 DNA molecules, i.e. the 2 single units (LD014_F1 & LD014_F2) and the 2 concatemers (LD014_C1 & LD014_C2), were digested with *Xba*I and *Xma*I and subcloned in pBluescriptII SK+ linearised by *Xba*I and *Xma*I digests, resulting in recombinant plasmids p1, p2, p3, & p4, respectively.

10 Double-stranded RNA production: dsRNA was synthesized using the commercially available kit T7 RibomaxTM Express RNAi System (Cat. Nr. P1700, Promega). First two separate single 5' T7 RNA polymerase promoter templates were generated in two separate PCR reactions, each reaction containing the target sequence in a different orientation relative to the T7 promoter. For LD014_F1, the sense T7 template was generated using the specific T7 forward primer oGBM159 and the specific reverse primer oGBM164 (represented herein as SEQ ID NO 204 and SEQ ID NO 205, respectively) in a PCR reaction with the following conditions: 4 minutes at 95°C, 15 followed by 35 cycles of 30 seconds at 95°C, 30 seconds at 55°C and 1 minute at 72°C, followed by 10 minutes at 72°C. The anti-sense T7 template was generated using the specific forward primer oGBM163 and the specific T7 reverse primer oGBM160 (represented herein as SEQ ID NO 206 and SEQ ID NO 207, respectively) in a PCR reaction with the same conditions as described above. The resulting PCR products were analyzed on agarose gel and purified by PCR purification 20 kit (Qiaquick PCR Purification Kit, Cat. Nr. 28106, Qiagen) and NaClO₄ precipitation. The generated T7 forward and reverse templates were mixed to be transcribed and the resulting RNA strands were annealed, Dnase and Rnase treated, and purified by sodium acetate, following the manufacturer's instructions. The sense strand of the resulting dsRNA is herein represented by SEQ ID NO 203.

25 For LD014_F2, the sense T7 template was generated using the specific T7 forward primer oGBM161 and the specific reverse primer oGBM166 (represented herein as SEQ ID NO 209 and SEQ ID NO 210, respectively) in a PCR reaction with the following conditions: 4 minutes at 95°C, followed by 35 cycles of 30 seconds at 95°C, 30 seconds at 55°C and 1 minute at 72°C, followed by 10 minutes at 72°C. The anti-sense T7 template was generated using the specific forward 30 primer oGBM165 and the specific T7 reverse primer oGBM162 (represented herein as SEQ ID NO 211 and SEQ ID NO 212, respectively) in a PCR reaction with the same conditions as described above. The resulting PCR products were analyzed on agarose gel and purified by PCR purification kit (Qiaquick PCR Purification Kit, Cat. Nr. 28106, Qiagen) and NaClO₄ precipitation. The generated T7 forward and reverse templates were mixed to be transcribed and the resulting RNA 35 strands were annealed, Dnase and Rnase treated, and purified by sodium acetate, following the manufacturer's instructions. The sense strand of the resulting dsRNA is herein represented by SEQ ID NO 208.

Also for the concatemers, separate single 5' T7 RNA polymerase promoter templates were generated in two separate PCR reactions, each reaction containing the target sequence in a 40 different orientation relative to the T7 promoter. The recombinant plasmids p3 and p4 containing

LD014_C1 & LD014_C2 were linearised with *Xba*I or *Xma*I, the two linear fragments for each construct purified and used as template for the *in vitro* transcription assay, using the T7 promoters flanking the cloning sites. Double-stranded RNA was prepared by *in vitro* transcription using the T7 RiboMAX™ Express RNAi System (Promega). The sense strands of the resulting dsRNA for LD014_C1 and LD014_C2 are herein represented by SEQ ID NO 213 and 2114, respectively.

Shorter sequences of target LD014 and concatemers were able to induce lethality in *Leptinotarsa decemlineata*, as shown in Figure 4-LD.

G. Screening dsRNAs at different concentrations using artificial diet for activity against *Leptinotarsa decemlineata*

Fifty µl of a solution of dsRNA at serial ten-fold concentrations from 1 µg/µl (for target LD027 from 0.1 µg/µl) down to 0.01 ng/µl was applied topically onto the solid artificial diet in the wells of a 24-well plate (Nunc). The diet was dried in a laminar flow cabin. Per treatment, twenty-four Colorado potato beetle larvae (2nd stage), with two insects per well, were tested. The plates were stored in the insect rearing chamber at 25 ± 2 °C, 60 % relative humidity, with a 16:8 hours light:dark photoperiod. The beetles were assessed as live or dead at regular intervals up to day 14. After seven days, the diet was replaced with fresh diet with topically applied dsRNA at the same concentrations. The dsRNA targets were compared to diet only.

Feeding artificial diet containing intact naked dsRNAs of different targets to *L. decemlineata* larvae resulted in high larval mortalities at concentrations as low as between 0.1 and 10 ng dsRNA/µl as shown in Figure 5-LD.

H. Adults are extremely susceptible to orally ingested dsRNA corresponding to target genes.

The example provided below highlights the finding that adult insects (and not only insects of the larval stage) are extremely susceptible to orally ingested dsRNA corresponding to target genes.

Four targets were chosen for this experiment: targets 2, 10, 14 and 16 (SEQ ID NO 168, 188, 198 and 220, respectively). GFP fragment dsRNA (SEQ ID NO 235) was used as a control. Young adults (2 to 3 days old) were picked at random from our laboratory-reared culture with no bias towards insect gender. Ten adults were chosen per treatment. The adults were prestarved for at least 6 hours before the onset of the treatment. On the first day of treatment, each adult was fed four potato leaf discs (diameter 1.5 cm²) which were pretreated with a topical application of 25 µl of 0.1 µg/µl target dsRNA (synthesized as described in Example 3A; topical application as described in Example 3E) per disc. Each adult was confined to a small petridish (diameter 3 cm) in order to make sure that all insects have ingested equal amounts of food and thus received equal doses of dsRNA. The following day, each adult was again fed four treated leaf discs as described above. On the third day, all ten adults per treatment were collected and placed together in a cage consisting of a plastic box (dimensions 30 cm x 20 cm x 15 cm) with a fine nylon mesh built into the lid to provide good aeration. Inside the box, some moistened filter paper was placed in the base. Some (untreated) potato foliage was placed on top of the paper to maintain the adults during the

experiment. From day 5, regular assessments were carried out to count the number of dead, alive (mobile) and moribund insects. For insect moribundity, adults were laid on their backs to check whether they could right themselves within several minutes; an insect was considered moribund only if it was not able to turn onto its front.

5 Clear specific toxic effects of double-stranded RNA corresponding to different targets towards adults of the Colorado potato beetle, *Leptinotarsa decemlineata*, were demonstrated in this experiment (Figure 6-LD). Double-stranded RNA corresponding to a gfp fragment showed no toxicity towards CPB adults on the day of the final assessment (day 19). This experiment clearly showed that the survival of CPB adults was severely reduced only after a few days of exposure to
10 dsRNA when delivered orally. For example, for target 10, on day 5, 5 out of 10 adults were moribund (sick and slow moving); on day 6, 4 out of 10 adults were dead with three of the survivors moribund; on day 9 all adults were observed dead.

As a consequence of this experiment, the application of target double-stranded RNAs against insect pests may be broadened to include the two life stages of an insect pest (i.e. larvae
15 and adults) which could cause extensive crop damage, as is the case with the Colorado potato beetle.

I. Laboratory trials to test transgenic potato plants against larvae of the Colorado potato beetle, *Leptinotarsa decemlineata*

The example provided below is an exemplification of the finding that transgenic potato
20 plants expressing CPB-gene-specific hairpin RNAs adversely affected Colorado potato beetles.

Potato transformation

Stably transformed potato plants were obtained using an adapted protocol received through Julie Gilbert at the NSF Potato Genome Project (<http://www.potatogenome.org/nsf5>). Stem internode explants of potato 'Line V' (obtained from the Laboratory of Plant Breeding at PRI
25 Wageningen, the Netherlands) which was derived from the susceptible diploid *Solanum tuberosum* 6487-9 were used as starting material for transformation.

In vitro derived explants were inoculated with *Agrobacterium tumefaciens* C58C₁Rif^R containing the hairpin constructs. After three days co-cultivation the explants were put onto a selective medium containing 100mg/l Kanamycin and 300mg/l Timentin. After 6 weeks post-
30 transformation the first putative shoots were removed and rooted on selective medium. Shoots originating from different explants were treated as independent events, shoots originating from the same callus were termed 'siblings' until their clonal status can be verified by Southern, and nodal cuttings of a shoot were referred to as 'clones'.

The transgenic status of the rooting shoots was checked either by GFP fluorescence or by
35 plus/minus PCR for the target sequence. Positive shoots were then clonally propagated in tissue culture to ensure enough replicates were available for the Colorado potato beetle assay with the first plants being available to test fourteen weeks post transformation.

Bioassay

Transgenic potato plants were grown to the 8-12 unfolded leaf stage in a plant growth room chamber with the following conditions: $23 \pm 2^{\circ}\text{C}$, 60 % relative humidity, 16:8 hour light:dark photoperiod. The plants were caged by placing a 500 ml bottle upside down over the plant with the neck of the bottle firmly placed in the soil in a pot and base cut open and covered with a fine nylon mesh to permit aeration, reduce condensation inside and prevent larval escape.

In this bioassay, seven neonate CPB larvae were placed on the foliage of each transgenic potato plant. Six transgenic potato siblings per transformation event (i.e. plants derived from one callus) of the hairpin construct LD002 (comprising SEQ ID NO 240) (labeled as pGBNB001/28A to F) and empty vector (labeled as pK7GWIWG2D(II)/11A to F), and two wild type plants were tested. Temperature, humidity and lighting conditions were the same as described above. At day 7 (7 days after the start of the bioassay), the number of survivors were counted and the average weight of larval survivors from each plant recorded. Data was analysed using the Spotfire® DecisionSite® 9.0 software (Version 17.1.779) from Spotfire Inc.

In this experiment, all larvae of the Colorado potato beetle on two sibling plants (labeled as pGBNB001/28A and pGBNB001/28F), harbouring hairpin construct LD002, generated from a single transformation event, were dead on day 7 (Figure 7-LD). Feeding damage by CPB larvae on these two plants was very low when compared to the empty vector transgenic plants or wild type line V plants.

Example 4: *Phaedon cochleariae* (mustard leaf beetle)

A. Cloning of a partial sequence of the *Phaedon cochleariae* (mustard leaf beetle) PC001, PC003, PC005, PC010, PC014, PC016 and PC027 genes via family PCR

High quality, intact RNA was isolated from the third larval stage of *Phaedon cochleariae* (mustard leaf beetle; source: Dr. Caroline Muller, Julius-von-Sachs-Institute for Biosciences, Chemical Ecology Group, University of Wuerzburg, Julius-von-Sachs-Platz 3, D-97082 Wuerzburg, Germany) using TRIzol Reagent (Cat. Nr. 15596-026/15596-018, Invitrogen, Rockville, Maryland, USA) following the manufacturer's instructions. Genomic DNA present in the RNA preparation was removed by DNase (Cat. Nr. 1700, Promega) treatment following the manufacturer's instructions. cDNA was generated using a commercially available kit (SuperScript™ III Reverse Transcriptase, Cat. Nr. 18080044, Invitrogen, Rockville, Maryland, USA) following the manufacturer's instructions.

To isolate cDNA sequences comprising a portion of the PC001, PC003, PC005, PC010, PC014, PC016 and PC027 genes, a series of PCR reactions with degenerate primers were performed using Amplitaq Gold (Cat. Nr. N8080240, Applied Biosystems) following the manufacturer's instructions.

The sequences of the degenerate primers used for amplification of each of the genes are given in Table 2-PC. These primers were used in respective PCR reactions with the following conditions: 10 minutes at 95°C , followed by 40 cycles of 30 seconds at 95°C , 1 minute at 55°C and 1 minute at 72°C , followed by 10 minutes at 72°C . The resulting PCR fragments were analyzed on agarose gel, purified (QIAquick Gel Extraction kit, Cat. Nr. 28706, Qiagen), cloned into the

pCR4/TOPO vector (Cat. Nr. K4530-20, Invitrogen) and sequenced. The sequences of the resulting PCR products are represented by the respective SEQ ID NOs as given in Table 2-PC and are referred to as the partial sequences.

The corresponding partial amino acid sequence are represented by the respective SEQ ID NOs as given in Table 3-PC. Table 3-PC provides amino acid sequences of cDNA clones, and the start of the reading frame is indicated in brackets.

B. dsRNA production of the *Phaedon cochleariae* genes

dsRNA was synthesized in milligram amounts using the commercially available kit T7 RibomaxTM Express RNAi System (Cat. Nr. P1700, Promega). First two separate single 5' T7 RNA polymerase promoter templates were generated in two separate PCR reactions, each reaction containing the target sequence in a different orientation relative to the T7 promoter.

For each of the target genes, the sense T7 template was generated using specific T7 forward and specific reverse primers. The sequences of the respective primers for amplifying the sense template for each of the target genes are given in Table 8-PC. Table 8-PC provides details for preparing ds RNA fragments of *Phaedon cochleariae* target sequences, including primer sequences.

The conditions in the PCR reactions were as follows: 1 minute at 95°C, followed by 20 cycles of 30 seconds at 95°C, 30 seconds at 60°C and 1 minute at 72°C, followed by 15 cycles of 30 seconds at 95°C, 30 seconds at 50°C and 1 minute at 72°C followed by 10 minutes at 72°C. The anti-sense T7 template was generated using specific forward and specific T7 reverse primers in a PCR reaction with the same conditions as described above. The sequences of the respective primers for amplifying the anti-sense template for each of the target genes are given in Table 8-PC. The resulting PCR products were analyzed on agarose gel and purified by PCR purification kit (Qiaquick PCR Purification Kit, Cat. Nr. 28106, Qiagen) and NaClO₄ precipitation. The generated T7 forward and reverse templates were mixed to be transcribed and the resulting RNA strands were annealed, DNase and RNase treated, and purified by sodium acetate, following the manufacturer's instructions. The sense strand of the resulting dsRNA for each of the target genes is given in Table 8-PC.

C. Recombination of the *Phaedon cochleariae* (mustard leaf beetle) genes into the plant vector pK7GWIWG2D(II)

Since the mechanism of RNA interference operates through dsRNA fragments, the target nucleotide sequences of the target genes, as selected above, were cloned in anti-sense and sense orientation, separated by the intron - CmR - intron, whereby CmR is the chloramphenicol resistance marker, to form a dsRNA hairpin construct. These hairpin constructs were generated using the LR recombination reaction between an attL- containing entry clone (see Example 4A) and an attR-containing destination vector (= pK7GWIWG2D(II)). The plant vector pK7GWIWG2D(II) was obtained from the VIB/Plant Systems Biology with a Material Transfer Agreement. LR recombination reaction was performed by using LR ClonaseTM II enzyme mix (Cat. Nr. 11791-020, Invitrogen) following the manufacturer's instructions. These cloning experiments resulted in a

hairpin construct for each of the PC001, PC010, PC014, PC016 and PC027 genes, having the promoter - sense - intron - CmR - intron - antisense orientation, and wherein the promoter is the plant operable 35S promoter. The binary vector pK7GWIWG2D(II) with the 35S promoter is suitable for transformation into *A. tumefaciens*.

5 Restriction enzyme digests were carried out on pCR8/GW/TOPO plasmids containing the different targets (see Example 4B): for PC001, a double digest with BsoBI & PvuI; for PC010, a double digest with PvuI & PvuII; for PC014, a triple digest with HincII, PvuI & XhoI; for PC016, a single digest with ApaLI; for PC027, a double digest with Aval & DrdI. The band containing the gene of interest flanked by the attL sites using Qiaquick Gel Extraction Kit (Cat. Nr. 28706, Qiagen)
 10 was purified. An amount of 150 ng of purified fragment and 150 ng pK7GWIWG2D(II) was added together with the LR clonase II enzyme and incubated for at least 1h at 25°C. After proteinase K solution treatment (10 min at 37°C), the whole recombination mix was transformed into Top 10 chemically competent cells. Positive clones were selected by restriction digest analyses. The complete sequence of the hairpin construct for:

- 15 - PC001 (sense - intron - CmR - intron - antisense) is represented in SEQ ID NO 508;
- PC010 (sense - intron - CmR - intron - antisense) is represented in SEQ ID NO 509;
- PC014 (sense - intron - CmR - intron - antisense) is represented in SEQ ID NO 510;
- PC016 (sense - intron - CmR - intron - antisense) is represented in SEQ ID NO 511;
- 20 - PC027 (sense - intron - CmR - intron - antisense) is represented in SEQ ID NO 512;

20

Table 9-PC provides sequences for each hairpin construct.

D. Laboratory trials to test dsRNA targets, using oilseed rape leaf discs for activity against *Phaedon cochleariae* larvae

The example provided below is an exemplification of the finding that the mustard leaf beetle (MLB) larvae are susceptible to orally ingested dsRNA corresponding to own target genes.
 25

To test the different double-stranded RNA samples against MLB larvae, a leaf disc assay was employed using oilseed rape (*Brassica napus* variety SW Oban; source: Nick Balaam, Sw Seed Ltd., 49 North Road, Abington, Cambridge, CB1 6AS, UK) leaf material as food source. The insect cultures were maintained on the same variety of oilseed rape in the insect chamber at 25 ± 2
 30 °C and 60 ± 5 % relative humidity with a photoperiod of 16h light/8h dark. Discs of approximately 1.1 cm in diameter (or 0.95 cm²) were cut out off leaves of 4- to 6-week old rape plants using a suitably-sized cork borer. Double-stranded RNA samples were diluted to 0.1 µg/µl in Milli-Q water containing 0.05% Triton X-100. Treated leaf discs were prepared by applying 25 µl of the diluted solution of target PC001, PC003, PC005, PC010, PC014, PC016, PC027 dsRNA and control gfp
 35 dsRNA or 0.05 % Triton X-100 on the adaxial leaf surface. The leaf discs were left to dry and placed individually in each of the 24 wells of a 24-well multiplate containing 1 ml of gellified 2% agar which helps to prevent the leaf disc from drying out. Two neonate MLB larvae were placed into each well of the plate, which was then covered with a multiwell plastic lid. The plate (one treatment containing 48 insects) was divided into 4 replicates of 12 insects per replicate (each row).

The plate containing the insects and leaf discs were kept in an insect chamber at 25 ± 2 °C and 60 ± 5 % relative humidity with a photoperiod of 16h light/8h dark. The insects were fed leaf discs for 2 days after which they were transferred to a new plate containing freshly treated leaf discs. Thereafter, 4 days after the start of the bioassay, the insects from each replicate were collected and transferred to a Petri dish containing untreated fresh oilseed rape leaves. Larval mortality and average weight were recorded at days 2, 4, 7, 9 and 11.

P. cochleariae larvae fed on intact naked target dsRNA-treated oilseed rape leaves resulted in significant increases in larval mortalities for all targets tested, as indicated in Figure 1(a). Tested double-stranded RNA for target PC010 led to 100 % larval mortality at day 9 and for target PC027 at day 11. For all other targets, significantly high mortality values were reached at day 11 when compared to control gfp dsRNA, 0.05% Triton X-100 alone or untreated leaf only: (average value in percentage \pm confidence interval with alpha 0.05) PC001 (94.4 ± 8.2); PC003 (86.1 ± 4.1); PC005 (83.3 ± 7.8); PC014 (63.9 ± 20.6); PC016 (75.0 ± 16.8); gfp dsRNA (11.1 ± 8.2); 0.05% Triton X-100 (19.4 ± 10.5); leaf only (8.3 ± 10.5).

Larval survivors were assessed based on their average weight. For all targets tested, the mustard leaf beetle larvae had significantly reduced average weights after day 4 of the bioassay; insects fed control gfp dsRNA or 0.05% Triton X-100 alone developed normally, as for the larvae on leaf only (Figure 1(b)-PC).

E. Laboratory trials to screen dsRNAs at different concentrations using oilseed rape leaf discs for activity against *Phaedon cochleariae* larvae

Twenty-five μ l of a solution of dsRNA from target PC010 or PC027 at serial ten-fold concentrations from 0.1 μ g/ μ l down to 0.1 ng/ μ l was applied topically onto the oilseed rape leaf disc, as described in Example 4D above. As a negative control, 0.05% Triton X-100 only was administered to the leaf disc. Per treatment, twenty-four mustard leaf beetle neonate larvae, with two insects per well, were tested. The plates were stored in the insect rearing chamber at 25 ± 2 °C, 60 ± 5 % relative humidity, with a 16:8 hours light:dark photoperiod. At day 2, the larvae were transferred on to a new plate containing fresh dsRNA-treated leaf discs. At day 4 for target PC010 and day 5 for target PC027, insects from each replicate were transferred to a Petri dish containing abundant untreated leaf material. The beetles were assessed as live or dead on days 2, 4, 7, 8, 9, and 11 for target PC010, and 2, 5, 8, 9 and 12 for target PC027.

Feeding oilseed rape leaf discs containing intact naked dsRNAs of the two different targets, PC010 and PC027, to *P. cochleariae* larvae resulted in high mortalities at concentrations down to as low as 1 ng dsRNA/ μ l solution, as shown in Figures 2 (a) and (b). Average mortality values in percentage \pm confidence interval with alpha 0.05 for different concentrations of dsRNA for target PC010 at day 11, 0 μ g/ μ l: 8.3 ± 9.4 ; 0.1 μ g/ μ l: 100; 0.01 μ g/ μ l: 79.2 ± 20.6 ; 0.001 μ g/ μ l: 58.3 ± 9.4 ; 0.0001 μ g/ μ l: 12.5 ± 15.6 ; and for target PC027 at day 12, 0 μ g/ μ l: 8.3 ± 9.4 ; 0.1 μ g/ μ l: 95.8 ± 8.2 ; 0.01 μ g/ μ l: 95.8 ± 8.2 ; 0.001 μ g/ μ l: 83.3 ± 13.3 ; 0.0001 μ g/ μ l: 12.5 ± 8.2 .

F. Laboratory trials of *Myzus persicae* (green peach aphid) infestation on transgenic *Arabidopsis thaliana* plants

Generation of transgenic plants

Arabidopsis thaliana plants were transformed using the floral dip method (Clough and Bent (1998) *Plant Journal* 16:735-743). Aerial parts of the plants were incubated for a few seconds in a solution containing 5% sucrose, resuspended *Agrobacterium tumefaciens* strain C58C1 Rif cells from an overnight culture and 0.03% of the surfactant Silwet L-77. After inoculation, plants were covered for 16 hours with a transparent plastic to maintain humidity. To increase the transformation efficiency, the procedure was repeated after one week. Watering was stopped as seeds matured and dry seeds were harvested and cold-treated for two days. After sterilization, seeds were plated on a kanamycin-containing growth medium for selection of transformed plants.

The selected plants are transferred to soil for optimal T2 seed production.

Bioassay

Transgenic *Arabidopsis thaliana* plants are selected by allowing the segregating T2 seeds to germinate on appropriate selection medium. When the roots of these transgenics are well-established they are then transferred to fresh artificial growth medium or soil and allowed to grow under optimal conditions. Whole transgenic plants are tested against nymphs of the green peach aphid (*Myzus persicae*) to show (1) a significant resistance to plant damage by the feeding nymph, (2) increased nymphal mortality, and/or (3) decreased weight of nymphal survivors (or any other aberrant insect development).

Example 5: *Epilachna varivetis* (Mexican bean beetle)

A. Cloning *Epilachna varivetis* partial gene sequences

High quality, intact RNA was isolated from 4 different larval stages of *Epilachna varivetis* (Mexican bean beetle; source: Thomas Dorsey, Supervising Entomologist, New Jersey Department of Agriculture, Division of Plant Industry, Bureau of Biological Pest Control, Phillip Alampi Beneficial Insect Laboratory, PO Box 330, Trenton, New Jersey 08625-0330, USA) using TRIzol Reagent (Cat. Nr. 15596-026/15596-018, Invitrogen, Rockville, Maryland, USA) following the manufacturer's instructions. Genomic DNA present in the RNA preparation was removed by DNase treatment following the manufacturer's instructions (Cat. Nr. 1700, Promega). cDNA was generated using a commercially available kit (SuperScript™ III Reverse Transcriptase, Cat. Nr. 18080044, Invitrogen, Rockville, Maryland, USA) following the manufacturer's instructions.

To isolate cDNA sequences comprising a portion of the EV005, EV009, EV010, EV015 and EV016 genes, a series of PCR reactions with degenerate primers were performed using Amplitaq Gold (Cat. Nr. N8080240, Applied Biosystems) following the manufacturer's instructions.

The sequences of the degenerate primers used for amplification of each of the genes are given in **Table 2-EV**, which displays *Epilachna varivetis* target genes including primer sequences and cDNA sequences obtained. These primers were used in respective PCR reactions with the following conditions: for EV005 and EV009, 10 minutes at 95°C, followed by 40 cycles of 30 seconds at 95°C, 1 minute at 50°C and 1 minute 30 seconds at 72°C, followed by 7 minutes at 72°C; for EV014, 10 minutes at 95°C, followed by 40 cycles of 30 seconds at 95°C, 1 minute at

53°C and 1 minute at 72°C, followed by 7 minutes at 72°C; for EV010 and EV016, 10 minutes at 95°C, followed by 40 cycles of 30 seconds at 95°C, 1 minute at 54°C and 1 minute 40 seconds at 72°C, followed by 7 minutes at 72°C. The resulting PCR fragments were analyzed on agarose gel, purified (QIAquick Gel Extraction kit, Cat. Nr. 28706, Qiagen), cloned into the pCR4/TOPO vector (Cat. Nr. K4530-20, Invitrogen), and sequenced. The sequences of the resulting PCR products are represented by the respective SEQ ID NOs as given in Table 2-EV and are referred to as the partial sequences. The corresponding partial amino acid sequences are represented by the respective SEQ ID NOs as given in Table 3-EV, where the start of the reading frame is indicated in brackets.

10 **B. dsRNA production of the *Epilachna varivetis* genes**

dsRNA was synthesized in milligram amounts using the commercially available kit T7 RibomaxTM Express RNAi System (Cat. Nr. P1700, Promega). First two separate single 5' T7 RNA polymerase promoter templates were generated in two separate PCR reactions, each reaction containing the target sequence in a different orientation relative to the T7 promoter.

15 For each of the target genes, the sense T7 template was generated using specific T7 forward and specific reverse primers. The sequences of the respective primers for amplifying the sense template for each of the target genes are given in Table 8-EV.

The conditions in the PCR reactions were as follows: 1 minute at 95°C, followed by 20 cycles of 30 seconds at 95°C, 30 seconds at 60°C and 1 minute at 72°C, followed by 15 cycles of 30 seconds at 95°C, 30 seconds at 50°C and 1 minute at 72°C followed by 10 minutes at 72°C. The anti-sense T7 template was generated using specific forward and specific T7 reverse primers in a PCR reaction with the same conditions as described above. The sequences of the respective primers for amplifying the anti-sense template for each of the target genes are given in Table 8-EV. The resulting PCR products were analyzed on agarose gel and purified by PCR purification kit (Qiaquick PCR Purification Kit, Cat. Nr. 28106, Qiagen) and NaClO₄ precipitation. The generated T7 forward and reverse templates were mixed to be transcribed and the resulting RNA strands were annealed, DNase and RNase treated, and purified by sodium acetate, following the manufacturer's instructions. The sense strand of the resulting dsRNA for each of the target genes is given in Table 8-EV.

30 **C. Recombination of the *Epilachna varivetis* genes into the plant vector pK7GWIWG2D(II)**

Since the mechanism of RNA interference operates through dsRNA fragments, the target nucleotide sequences of the target genes, as selected above, are cloned in anti-sense and sense orientation, separated by the intron - CmR - intron, whereby CmR is the chloramphenicol resistance marker, to form a dsRNA hairpin construct. These hairpin constructs are generated using the LR recombination reaction between an attL- containing entry clone (see Example 5A) and an attR-containing destination vector (= pK7GWIWG2D(II)). The plant vector pK7GWIWG2D(II) is obtained from the VIB/Plant Systems Biology with a Material Transfer Agreement. LR recombination reaction is performed by using LR ClonaseTM II enzyme mix (Cat. Nr. 11791-020, Invitrogen) following the

manufacturer's instructions. These cloning experiments result in a hairpin construct for each of the target genes, having the promoter - sense - intron - CmR - intron - antisense orientation, and wherein the promoter is the plant operable 35S promoter. The binary vector pK7GWIWG2D(II) with the 35S promoter is suitable for transformation into *A. tumefaciens*.

- 5 Restriction enzyme digests were carried out on pCR8/GW/TOPO plasmids containing the different targets (see Example B). The band containing the gene of interest flanked by the attL sites using Qiaquick Gel Extraction Kit (Cat. Nr. 28706, Qiagen) is purified. An amount of 150 ng of purified fragment and 150 ng pK7GWIWG2D(II) is added together with the LR clonase II enzyme and incubated for at least 1h at 25°C. After proteinase K solution treatment (10 min at 37°C), the whole recombination mix is transformed into Top 10 chemically competent cells. Positive clones are selected by restriction digest analyses.

D. Laboratory trials to test dsRNA targets using bean leaf discs for activity against *Epilachna varivestis* larvae

- 15 The example provided below is an exemplification of the finding that the Mexican bean beetle (MBB) larvae are susceptible to orally ingested dsRNA corresponding to own target genes.

- To test the different double-stranded RNA samples against MBB larvae, a leaf disc assay was employed using snap bean (*Phaseolus vulgaris* variety Montano; source: Aveve NV, Belgium) leaf material as food source. The same variety of beans was used to maintain insect cultures in the insect chamber at 25 ± 2 °C and 60 ± 5 % relative humidity with a photoperiod of 16h light/8h dark.
- 20 Discs of approximately 1.1 cm in diameter (or 0.95 cm²) were cut out off leaves of 1- to 2-week old bean plants using a suitably-sized cork borer. Double-stranded RNA samples were diluted to 1 µg/µl in Milli-Q water containing 0.05% Triton X-100. Treated leaf discs were prepared by applying 25 µl of the diluted solution of target Ev005, Ev010, Ev015, Ev016 dsRNA and control gfp dsRNA or 0.05 % Triton X-100 on the adaxial leaf surface. The leaf discs were left to dry and placed
- 25 individually in each of the 24 wells of a 24-well multiplate containing 1 ml of gellified 2 % agar which helps to prevent the leaf disc from drying out. A single neonate MBB larva was placed into each well of a plate, which was then covered with a multiwell plastic lid. The plate was divided into 3 replicates of 8 insects per replicate (row). The plate containing the insects and leaf discs were kept in an insect chamber at 25 ± 2 °C and 60 ± 5 % relative humidity with a photoperiod of 16h light/8h
- 30 dark. The insects were fed on the leaf discs for 2 days after which the insects were transferred to a new plate containing freshly treated leaf discs. Thereafter, 4 days after the start of the bioassay, the insects were transferred to a petriplate containing untreated fresh bean leaves every day until day 10. Insect mortality was recorded at day 2 and every other day thereafter.

- Feeding snap bean leaves containing surface-applied intact naked target dsRNAs to *E. varivestis* larvae resulted in significant increases in larval mortalities, as indicated in Figure 1.
- 35 Tested double-stranded RNAs of targets Ev010, Ev015, & Ev016 led to 100 % mortality after 8 days, whereas dsRNA of target Ev005 took 10 days to kill all larvae. The majority of the insects fed on treated leaf discs containing control gfp dsRNA or only the surfactant Triton X-100 were sustained throughout the bioassay (Figure 1-EV).

E. Laboratory trials to test dsRNA targets using bean leaf discs for activity against *Epilachna varivestis* adults

The example provided below is an exemplification of the finding that the Mexican bean beetle adults are susceptible to orally ingested dsRNA corresponding to own target genes.

5 In a similar bioassay set-up as for Mexican bean beetle larvae, adult MBBs were tested against double-stranded RNAs topically-applied to bean leaf discs. Test dsRNA from each target Ev010, Ev015 and Ev016 was diluted in 0.05 % Triton X-100 to a final concentration of 0.1 µg/µl. Bean leaf discs were treated by topical application of 30 µl of the test solution onto each disc. The discs were allowed to dry completely before placing each on a slice of gellified 2 % agar in each
10 well of a 24-well multiwell plate. Three-day-old adults were collected from the culture cages and fed nothing for 7-8 hours prior to placing one adult to each well of the bioassay plate (thus 24 adults per treatment). The plates were kept in the insect rearing chamber (under the same conditions as for MBB larvae for 24 hours) after which the adults were transferred to a new plate containing fresh dsRNA-treated leaf discs. After a further 24 hours, the adults from each treatment were collected
15 and placed in a plastic box with dimensions 30 cm x 15 cm x 10 cm containing two potted and untreated 3-week-old bean plants. Insect mortality was assessed from day 4 until day 11.

All three target dsRNAs (Ev010, Ev015 and Ev016) ingested by adults of *Epilachna varivestis* resulted in significant increases in mortality from day 4 (4 days post bioassay start), as shown in **Figure 2-EV(a)**. From day 5, dramatic changes in feeding patterns were observed
20 between insects fed initially with target-dsRNA-treated bean leaf discs and those that were fed discs containing control gfp dsRNA or surfactant Triton X-100. Reductions in foliar damage by MBB adults of untreated bean plants were clearly visible for all three targets when compared to gfp dsRNA and surfactant only controls, albeit at varying levels; insects fed target 15 caused the least damage to bean foliage (**Figure 2-EV(b)**).

25

Example 6: *Anthonomus grandis* (cotton boll weevil)

A. Cloning *Anthonomus grandis* partial sequences

High quality, intact RNA was isolated from the 3 instars of *Anthonomus grandis* (cotton boll weevil; source: Dr. Gary Benzon, Benzon Research Inc., 7 Kuhn Drive, Carlisle, Pennsylvania
30 17013, USA) using TRIzol Reagent (Cat. Nr. 15596-026/15596-018, Invitrogen, Rockville, Maryland, USA) following the manufacturer's instructions. Genomic DNA present in the RNA preparation was removed by DNase treatment following the manufacturer's instructions (Cat. Nr. 1700, Promega). cDNA was generated using a commercially available kit (SuperScript™ III Reverse Transcriptase, Cat. Nr. 18080044, Invitrogen, Rockville, Maryland, USA) following the
35 manufacturer's instructions.

To isolate cDNA sequences comprising a portion of the AG001, AG005, AG010, AG014 and AG016 genes, a series of PCR reactions with degenerate primers were performed using Amplitaq Gold (Cat. Nr. N8080240, Applied Biosystems) following the manufacturer's instructions.

The sequences of the degenerate primers used for amplification of each of the genes are given in **Table 2-AG**. These primers were used in respective PCR reactions with the following conditions: for AG001, AG005 and AG016, 10 minutes at 95°C, followed by 40 cycles of 30 seconds at 95°C, 1 minute at 50°C and 1 minute and 30 seconds at 72°C, followed by 7 minutes at 72°C; for AG010, 10 minutes at 95°C, followed by 40 cycles of 30 seconds at 95°C, 1 minute at 54°C and 2 minutes and 30 seconds at 72°C, followed by 7 minutes at 72°C; for AG014, 10 minutes at 95°C, followed by 40 cycles of 30 seconds at 95°C, 1 minute at 55°C and 1 minute at 72°C, followed by 7 minutes at 72°C. The resulting PCR fragments were analyzed on agarose gel, purified (QIAquick Gel Extraction kit, Cat. Nr. 28706, Qiagen), cloned into the pCR8/GW/TOPO vector (Cat. Nr. K2500-20, Invitrogen) and sequenced. The sequences of the resulting PCR products are represented by the respective SEQ ID NOs as given in **Table 2-AG** and are referred to as the partial sequences. The corresponding partial amino acid sequence are represented by the respective SEQ ID NOs as given in **Table 3-AG**.

B. dsRNA production of the *Anthonomus grandis* (cotton boll weevil) genes

dsRNA was synthesized in milligram amounts using the commercially available kit T7 RibomaxTM Express RNAi System (Cat. Nr. P1700, Promega). First two separate single 5' T7 RNA polymerase promoter templates were generated in two separate PCR reactions, each reaction containing the target sequence in a different orientation relative to the T7 promoter.

For each of the target genes, the sense T7 template was generated using specific T7 forward and specific reverse primers. The sequences of the respective primers for amplifying the sense template for each of the target genes are given in **Table 8-AG**. A touchdown PCR was performed as follows: 1 minute at 95°C, followed by 20 cycles of 30 seconds at 95°C, 30 seconds at 60°C with a decrease in temperature of 0.5°C per cycle and 1 minute at 72°C, followed by 15 cycles of 30 seconds at 95°C, 30 seconds at 50°C and 1 minute at 72°C, followed by 10 minutes at 72°C. The anti-sense T7 template was generated using specific forward and specific T7 reverse primers in a PCR reaction with the same conditions as described above. The sequences of the respective primers for amplifying the anti-sense template for each of the target genes are given in **Table 8-AG**. The resulting PCR products were analyzed on agarose gel and purified by PCR purification kit (Qiaquick PCR Purification Kit, Cat. Nr. 28106, Qiagen) and NaClO₄ precipitation. The generated T7 forward and reverse templates were mixed to be transcribed and the resulting RNA strands were annealed, DNase and RNase treated, and purified by sodium acetate, following the manufacturer's instructions. The sense strand of the resulting dsRNA for each of the target genes is given in **Table 8-AG**.

C. Recombination of *Anthonomus grandis* genes into the plant vector pK7GWIWG2D(II)

Since the mechanism of RNA interference operates through dsRNA fragments, the target nucleotide sequences of the target genes, as selected above, are cloned in anti-sense and sense orientation, separated by the intron - CmR - intron, whereby CmR is the chloramphenicol resistance marker, to form a dsRNA hairpin construct. These hairpin constructs are generated using the LR

recombination reaction between an attL- containing entry clone (see Example 6A) and an attR- containing destination vector (= pK7GWIWG2D(II)). The plant vector pK7GWIWG2D(II) is obtained from the VIB/Plant Systems Biology with a Material Transfer Agreement. LR recombination reaction is performed by using LR Clonase™ II enzyme mix (Cat. Nr. 11791-020, Invitrogen) following the manufacturer's instructions. These cloning experiments result in a hairpin construct for each of the target genes, having the promoter - sense - intron - CmR - intron - antisense orientation, and wherein the promoter is the plant operable 35S promoter. The binary vector pK7GWIWG2D(II) with the 35S promoter is suitable for transformation into *A. tumefaciens*.

Restriction enzyme digests were carried out on pCR8/GW/TOPO plasmids containing the different targets (see Example 6B). The band containing the gene of interest flanked by the attL sites using Qiaquick Gel Extraction Kit (Cat. Nr. 28706, Qiagen) is purified. An amount of 150 ng of purified fragment and 150 ng pK7GWIWG2D(II) is added together with the LR clonase II enzyme and incubated for at least 1h at 25°C . After proteinase K solution treatment (10 min at 37°C), the whole recombination mix is transformed into Top 10 chemically competent cells. Positive clones are selected by restriction digest analyses.

D. Laboratory trials to test *Escherichia coli* expressing dsRNA targets against *Anthonomus grandis*

Plant-based bioassays

Whole plants are sprayed with suspensions of chemically induced bacteria expressing dsRNA prior to feeding the plants to CBW. The are grown from in a plant growth room chamber. The plants are caged by placing a 500 ml plastic bottle upside down over the plant with the neck of the bottle firmly placed in the soil in a pot and the base cut open and covered with a fine nylon mesh to permit aeration; reduce condensation inside and prevent insect escape. CBW are placed on each treated plant in the cage. Plants are treated with a suspension of *E. coli* AB301-105(DE3) harboring the pGXXX0XX plasmids or pGN29 plasmid. Different quantities of bacteria are applied to the plants: for instance 66, 22, and 7 units, where one unit is defined as 10^9 bacterial cells in 1 ml of a bacterial suspension at optical density value of 1 at 600 nm wavelength. In each case, a total volume of between 1 and 10 ml s sprayed on the plant with the aid of a vaporizer. One plant is used per treatment in this trial. The number of survivors are counted and the weight of each survivor recorded.

Spraying plants with a suspension of *E. coli* bacterial strain AB301-105(DE3) expressing target dsRNA from pGXXX0XX lead to a dramatic increase in insect mortality when compared to pGN29 control. These experiments show that double-stranded RNA corresponding to an insect gene target sequence produced in either wild-type or RNaseIII-deficient bacterial expression systems is toxic towards the insect in terms of substantial increases in insect mortality and growth/development delay for larval survivors. It is also clear from these experiments that an exemplification is provided for the effective protection of plants/crops from insect damage by the use of a spray of a formulation consisting of bacteria expressing double-stranded RNA corresponding to an insect gene target.

Example 7: *Tribolium castaneum* (red flour beetle)**A. Cloning *Tribolium castaneum* partial sequences**

High quality, intact RNA was isolated from all the different insect stages of *Tribolium*
 5 *castaneum* (red flour beetle; source: Dr. Lara Senior, Insect Investigations Ltd., Capital Business
 Park, Wentloog, Cardiff, CF3 2PX, Wales, UK) using TRIzol Reagent (Cat. Nr. 15596-026/15596-
 018, Invitrogen, Rockville, Maryland, USA) following the manufacturer's instructions. Genomic DNA
 present in the RNA preparation was removed by DNase treatment following the manufacturer's
 instructions (Cat. Nr. 1700, Promega). cDNA was generated using a commercially available kit
 10 (SuperScript™ III Reverse Transcriptase, Cat. Nr. 18080044, Invitrogen, Rockville, Maryland,
 USA) following the manufacturer's instructions.

To isolate cDNA sequences comprising a portion of the TC001, TC002, TC010, TC014 and
 TC015 genes, a series of PCR reactions with degenerate primers were performed using Amplitaq
 Gold (Cat. Nr. N8080240, Applied Biosystems) following the manufacturer's instructions.

15 The sequences of the degenerate primers used for amplification of each of the genes are
 given in **Table 2-TC**. These primers were used in respective PCR reactions with the following
 conditions: 10 minutes at 95°C, followed by 40 cycles of 30 seconds at 95°C, 1 minute at 50°C and
 1 minute and 30 seconds at 72°C, followed by 7 minutes at 72°C (TC001, TC014, TC015); 10
 minutes at 95°C, followed by 40 cycles of 30 seconds at 95°C, 1 minute at 54°C and 2 minutes and
 20 30 seconds at 72°C, followed by 7 minutes at 72°C (TC010); 10 minutes at 95°C, followed by 40
 cycles of 30 seconds at 95°C, 1 minute at 53°C and 1 minute at 72°C, followed by 7 minutes at
 72°C (TC002). The resulting PCR fragments were analyzed on agarose gel, purified (QIAquick Gel
 Extraction kit, Cat. Nr. 28706, Qiagen), cloned into the pCR8/GW/TOPO vector (Cat. Nr. K2500-20,
 Invitrogen), and sequenced. The sequences of the resulting PCR products are represented by the
 25 respective SEQ ID NOs as given in **Table 2-TC** and are referred to as the partial sequences. The
 corresponding partial amino acid sequences are represented by the respective SEQ ID NOs as
 given in **Table 3-TC**.

B. dsRNA production of the *Tribolium castaneum* genes

dsRNA was synthesized in milligram amounts using the commercially available kit T7
 30 Ribomax™ Express RNAi System (Cat. Nr. P1700, Promega). First two separate single 5' T7 RNA
 polymerase promoter templates were generated in two separate PCR reactions, each reaction
 containing the target sequence in a different orientation relative to the T7 promoter.

For each of the target genes, the sense T7 template was generated using specific T7
 forward and specific reverse primers. The sequences of the respective primers for amplifying the
 35 sense template for each of the target genes are given in **Table 8-TC**. The conditions in the PCR
 reactions were as follows: 1 minute at 95°C, followed by 20 cycles of 30 seconds at 95°C, 30
 seconds at 60°C (-0.5°C/cycle) and 1 minute at 72°C, followed by 15 cycles of 30 seconds at 95°C,
 30 seconds at 50°C and 1 minute at 72°C, followed by 10 minutes at 72°C. The anti-sense T7
 template was generated using specific forward and specific T7 reverse primers in a PCR reaction

with the same conditions as described above. The sequences of the respective primers for amplifying the anti-sense template for each of the target genes are given in Table 8-TC. The resulting PCR products were analyzed on agarose gel and purified by PCR purification kit (Qiaquick PCR Purification Kit, Cat. Nr. 28106, Qiagen) and NaClO₄ precipitation. The generated T7 forward and reverse templates were mixed to be transcribed and the resulting RNA strands were annealed, DNase and RNase treated, and purified by sodium acetate, following the manufacturer's instructions. The sense strand of the resulting dsRNA for each of the target genes is given in Table 8-TC.

10 C. Recombination of *Tribolium castaneum* genes into the plant vector pK7GWIWG2D(II)

Since the mechanism of RNA interference operates through dsRNA fragments, the target nucleotide sequences of the target genes, as selected above, are cloned in anti-sense and sense orientation, separated by the intron - CmR - intron, whereby CmR is the chloramphenicol resistance marker, to form a dsRNA hairpin construct. These hairpin constructs are generated using the LR recombination reaction between an attL- containing entry clone (see Example 7A) and an attR- containing destination vector (= pK7GWIWG2D(II)). The plant vector pK7GWIWG2D(II) is obtained from the VIB/Plant Systems Biology with a Material Transfer Agreement. LR recombination reaction is performed by using LR Clonase™ II enzyme mix (Cat. Nr. 11791-020, Invitrogen) following the manufacturer's instructions. These cloning experiments result in a hairpin construct for each of the target genes, having the promoter - sense - intron - CmR - intron - antisense orientation, and wherein the promoter is the plant operable 35S promoter. The binary vector pK7GWIWG2D(II) with the 35S promoter is suitable for transformation into *A. tumefaciens*.

Restriction enzyme digests were carried out on pCR8/GW/TOPO plasmids containing the different targets (see Example 7B). The band containing the gene of interest flanked by the attL sites using Qiaquick Gel Extraction Kit (Cat. Nr. 28706, Qiagen) is purified. An amount of 150 ng of purified fragment and 150 ng pK7GWIWG2D(II) is added together with the LR clonase II enzyme and incubated for at least 1h at 25°C. After proteinase K solution treatment (10 min at 37°C), the whole recombination mix is transformed into Top 10 chemically competent cells. Positive clones are selected by restriction digest analyses.

30 D. Laboratory trials to test dsRNA targets, using artificial diet for activity against *Tribolium castaneum* larvae

The example provided below is an exemplification of the finding that the red flour beetle (RFB) larvae are susceptible to orally ingested dsRNA corresponding to own target genes.

Red flour beetles, *Tribolium castaneum*, were maintained at Insect Investigations Ltd. (origin: Imperial College of Science, Technology and Medicine, Silwood Park, Berkshire, UK). Insects were cultured according to company SOP/251/01. Briefly, the beetles were housed in plastic jars or tanks. These have an open top to allow ventilation. A piece of netting was fitted over the top and secured with an elastic band to prevent escape. The larval rearing medium (flour) was

placed in the container where the beetles can breed. The stored product beetle colonies were maintained in a controlled temperature room at $25 \pm 3^\circ\text{C}$ with a 16:8 hour light:dark cycle.

Double-stranded RNA from target TC014 (with sequence corresponding to SEQ ID NO - 799) was incorporated into a mixture of flour and milk powder (wholemeal flour: powdered milk in the ratio 4:1) and left to dry overnight. Each replicate was prepared separately: 100 μl of a 10 $\mu\text{g}/\mu\text{l}$ dsRNA solution (1 mg dsRNA) was added to 0.1 g flour/milk mixture. The dried mixture was ground to a fine powder. Insects were maintained within Petri dishes (55 mm diameter), lined with a double layer of filter paper. The treated diet was placed between the two filter paper layers. Ten first instar, mixed sex larvae were placed in each dish (replicate). Four replicates were performed for each treatment. Control was Milli-Q water. Assessments (number of survivors) were made on a regular basis. During the trial, the test conditions were $25 - 33^\circ\text{C}$ and 20 – 25 % relative humidity, with a 12:12 hour light:dark photoperiod.

Survival of larvae of *T. castaneum* over time on artificial diet treated with target TC014 dsRNA was significantly reduced when compared to diet only control, as shown in Figure 1-TC.

Example 8: *Myzus persicae* (green peach aphid)

A. Cloning *Myzus persicae* partial sequences

High quality, intact RNA was isolated from nymphs of *Myzus persicae* (green peach aphid; source: Dr. Rachel Down, Insect & Pathogen Interactions, Central Science Laboratory, Sand Hutton, York, YO41 1LZ, UK) using TRIzol Reagent (Cat. Nr. 15596-026/15596-018, Invitrogen, Rockville, Maryland, USA) following the manufacturer's instructions. Genomic DNA present in the RNA preparation was removed by DNase treatment following the manufacturer's instructions (Cat. Nr. 1700, Promega). cDNA was generated using a commercially available kit (SuperScriptTM III Reverse Transcriptase, Cat. Nr. 18080044, Invitrogen, Rockville, Maryland, USA) following the manufacturer's instructions.

To isolate cDNA sequences comprising a portion of the MP001, MP002, MP010, MP016 and MP027 genes, a series of PCR reactions with degenerate primers were performed using Amplitaq Gold (Cat. Nr. N8080240, Applied Biosystems) following the manufacturer's instructions.

The sequences of the degenerate primers used for amplification of each of the genes are given in Table 2-MP. These primers were used in respective PCR reactions with the following conditions: for MP001, MP002 and MP016, 10 minutes at 95°C , followed by 40 cycles of 30 seconds at 95°C , 1 minute at 50°C and 1 minute 30 seconds at 72°C , followed by 7 minutes at 72°C ; for MP027, a touchdown program was used: 10 minutes at 95°C , followed by 10 cycles of 30 seconds at 95°C , 40 seconds at 60°C with a decrease in temperature of 1°C per cycle and 1 minute 10 seconds at 72°C , followed by 30 cycles of 30 seconds at 95°C , 40 seconds at 50°C and 1 minute 10 seconds at 72°C , followed by 7 minutes at 72°C ; for MP010, 10 minutes at 95°C , followed by 40 cycles of 30 seconds at 95°C , 1 minute at 54°C and 3 minutes at 72°C , followed by 7 minutes at 72°C . The resulting PCR fragments were analyzed on agarose gel, purified (QIAquick Gel Extraction kit, Cat. Nr. 28706, Qiagen), cloned into the pCR8/GW/TOPO vector (Cat. Nr.

K2500-20, Invitrogen), and sequenced. The sequences of the resulting PCR products are represented by the respective SEQ ID NOs as given in **Table 2-MP** and are referred to as the partial sequences. The corresponding partial amino acid sequences are represented by the respective SEQ ID NOs as given in **Table 3-MP**.

5 **B. dsRNA production of *Myzus persicae* genes**

dsRNA was synthesized in milligram amounts using the commercially available kit T7 Ribomax™ Express RNAi System (Cat. Nr. P1700, Promega). First two separate single 5' T7 RNA polymerase promoter templates were generated in two separate PCR reactions, each reaction containing the target sequence in a different orientation relative to the T7 promoter.

10 For each of the target genes, the sense T7 template was generated using specific T7 forward and specific reverse primers. The sequences of the respective primers for amplifying the sense template for each of the target genes are given in **Table 8-MP**. A touchdown PCR was performed as follows: 1 minute at 95°C, followed by 20 cycles of 30 seconds at 95°C, 30 seconds at 55°C (for MP001, MP002, MP016, MP027 and gfp) or 30 seconds at 50°C (for MP010) with a
15 decrease in temperature of 0.5°C per cycle and 1 minute at 72°C, followed by 15 cycles of 30 seconds at 95°C, 30 seconds at 45°C and 1 minute at 72°C followed by 10 minutes at 72°C. The anti-sense T7 template was generated using specific forward and specific T7 reverse primers in a PCR reaction with the same conditions as described above. The sequences of the respective primers for amplifying the anti-sense template for each of the target genes are given in **Table 8-MP**.
20 The resulting PCR products were analyzed on agarose gel and purified by PCR purification kit (Qiaquick PCR Purification Kit, Cat. Nr. 28106, Qiagen) and NaClO₄ precipitation. The generated T7 forward and reverse templates were mixed to be transcribed and the resulting RNA strands were annealed, DNase and RNase treated, and purified by sodium acetate, following the manufacturer's instructions. The sense strand of the resulting dsRNA for each of the target genes
25 is given in **Table 8-MP**.

C. Recombination of *Myzus persicae* genes into the plant vector pK7GWIWG2D(II)

Since the mechanism of RNA interference operates through dsRNA fragments, the target nucleotide sequences of the target genes, as selected above, were cloned in anti-sense and sense orientation, separated by the intron - CmR - intron, whereby CmR is the chloramphenicol resistance
30 marker, to form a dsRNA hairpin construct. These hairpin constructs were generated using the LR recombination reaction between an attL- containing entry clone (see Example 8A) and an attR-containing destination vector (= pK7GWIWG2D(II)). The plant vector pK7GWIWG2D(II) was obtained from the VIB/Plant Systems Biology with a Material Transfer Agreement. LR recombination reaction was performed by using LR Clonase™ II enzyme mix (Cat. Nr. 11791-020,
35 Invitrogen) following the manufacturer's instructions. These cloning experiments resulted in a hairpin construct for each of the MP001, MP002, MP010, MP016 and MP026 genes, having the promoter - sense - intron - CmR - intron - antisense orientation and wherein the promoter is the plant operable 35S promoter. The binary vector pK7GWIWG2D(II) with the 35S promoter is suitable for transformation into *A. tumefaciens*.

A digest with restriction enzyme Alw44I was done for all the targets cloned into pCR8/GW/topo (see Example 8B). The band containing the gene of interest flanked by the attL sites using Qiaquick Gel Extraction Kit (Cat. Nr. 28706, Qiagen) was purified. An amount of 150 ng of purified fragment and 150 ng pK7GWIWG2D(II) was added together with the LR clonase II enzyme and incubated for at least 1h at 25°C. After proteinase K solution treatment (10 min at 37°C), the whole recombination mix was transformed into Top 10 chemically competent cells. Positive clones were selected by restriction digest analysis. The complete sequence of the hairpin construct for:

- MP001 (sense - intron - CmR - intron - antisense) is represented in SEQ ID NO 1066;
- MP002 (sense - intron - CmR - intron - antisense) is represented in SEQ ID NO 1067;
- MP010 (sense - intron - CmR - intron - antisense) is represented in SEQ ID NO 1068;
- MP016 (sense - intron - CmR - intron - antisense) is represented in SEQ ID NO 1069;
- MP027 (sense - intron - CmR - intron - antisense) is represented in SEQ ID NO 1070.

Table 9-MP provides complete sequences for each hairpin construct.

15 D. Laboratory trials to test dsRNA targets using liquid artificial diet for activity against *Myzus persicae*

Liquid artificial diet for the green peach aphid, *Myzus persicae*, was prepared based on the diet suitable for pea aphids (*Acyrtosiphon pisum*), as described by Febvay et al. (1988) [Influence of the amino acid balance on the improvement of an artificial diet for a biotype of *Acyrtosiphon pisum* (Homoptera: Aphididae). *Can. J. Zool.* 66: 2449–2453], but with some modifications. The amino acids component of the diet was prepared as follows: in mg/100ml, alanine 178.71, beta-alanine 6.22, arginine 244.9, asparagine 298.55, aspartic acid 88.25, cysteine 29.59, glutamic acid 149.36, glutamine 445.61, glycine 166.56, histidine 136.02, isoleucine 164.75, leucine 231.56, lysine hydrochloride 351.09, methionine 72.35, ornithine (HCl) 9.41, phenylalanine 293, proline 129.33, serine 124.28, threonine 127.16, tryptophane 42.75, tyrosine 38.63, L-valine 190.85. The amino acids were dissolved in 30 ml Milli-Q H₂O except for tyrosine which was first dissolved in a few drops of 1 M HCl before adding to the amino acid mix. The vitamin mix component of the diet was prepared as a 5 x concentrate stock as follows: in mg/L, amino benzoic acid 100, ascorbic acid 1000, biotin 1, calcium panthothenate 50, choline chloride 500, folic acid 10, myoinositol 420, nicotinic acid 100, pyridoxine hydrochloride 25, riboflavin 5, thiamine hydrochloride 25. The riboflavin was dissolved in 1 ml H₂O at 50 °C and then added to the vitamin mix stock. The vitamin mix was aliquoted in 20 ml per aliquot and stored at -20 °C. One aliquot of vitamin mix was added to the amino acid solution. Sucrose and MgSO₄·7H₂O was added with the following amounts to the mix: 20 g and 242 mg, respectively. Trace metal stock solution was prepared as follows: in mg/100ml, CuSO₄·5H₂O 4.7, FeCl₃·6H₂O 44.5, MnCl₂·4H₂O 6.5, NaCl 25.4, ZnCl₂ 8.3. Ten ml of the trace metal solution and 250 mg KH₂PO₄ was added to the diet and Milli-Q water was added to a final liquid diet volume of 100 ml. The pH of the diet was adjusted to 7 with 1 M KOH solution. The liquid diet was filter-sterilised through an 0.22 µm filter disc (Millipore).

Green peach aphids (*Myzus persicae*; source: Dr. Rachel Down, Insect & Pathogen Interactions, Central Science Laboratory, Sand Hutton, York, YO41 1LZ, UK) were reared on 4- to 6-week-old oilseed rape (*Brassica napus* variety SW Oban; source: Nick Balaam, Sw Seed Ltd., 49 North Road, Abington, Cambridge, CB1 6AS, UK) in aluminium-framed cages containing 70 µm mesh in a controlled environment chamber with the following conditions: 23 ±2 °C and 60 ±5 % relative humidity, with a 16:8 hours light:dark photoperiod.

One day prior to the start of the bioassay, adults were collected from the rearing cages and placed on fresh detached oilseed rape leaves in a Petri dish and left overnight in the insect chamber. The following day, first-instar nymphs were picked and transferred to feeding chambers. A feeding chamber comprised of 10 first instar nymphs placed in a small Petri dish (with diameter 3 cm) covered with a single layer of thinly stretched parafilm M onto which 50 µl of diet was added. The chamber was sealed with a second layer of parafilm and incubated under the same conditions as the adult cultures. Diet with dsRNA was refreshed every other day and the insects' survival assessed on day 8 i.e. 8th day post bioassay start. Per treatment, 5 bioassay feeding chambers (replicates) were set up simultaneously. Test and control (gfp) dsRNA solutions were incorporated into the diet to a final concentration of 2 µg/µl. The feeding chambers were kept at 23 ±2 °C and 60 ±5 % relative humidity, with a 16:8 hours light:dark photoperiod. A Mann-Whitney test was determined by GraphPad Prism version 4 to establish whether the medians do differ significantly between target 27 (MP027) and GFP dsRNA.

In the bioassay, feeding liquid artificial diet supplemented with intact naked dsRNA from target 27 (SEQ ID NO 1061) to nymphs of *Myzus persicae* using a feeding chamber, resulted in a significant increase in mortality, as shown in Figure 1. Average percentage survivors for target 27, GFP dsRNA and diet only treatment were 2, 34 and 82, respectively. Comparison of target 027 with GFP dsRNA groups using the Mann-Whitney test resulted in a one-tailed P-value of 0.004 which indicates that the median of target 027 is significantly different ($P < 0.05$) from the expected larger median of GFP dsRNA. The green peach aphids on the liquid diet with incorporated target 27 dsRNA were noticeably smaller than those that were fed on diet only or with GFP dsRNA control (data not presented).

E. Laboratory trials of *Myzus persicae* (green peach aphid) infestation on transgenic *Arabidopsis thaliana* plants

Generation of transgenic plants

Arabidopsis thaliana plants were transformed using the floral dip method (Clough and Bent (1998) *Plant Journal* 16:735-743). Aerial parts of the plants were incubated for a few seconds in a solution containing 5% sucrose, resuspended *Agrobacterium tumefaciens* strain C58C1 Rif cells from an overnight culture and 0.03% of the surfactant Silwet L-77. After inoculation, plants were covered for 16 hours with a transparent plastic to maintain humidity. To increase the transformation efficiency, the procedure was repeated after one week. Watering was stopped as seeds matured and dry seeds were harvested and cold-treated for two days. After sterilization, seeds were plated on a kanamycin-containing growth medium for selection of transformed plants.

The selected plants are transferred to soil for optimal T2 seed production.

Bioassay

Transgenic *Arabidopsis thaliana* plants are selected by allowing the segregating T2 seeds to germinate on appropriate selection medium. When the roots of these transgenics are well-established they are then transferred to fresh artificial growth medium or soil and allowed to grow under optimal conditions. Whole transgenic plants are tested against nymphs of the green peach aphid (*Myzus persicae*) to show (1) a significant resistance to plant damage by the feeding nymph, (2) increased nymphal mortality, and/or (3) decreased weight of nymphal survivors (or any other aberrant insect development).

Example 9: *Nilaparvata lugens* (Brown Plant Hopper)

A. Cloning *Nilaparvata lugens* partial sequences

From high quality total RNA of *Nilaparvata lugens* (source: Dr. J. A. Gatehouse, Dept. Biological Sciences, Durham University, UK) cDNA was generated using a commercially available kit (SuperScript™ III Reverse Transcriptase, Cat N°. 18080044, Invitrogen, Rockville, Maryland, USA) following the manufacturer's protocol.

To isolate cDNA sequences comprising a portion of the *Nilaparvata lugens* NL001, NL002, NL003, NL004, NL005, NL006, NL007, NL008, NL009, NL010, NL011, NL012, NL013, NL014, NL015, NL016, NL018, NL019, NL021, NL022, and NL027 genes, a series of PCR reactions with degenerate primers were performed using Amplitaq Gold (Cat N°. N8080240; Applied Biosystems) following the manufacturer's protocol.

The sequences of the degenerate primers used for amplification of each of the genes are given in Table 2-NL. These primers were used in respective PCR reactions with the following conditions: for NL001: 5 minutes at 95°C, followed by 40 cycles of 30 seconds at 95°C, 1 minute at 55°C and 1 minute at 72°C, followed by 10 minutes at 72°C; for NL002: 3 minutes at 95°C, followed by 40 cycles of 30 seconds at 95°C, 1 minute at 55°C and 1 minute at 72°C, followed by 10 minutes at 72°C; for NL003: 3 minutes at 95 °C, followed by 40 cycles of 30 seconds at 95 °C, 1 minute at 61 °C and 1 minute at 72 °C, followed by 10 minutes at 72°C; for NL004: 10 minutes at 95 °C, followed by 40 cycles of 30 seconds at 95 °C, 1 minute at 51 °C and 1 minute at 72 °C; for NL005: 10 minutes at 95 °C, followed by 40 cycles of 30 seconds at 95 °C, 1 minute at 54 °C and 1 minute at 72 °C, followed by 10 minutes at 72°C; for NL006: 10 minutes at 95 °C, followed by 40 cycles of 30 seconds at 95 °C, 1 minute at 55 °C and 3 minute 30 seconds at 72 °C, followed by 10 minutes at 72°C; for NL007: 10 minutes at 95 °C, followed by 40 cycles of 30 seconds at 95 °C, 1 minute at 54 °C and 1 minute 15 seconds at 72 °C, followed by 10 minutes at 72°C; for NL008 & NL014: 10 minutes at 95 °C, followed by 40 cycles of 30 seconds at 95 °C, 1 minute at 53 °C and 1 minute at 72 °C, followed by 10 minutes at 72°C; for NL009, NL011, NL012 & NL019: 10 minutes at 95 °C, followed by 40 cycles of 30 seconds at 95 °C, 1 minute at 55 °C and 1 minute at 72 °C, followed by 10 minutes at 72°C; for NL010: 10 minutes at 95 °C, followed by 40 cycles of 30 seconds at 95 °C, 1 minute at 54 °C and 2 minute 30 seconds at 72 °C, followed by 10 minutes at

72°C; for NL013: 10 minutes at 95 °C, followed by 40 cycles of 30 seconds at 95 °C, 1 minute at 54 °C and 1 minute 10 seconds at 72 °C, followed by 10 minutes at 72°C; for NL015 & NL016: 10 minutes at 95 °C, followed by 40 cycles of 30 seconds at 95 °C, 1 minute at 54 °C and 1 minute 40 seconds at 72 °C, followed by 10 minutes at 72°C; for NL018: 10 minutes at 95 °C, followed by 40 cycles of 30 seconds at 95 °C, 1 minute at 54 °C and 1 minute 35 seconds at 72 °C, followed by 10 minutes at 72°C; for NL021, NL022 & NL027: 10 minutes at 95 °C, followed by 40 cycles of 30 seconds at 95 °C, 1 minute at 54 °C and 1 minute 45 seconds at 72 °C, followed by 10 minutes at 72°C. The resulting PCR fragments were analyzed on agarose gel, purified (QIAquick Gel Extraction kit, Cat. Nr. 28706, Qiagen), cloned into the pCR8/GW/topo vector (Cat. Nr. K2500 20, Invitrogen), and sequenced. The sequences of the resulting PCR products are represented by the respective SEQ ID NOs as given in Table 2-NL and are referred to as the partial sequences. The corresponding partial amino acid sequences are represented by the respective SEQ ID NOs as given in Table 3-NL.

15 B. Cloning of a partial sequence of the *Nilaparvata lugens* NL023 gene via EST sequence

From high quality total RNA of *Nilaparvata lugens* (source: Dr. J. A. Gatehouse, Dept. Biological Sciences, Durham University, UK) cDNA was generated using a commercially available kit (SuperScript™ III Reverse Transcriptase, Cat N°. 18080044, Invitrogen, Rockville, Maryland, USA) following the manufacturer's protocol.

20 A partial cDNA sequence, NL023, was amplified from *Nilaparvata lugens* cDNA which corresponded to a *Nilaparvata lugens* EST sequence in the public database Genbank with accession number CAH65679.2. To isolate cDNA sequences comprising a portion of the NL023 gene, a series of PCR reactions with EST based specific primers were performed using PerfectShot™ ExTaq (Cat N°. RR005A, Takara Bio Inc.) following the manufacturer's protocol.

25 For NL023, the specific primers oGBKW002 and oGBKW003 (represented herein as SEQ ID NO 1157 and SEQ ID NO 1158, respectively) were used in two independent PCR reactions with the following conditions: 3 minutes at 95 °C, followed by 30 cycles of 30 seconds at 95 °C, 30 seconds at 56 °C and 2 minutes at 72 °C, followed by 10 minutes at 72°C. The resulting PCR products were analyzed on agarose gel, purified (QIAquick® Gel Extraction Kit; Cat. N°. 28706, Qiagen), cloned into the pCR4-TOPO vector (Cat N°. K4575-40, Invitrogen) and sequenced. The consensus sequence resulting from the sequencing of both PCR products is herein represented by SEQ ID NO 1111 and is referred to as the partial sequence of the NL023 gene. The corresponding partial amino acid sequence is herein represented as SEQ ID NO 1112.

35 C. dsRNA production of *Nilaparvata lugens* genes

dsRNA was synthesized in milligram amounts using the commercially available kit T7 Ribomax™ Express RNAi System (Cat. Nr. P1700, Promega). First two separate single 5' T7 RNA polymerase promoter templates were generated in two separate PCR reactions, each reaction containing the target sequence in a different orientation relative to the T7 promoter.

For each of the target genes, the sense T7 template was generated using specific T7 forward and specific reverse primers. The sequences of the respective primers for amplifying the sense template for each of the target genes are given in **Table 8-NL**. The conditions in the PCR reactions were as follows: for NL001 & NL002: 4 minutes at 94 °C, followed by 35 cycles of 30 seconds at 94 °C, 30 seconds at 60 °C and 1 minute at 72 °C, followed by 10 minutes at 72°C; for NL003: 4 minutes at 94 °C, followed by 35 cycles of 30 seconds at 94 °C, 30 seconds at 66 °C and 1 minute at 72 °C, followed by 10 minutes at 72°C; for NL004, NL006, NL008, NL009, NL010 & NL019: 4 minutes at 95 °C, followed by 35 cycles of 30 seconds at 95 °C, 30 seconds at 54 °C and 1 minute at 72 °C, followed by 10 minutes at 72°C; for NL005 & NL016: 4 minutes at 95 °C, followed by 35 cycles of 30 seconds at 95 °C, 30 seconds at 57 °C and 1 minute at 72 °C, followed by 10 minutes at 72°C; for NL007 & NL014: 4 minutes at 95 °C, followed by 35 cycles of 30 seconds at 95 °C, 30 seconds at 51 °C and 1 minute at 72 °C, followed by 10 minutes at 72°C; for NL011, NL012 & NL022: 4 minutes at 95 °C, followed by 35 cycles of 30 seconds at 95 °C, 30 seconds at 53 °C and 1 minute at 72 °C, followed by 10 minutes at 72°C; for NL013, NL015, NL018 & NL021: 4 minutes at 95 °C, followed by 35 cycles of 30 seconds at 95 °C, 30 seconds at 55 °C and 1 minute at 72 °C, followed by 10 minutes at 72°C; for NL023 & NL027: 4 minutes at 95 °C, followed by 35 cycles of 30 seconds at 95 °C, 30 seconds at 52 °C and 1 minute at 72 °C, followed by 10 minutes at 72°C. The anti-sense T7 template was generated using specific forward and specific T7 reverse primers in a PCR reaction with the same conditions as described above. The sequences of the respective primers for amplifying the anti-sense template for each of the target genes are given in **Table 8-NL**. The resulting PCR products were analyzed on agarose gel and purified by PCR purification kit (Qiaquick PCR Purification Kit, Cat. Nr. 28106, Qiagen). The generated T7 forward and reverse templates were mixed to be transcribed and the resulting RNA strands were annealed, DNase and RNase treated, and purified by sodium acetate, following the manufacturer's instructions, but with the following modification: RNA pepet is washed twice in 70% ethanol. The sense strand of the resulting dsRNA for each of the target genes is given in **Table 8-NL**.

The template DNA used for the PCR reactions with T7 primers on the green fluorescent protein (gfp) control was the plasmid pPD96.12 (the Fire Lab, <http://genome-www.stanford.edu/group/fire/>), which contains the wild-type gfp coding sequence interspersed by 3 synthetic introns. Double-stranded RNA was synthesized using the commercially available kit T7 RiboMAX™ Express RNAi System (Cat.N°. P1700, Promega). First two separate single 5' T7 RNA polymerase promoter templates were generated in two separate PCR reactions, each reaction containing the target sequence in a different orientation relative to the T7 promoter. For gfp, the sense T7 template was generated using the specific T7 FW primer oGAU183 and the specific RV primer oGAU182 (represented herein as SEQ ID NO 236 and SEQ ID NO 237 , respectively) in a PCR reaction with the following conditions: 4 minutes at 95 °C, followed by 35 cycles of 30 seconds at 95 °C, 30 seconds at 55 °C and 1 minute at 72 °C, followed by 10 minutes at 72°C. The anti-sense T7 template was generated using the specific FW primer oGAU181 and the specific T7 RV primer oGAU184 (represented herein as SEQ ID NO 238 and SEQ ID NO 239 , respectively) in a

PCR reaction with the same conditions as described above. The resulting PCR products were analyzed on agarose gel and purified (QIAquick® PCR Purification Kit; Cat. N°. 28106, Qiagen). The generated T7 FW and RV templates were mixed to be transcribed and the resulting RNA strands were annealed, DNase and RNase treated, and purified by precipitation with sodium acetate and isopropanol, following the manufacturer's protocol, but with the following modification: RNA prep is washed twice in 70% ethanol. The sense strands of the resulting dsRNA is herein represented by SEQ ID NO 235.

D. Laboratory trials to screen dsRNA targets using liquid artificial diet for activity against *Nilaparvata lugens*

Liquid artificial diet (MMD-1) for the rice brown planthopper, *Nilaparvata lugens*, was prepared as described by Koyama (1988) [Artificial rearing and nutritional physiology of the planthoppers and leafhoppers (Homoptera: Delphacidae and Deltocephalidae) on a holidic diet. JARQ 22: 20–27], but with a modification in final concentration of diet component sucrose: 14.4 % (weight over volume) was used. Diet components were prepared as separate concentrates: 10 x mineral stock (stored at 4 °C), 2 x amino acid stock (stored at -20 °C) and 10 x vitamin stock (stored at -20 °C). The stock components were mixed immediately prior to the start of a bioassay to 4/3 x concentration to allow dilution with the test dsRNA solution (4 x concentration), pH adjusted to 6.5, and filter-sterilised into approximately 500 µl aliquots.

Rice brown planthopper (*Nilaparvata lugens*) was reared on two-to-three month old rice (*Oryza sativa* cv Taichung Native 1) plants in a controlled environment chamber: 27 ± 2 °C, 80 % relative humidity, with a 16:8 hours light:dark photoperiod. A feeding chamber comprised 10 first or second instar nymphs placed in a small petri dish (with diameter 3 cm) covered with a single layer of thinly stretched parafilm M onto which 50 µl of diet was added. The chamber was sealed with a second layer of parafilm and incubated under the same conditions as the adult cultures but with no direct light exposure. Diet with dsRNA was refreshed every other day and the insects' survival assessed daily. Per treatment, 5 bioassay feeding chambers (replicates) were set up simultaneously. Test and control (gfp) dsRNA solutions were incorporated into the diet to a final concentration of 2 mg/ml. The feeding chambers were kept at 27 ± 2 °C, 80 % relative humidity, with a 16:8 hours light:dark photoperiod. Insect survival data were analysed using the Kaplan-Meier survival curve model and the survival between groups were compared using the logrank test (Prism version 4.0).

Feeding liquid artificial diet supplemented with intact naked dsRNAs to *Nilaparvata lugens* *in vitro* using a feeding chamber resulted in significant increases in nymphal mortalities as shown in four separate bioassays (Figures 1(a)-(d)-NL; Tables 10-NL(a)-(d)) (Durham University). These results demonstrate that dsRNAs corresponding to different essential BPH genes showed significant toxicity towards the rice brown planthopper.

Effect of gfp dsRNA on BPH survival in these bioassays is not significantly different to survival on diet only

Tables 10-NL(a)-(d) show a summary of the survival of *Nilaparvata lugens* on artificial diet supplemented with 2 mg/ml (final concentration) of the following targets; in Table 10-NL(a): NL002, NL003, NL005, NL010; in Table 10-NL(b): NL009, NL016; in Table 10-NL(c): NL014, NL018; and in Table 10-NL(d): NL013, NL015, NL021. In the survival analysis column, the effect of RNAi is indicated as follows: + = significantly decreased survival compared to gfp dsRNA control ($\alpha < 0.05$); - = no significant difference in survival compared to gfp dsRNA control. Survival curves were compared (between diet only and diet supplemented with test dsRNA, gfp dsRNA and test dsRNA, and diet only and gfp dsRNA) using the logrank test.

10 E. Laboratory trials to screen dsRNAs at different concentrations using artificial diet for activity against *Nilaparvata lugens*

Fifty μ l of liquid artificial diet supplemented with different concentrations of target NL002 dsRNA, namely 1, 0.2, 0.08, and 0.04 mg/ml (final concentration), was applied to the brown planthopper feeding chambers. Diet with dsRNA was refreshed every other day and the insects' survival assessed daily. Per treatment, 5 bioassay feeding chambers (replicates) were set up simultaneously. The feeding chambers were kept at 27 ± 2 °C, 80 % relative humidity, with a 16:8 hours light:dark photoperiod. Insect survival data were analysed using the Kaplan-Meier survival curve model and the survival between groups were compared using the logrank test (Prism version 4.0).

Feeding liquid artificial diet supplemented with intact naked dsRNAs of target NL002 at different concentrations resulted in significantly higher BPH mortalities at final concentrations of as low as 0.04 mg dsRNA per ml diet when compared with survival on diet only, as shown in Figure 2-NL and Table 11-NL. Table 11-NL summarizes the survival of *Nilaparvata lugens* artificial diet feeding trial supplemented with 1, 0.2, 0.08, & 0.04 mg/ml (final concentration) of target NL002. In the survival analysis column the effect of RNAi is indicated as follows: + = significantly decreases survival compared to diet only control ($\alpha < 0.05$); - = no significant differences in survival compared to diet only control. Survival curves were compared using the logrank test.

Example 10: *Chilo suppressalis* (rice striped stem borer)

30 A. Cloning of partial sequence of the *Chilo suppressalis* genes via family PCR

High quality, intact RNA was isolated from the 4 different larval stages of *Chilo suppressalis* (rice striped stem borer) using TRIzol Reagent (Cat. Nr. 15596-026/15596-018, Invitrogen, Rockville, Maryland, USA) following the manufacturer's instructions. Genomic DNA present in the RNA preparation was removed by DNase treatment following the manufacturer's instructions (Cat. Nr. 1700, Promega). cDNA was generated using a commercially available kit (SuperScriptTM III Reverse Transcriptase, Cat. Nr. 18080044, Invitrogen, Rockville, Maryland, USA) following the manufacturer's instructions.

To isolate cDNA sequences comprising a portion of the CS001, CS002, CS003, CS006, CS007, CS009, CS011, CS013, CS014, CS015, CS016 and CS018 genes, a series of PCR

reactions with degenerate primers were performed using Amplitaq Gold (Cat. Nr. N8080240, Applied Biosystems) following the manufacturer's instructions.

The sequences of the degenerate primers used for amplification of each of the genes are given in **Table 2-CS**. These primers were used in respective PCR reactions with the following conditions: 10 minutes at 95°C, followed by 40 cycles of 30 seconds at 95°C, 1 minute at 55°C and 1 minute at 72°C, followed by 10 minutes at 72°C. The resulting PCR fragments were analyzed on agarose gel, purified (QIAquick Gel Extraction kit, Cat. Nr. 28706, Qiagen), cloned into the pCR4/TOPO vector (Cat. Nr. K2500-20, Invitrogen), and sequenced. The sequences of the resulting PCR products are represented by the respective SEQ ID NOs as given in **Table 2-CS** and are referred to as the partial sequences. The corresponding partial amino acid sequences are represented by the respective SEQ ID NOs as given in **Table 3-CS**.

B. dsRNA production of the *Chilo suppressalis* genes

dsRNA was synthesized in milligram amounts using the commercially available kit T7 RibomaxTM Express RNAi System (Cat. Nr. P1700, Promega). First two separate single 5' T7 RNA polymerase promoter templates were generated in two separate PCR reactions, each reaction containing the target sequence in a different orientation relative to the T7 promoter.

For each of the target genes, the sense T7 template was generated using specific T7 forward and specific reverse primers. The sequences of the respective primers for amplifying the sense template for each of the target genes are given in **Table 8-CS**. The conditions in the PCR reactions were as follows: 4 minutes at 95°C, followed by 35 cycles of 30 seconds at 95°C, 30 seconds at 55°C and 1 minute at 72°C, followed by 10 minutes at 72°C. The anti-sense T7 template was generated using specific forward and specific T7 reverse primers in a PCR reaction with the same conditions as described above. The sequences of the respective primers for amplifying the anti-sense template for each of the target genes are given in **Table 8-CS**. The resulting PCR products were analyzed on agarose gel and purified by PCR purification kit (QIAquick PCR Purification Kit, Cat. Nr. 28106, Qiagen) and NaClO₄ precipitation. The generated T7 forward and reverse templates were mixed to be transcribed and the resulting RNA strands were annealed, DNase and RNase treated, and purified by sodium acetate, following the manufacturer's instructions. The sense strand of the resulting dsRNA for each of the target genes is given in **Table 8-CS**.

C. Recombination of the *Chilo suppressalis* genes into the plant vector pK7GWIWG2D(II)

Since the mechanism of RNA interference operates through dsRNA fragments, the target nucleotide sequences of the target genes, as selected above, are cloned in anti-sense and sense orientation, separated by the intron - CmR - intron, whereby CmR is the chloramphenicol resistance marker, to form a dsRNA hairpin construct. These hairpin constructs are generated using the LR recombination reaction between an attL- containing entry clone (see Example 10A) and an attR-containing destination vector (= pK7GWIWG2D(II)). The plant vector pK7GWIWG2D(II) is obtained from the VIB/Plant Systems Biology with a Material Transfer Agreement. LR recombination reaction

is performed by using LR Clonase™ II enzyme mix (Cat. Nr. 11791-020, Invitrogen) following the manufacturer's instructions. These cloning experiments result in a hairpin construct for each of the target genes, having the promoter - sense - intron - CmR - intron - antisense orientation, and wherein the promoter is the plant operable 35S promoter. The binary vector pK7GWIWG2D(II) with the 35S promoter is suitable for transformation into *A. tumefaciens*.

Restriction enzyme digests were carried out on pCR8/GW/TOPO plasmids containing the different targets (see Example 10B). The band containing the gene of interest flanked by the attL sites using Qiaquick Gel Extraction Kit (Cat. Nr. 28706, Qiagen) is purified. An amount of 150 ng of purified fragment and 150 ng pK7GWIWG2D(II) is added together with the LR clonase II enzyme and incubated for at least 1h at 25°C. After proteinase K solution treatment (10 min at 37°C), the whole recombination mix is transformed into Top 10 chemically competent cells. Positive clones are selected by restriction digest analyses.

D. Laboratory trials to test dsRNA targets, using artificial diet for activity against *Chilo suppressalis* larvae

Rice striped stem borers, *Chilo suppressalis*, (origin: Syngenta, Stein, Switzerland) were maintained on a modified artificial diet based on that described by Kamano and Sato, 1985 (in: Handbook of Insect Rearing. Volumes I & II. P Singh and RF Moore, eds., Elsevier Science Publishers, Amsterdam and New York, 1985, pp 448). Briefly, a litre diet was made up as follows: 20 g of agar added to 980 ml of Milli-Q water and autoclaved; the agar solution was cooled down to approximately 55 °C and the remaining ingredients were added and mixed thoroughly: 40 g corn flour (Polenta), 20 g cellulose, 30 g sucrose, 30 g casein, 20 g wheat germ (toasted), 8 g Wesson salt mixture, 12 g Vanderzant vitamin mix, 1.8 g sorbic acid, 1.6 g nipagin (methylparaben), 0.3 g aureomycin, 0.4 g cholesterol and 0.6 g L-cysteine. The diet was cooled down to approx. 45 °C and poured into rearing trays or cups. The diet was left to set in a horizontal laminar flow cabin. Rice leaf sections with oviposited eggs were removed from a cage housing adult moths and pinned to the solid diet in the rearing cup or tray. Eggs were left to hatch and neonate larvae were available for bioassays and the maintenance of the insect cultures. During the trials and rearings, the conditions were 28 ± 2 °C and 80 ± 5 % relative humidity, with a 16:8 hour light:dark photoperiod.

The same artificial diet is used for the bioassays but in this case the diet is poured equally in 24 multiwell plates, with each well containing 1 ml diet. Once the diet is set, the test formulations are applied to the diet's surface (2 cm²), at the rate of 50 µl of 1 µg/µl dsRNA of target. The dsRNA solutions are left to dry and two first instar moth larvae are placed in each well. After 7 days, the larvae are transferred to fresh treated diet in multiwell plates. At day 14 (i.e. 14 days post bioassay start) the number of live and dead insects is recorded and examined for abnormalities. Twenty-four larvae in total are tested per treatment.

An alternative bioassay is performed in which treated rice leaves are fed to neonate larvae of the rice striped stem borer. Small leaf sections of *Indica* rice variety Taichung native 1 are dipped in 0.05 % Triton X-100 solution containing 1 µg/µl of target dsRNA, left to dry and each section placed in a well of a 24 multiwell plate containing gellified 2 % agar. Two neonates are transferred

from the rearing tray to each dsRNA treated leaf section (24 larvae per treatment). After 4 and 8 days, the larvae are transferred to fresh treated rice leaf sections. The number of live and dead larvae are assessed on days 4, 8 and 12; any abnormalities are also recorded.

5 **Example 11: *Plutella xylostella* (Diamondback moth)**

A. Cloning of a partial sequence of the *Plutella xylostella*

High quality, intact RNA was isolated from all the different larval stages of *Plutella xylostella* (Diamondback moth; source: Dr. Lara Senior, Insect Investigations Ltd., Capital Business Park, Wentloog, Cardiff, CF3 2PX, Wales, UK) using TRIzol Reagent (Cat. Nr. 15596-026/15596-018, Invitrogen, Rockville, Maryland, USA) following the manufacturer's instructions. Genomic DNA present in the RNA preparation was removed by DNase treatment following the manufacturer's instructions (Cat. Nr. 1700, Promega). cDNA was generated using a commercially available kit (SuperScript™ III Reverse Transcriptase, Cat. Nr. 18080044, Invitrogen, Rockville, Maryland, USA) following the manufacturer's instructions.

15 To isolate cDNA sequences comprising a portion of the PX001, PX009, PX010, PX015, PX016 genes, a series of PCR reactions with degenerate primers were performed using Amplitaq Gold (Cat. Nr. N8080240, Applied Biosystems) following the manufacturer's instructions.

The sequences of the degenerate primers used for amplification of each of the genes are given in **Table 2-PX**. These primers were used in respective PCR reactions with the following conditions: 10 minutes at 95°C, followed by 40 cycles of 30 seconds at 95°C, 1 minute at 50°C and 1 minute and 30 seconds at 72°C, followed by 7 minutes at 72°C (for PX001, PX009, PX015, PX016); 10 minutes at 95°C, followed by 40 cycles of 30 seconds at 95°C, 1 minute at 54°C and 2 minute and 30 seconds at 72°C, followed by 7 minutes at 72°C (for PX010). The resulting PCR fragments were analyzed on agarose gel, purified (QIAquick Gel Extraction kit, Cat. Nr. 28706, Qiagen), cloned into the pCR8/GW/TOPO vector (Cat. Nr. K2500-20, Invitrogen) and sequenced. The sequences of the resulting PCR products are represented by the respective SEQ ID NOs as given in **Table 2-PX** and are referred to as the partial sequences. The corresponding partial amino acid sequence are represented by the respective SEQ ID NOs as given in **Table 3-PX**.

B. dsRNA production of the *Plutella xylostella* genes

30 dsRNA was synthesized in milligram amounts using the commercially available kit T7 Ribomax™ Express RNAi System (Cat. Nr. P1700, Promega). First two separate single 5' T7 RNA polymerase promoter templates were generated in two separate PCR reactions, each reaction containing the target sequence in a different orientation relative to the T7 promoter.

35 For each of the target genes, the sense T7 template was generated using specific T7 forward and specific reverse primers. The sequences of the respective primers for amplifying the sense template for each of the target genes are given in **Table 8-PX**. The conditions in the PCR reactions were as follows: 1 minute at 95°C, followed by 20 cycles of 30 seconds at 95°C, 30 seconds at 60°C (-0.5°C/cycle) and 1 minute at 72°C, followed by 15 cycles of 30 seconds at 95°C, 30 seconds at 50°C and 1 minute at 72°C, followed by 10 minutes at 72°C. The anti-sense T7

template was generated using specific forward and specific T7 reverse primers in a PCR reaction with the same conditions as described above. The sequences of the respective primers for amplifying the anti-sense template for each of the target genes are given in Table 8-PX. The resulting PCR products were analyzed on agarose gel and purified by PCR purification kit (Qiaquick PCR Purification Kit, Cat. Nr. 28106, Qiagen) and NaClO₄ precipitation. The generated T7 forward and reverse templates were mixed to be transcribed and the resulting RNA strands were annealed, DNase and RNase treated, and purified by sodium acetate, following the manufacturer's instructions. The sense strand of the resulting dsRNA for each of the target genes is given in Table 8-PX.

10 C. Recombination of the *Plutella xylostella* genes into the plant vector pK7GWIWG2D(II)

Since the mechanism of RNA interference operates through dsRNA fragments, the target nucleotide sequences of the target genes, as selected above, are cloned in anti-sense and sense orientation, separated by the intron - CmR - intron, whereby CmR is the chloramphenicol resistance marker, to form a dsRNA hairpin construct. These hairpin constructs are generated using the LR recombination reaction between an attL- containing entry clone (see Example 11A) and an attR- containing destination vector (= pK7GWIWG2D(II)). The plant vector pK7GWIWG2D(II) is obtained from the VIB/Plant Systems Biology with a Material Transfer Agreement. LR recombination reaction is performed by using LR ClonaseTM II enzyme mix (Cat. Nr. 11791-020, Invitrogen) following the manufacturer's instructions. These cloning experiments result in a hairpin construct for each of the target genes, having the promoter - sense - intron - CmR - intron - antisense orientation, and wherein the promoter is the plant operable 35S promoter. The binary vector pK7GWIWG2D(II) with the 35S promoter is suitable for transformation into *A. tumefaciens*.

Restriction enzyme digests were carried out on pCR8/GW/TOPO plasmids containing the different targets (see Example 11B). The band containing the gene of interest flanked by the attL sites using Qiaquick Gel Extraction Kit (Cat. Nr. 28706, Qiagen) is purified. An amount of 150 ng of purified fragment and 150 ng pK7GWIWG2D(II) is added together with the LR clonase II enzyme and incubated for at least 1h at 25°C. After proteinase K solution treatment (10 min at 37°C), the whole recombination mix is transformed into Top 10 chemically competent cells. Positive clones are selected by restriction digest analyses.

25 D. Laboratory trials to test dsRNA targets, using artificial diet for activity against *Plutella xylostella* larvae

Diamond-back moths, *Plutella xylostella*, were maintained at Insect Investigations Ltd. (origin: Newcastle University, Newcastle-upon-Tyne, UK). The insects were reared on cabbage leaves. First instar, mixed sex larvae (approximately 1 day old) were selected for use in the trial. Insects were maintained in Eppendorf tubes (1.5 ml capacity). Commercially available Diamond-back moth diet (Bio-Serv, NJ, USA), prepared following the manufacturer's instructions, was placed in the lid of each tube (0.25 ml capacity, 8 mm diameter). While still liquid, the diet was smoother over to remove excess and produce an even surface.

Once the diet has set the test formulations are applied to the diet's surface, at the rate of 25 µl undiluted formulation (1 µg/µl dsRNA of targets) per replicate. The test formulations are allowed to dry and one first instar moth larva is placed in each tube. The larva is placed on the surface of the diet in the lid and the tube carefully closed. The tubes are stored upside down, on their lids such that each larva remains on the surface of the diet. Twice weekly the larvae are transferred to new Eppendorf tubes with fresh diet. The insects are provided with treated diet for the first two weeks of the trial and thereafter with untreated diet.

Assessments are made twice weekly for a total of 38 days at which point all larvae are dead. At each assessment the insects are assessed as live or dead and examined for abnormalities. Forty single larva replicates are performed for each of the treatments. During the trial the test conditions are 23 to 26 °C and 50 to 65 % relative humidity, with a 16:8 hour light:dark photoperiod.

Example 12: *Acheta domesticus* (house cricket)

A. Cloning *Acheta domesticus* partial sequences

High quality, intact RNA was isolated from all the different insect stages of *Acheta domesticus* (house cricket; source: Dr. Lara Senior, Insect Investigations Ltd., Capital Business Park, Wentloog, Cardiff, CF3 2PX, Wales, UK) using TRIzol Reagent (Cat. Nr. 15596-026/15596-018, Invitrogen, Rockville, Maryland, USA) following the manufacturer's instructions. Genomic DNA present in the RNA preparation was removed by DNase treatment following the manufacturer's instructions (Cat. Nr. 1700, Promega). cDNA was generated using a commercially available kit (SuperScript™ III Reverse Transcriptase, Cat. Nr. 18080044, Invitrogen, Rockville, Maryland, USA) following the manufacturer's instructions.

To isolate cDNA sequences comprising a portion of the AD001, AD002, AD009, AD015 and AD016 genes, a series of PCR reactions with degenerate primers were performed using Amplitaq Gold (Cat. Nr. N8080240, Applied Biosystems) following the manufacturer's instructions.

The sequences of the degenerate primers used for amplification of each of the genes are given in **Table 2-AD**. These primers were used in respective PCR reactions with the following conditions: 10 minutes at 95°C, followed by 40 cycles of 30 seconds at 95°C, 1 minute at 50°C and 1 minute and 30 seconds at 72°C, followed by 7 minutes at 72°C. The resulting PCR fragments were analyzed on agarose gel, purified (QIAquick Gel Extraction kit, Cat. Nr. 28706, Qiagen), cloned into the pCR8/GW/topo vector (Cat. Nr. K2500 20, Invitrogen) and sequenced. The sequences of the resulting PCR products are represented by the respective SEQ ID NOs as given in **Table 2-AD** and are referred to as the partial sequences. The corresponding partial amino acid sequence are represented by the respective SEQ ID NOs as given in **Table 3-AD**.

B. dsRNA production of the *Acheta domesticus* genes

dsRNA was synthesized in milligram amounts using the commercially available kit T7 Ribomax™ Express RNAi System (Cat. Nr. P1700, Promega). First two separate single 5' T7 RNA polymerase promoter templates were generated in two separate PCR reactions, each reaction containing the target sequence in a different orientation relative to the T7 promoter.

5 For each of the target genes, the sense T7 template was generated using specific T7 forward and specific reverse primers. The sequences of the respective primers for amplifying the sense template for each of the target genes are given in Table 8-AD. The conditions in the PCR reactions were as follows: 1 minute at 95°C, followed by 20 cycles of 30 seconds at 95°C, 30 seconds at 60°C (-0.5°C/cycle) and 1 minute at 72°C, followed by 15 cycles of 30 seconds at 95°C, 10 30 seconds at 50°C and 1 minute at 72°C, followed by 10 minutes at 72°C. The anti-sense T7 template was generated using specific forward and specific T7 reverse primers in a PCR reaction with the same conditions as described above. The sequences of the respective primers for amplifying the anti-sense template for each of the target genes are given in Table 8-AD. The resulting PCR products were analyzed on agarose gel and purified by PCR purification kit 15 (Qiaquick PCR Purification Kit, Cat. Nr. 28106, Qiagen) and NaClO₄ precipitation. The generated T7 forward and reverse templates were mixed to be transcribed and the resulting RNA strands were annealed, DNase and RNase treated, and purified by sodium acetate, following the manufacturer's instructions. The sense strand of the resulting dsRNA for each of the target genes is given in Table 8-AD.

20 C. Recombination of the *Acheta domesticus* genes into the plant vector pK7GWIWG2D(II)

Since the mechanism of RNA interference operates through dsRNA fragments, the target nucleotide sequences of the target genes, as selected above, are cloned in anti-sense and sense orientation, separated by the intron - CmR - intron, whereby CmR is the chloramphenicol resistance marker, to form a dsRNA hairpin construct. These hairpin constructs are generated using the LR 25 recombination reaction between an attL- containing entry clone (see Example 12A) and an attR-containing destination vector (= pK7GWIWG2D(II)). The plant vector pK7GWIWG2D(II) is obtained from the VIB/Plant Systems Biology with a Material Transfer Agreement. LR recombination reaction is performed by using LR Clonase™ II enzyme mix (Cat. Nr. 11791-020, Invitrogen) following the 30 manufacturer's instructions. These cloning experiments result in a hairpin construct for each of the target genes, having the promoter - sense - intron - CmR - intron - antisense orientation, and wherein the promoter is the plant operable 35S promoter. The binary vector pK7GWIWG2D(II) with the 35S promoter is suitable for transformation into *A. tumefaciens*.

35 Restriction enzyme digests were carried out on pCR8/GW/TOPO plasmids containing the different targets (see Example 12B). The band containing the gene of interest flanked by the attL sites using Qiaquick Gel Extraction Kit (Cat. Nr. 28706, Qiagen) is purified. An amount of 150 ng of purified fragment and 150 ng pK7GWIWG2D(II) is added together with the LR clonase II enzyme and incubated for at least 1h at 25°C. After proteinase K solution treatment (10 min at 37°C), the

whole recombination mix is transformed into Top 10 chemically competent cells. Positive clones are selected by restriction digest analyses.

D. Laboratory trials to test dsRNA targets, using artificial diet for activity against *Acheta domesticus* larvae

5 House crickets, *Acheta domesticus*, were maintained at Insect Investigations Ltd. (origin: Blades Biological Ltd., Kent, UK). The insects were reared on bran pellets and cabbage leaves. Mixed sex nymphs of equal size and no more than 5 days old were selected for use in the trial. Double-stranded RNA is mixed with a wheat-based pelleted rodent diet (rat and mouse standard diet, B & K Universal Ltd., Grimston, Aldbrough, Hull, UK). The diet, BK001P, contains the following
10 ingredients in descending order by weight: wheat, soya, wheatfeed, barley, pellet binder, rodent 5 vit min, fat blend, dicalcium phosphate, mould carb. The pelleted rodent diet is finely ground and heat-treated in a microwave oven prior to mixing, in order to inactivate any enzyme components. All rodent diet is taken from the same batch in order to ensure consistency. The ground diet and dsRNA are mixed thoroughly and formed into small pellets of equal weight, which are allowed to
15 dry overnight at room temperature.

Double-stranded RNA samples from targets and gfp control at concentrations 10 µg/µl were applied in the ratio 1 g ground diet plus 1 ml dsRNA solution, thereby resulting in an application rate of 10 mg dsRNA per g pellet. Pellets are replaced weekly. The insects are provided with treated pellets for the first three weeks of the trial. Thereafter untreated pellets are provided.
20 Insects are maintained within lidded plastic containers (9 cm diameter, 4.5 cm deep), ten per container. Each arena contains one treated bait pellet and one water source (damp cotton wool ball), each placed in a separate small weigh boat. The water is replenished *ad lib* throughout the experiment.

Assessments are made at twice weekly intervals, with no more than four days between
25 assessments, until all the control insects had either died or moulted to the adult stage (84 days). At each assessment the insects are assessed as live or dead, and examined for abnormalities. From day 46 onwards, once moulting to adult has commenced, all insects (live and dead) are assessed as nymph or adult. Surviving insects are weighed on day 55 of the trial. Four replicates are performed for each of the treatments. During the trial the test conditions are 25 to 33 °C and 20 to
30 25 % relative humidity, with a 12:12 hour light:dark photoperiod.

Table 1A

C. elegans id	D. melanogaster id	description	devgen RNAi screen
B0250.1	CG1263	large ribosomal subunit L8 protein.	Acute lethal or lethal
B0336.10	CG3661	large ribosomal subunit L23 protein.	Acute lethal or lethal
B0336.2	CG8385	ADP-ribosylation factor	Acute lethal or lethal
B0464.1	CG3821	Putative aspartyl(D) tRNA synthetase.	Acute lethal or lethal
C01G8.5	CG10701	Ortholog of the ERM family of cytoskeletal linkers	Acute lethal or lethal
C01H6.5	CG33183	Nuclear hormone receptor that is required in all larval molts	Acute lethal or lethal
C02C6.1	CG18102	Member of the DYNamin related gene class	Acute lethal or lethal
C03D6.8	CG6764	Large ribosomal subunit L24 protein (Rlp24p)	Acute lethal or lethal
C04F12.4	CG6253	rpl-14 encodes a large ribosomal subunit L14 protein.	Acute lethal or lethal
C04H5.6	CG10689	Product with RNA helicase activity (EC:2.7.7.-) involved in nuclear mRNA splicing, via spliceosome which is a component of the spliceosome complex	Embryonic lethal or sterile
C13B9.3	CG14813	Delta subunit of the coatomer (COPI) complex	Acute lethal or lethal
C17H12.14	CG1088	Member of the Vacuolar H ATPase gene class	Acute lethal or lethal
C26E6.4	CG3180	DNA-directed RNA polymerase II	Acute lethal or lethal
F23F12.6	CG16916	Triple A ATPase subunit of the 26S proteasome's 19S regulatory particle (RP) base subcomplex	Acute lethal or lethal
F57B9.10	CG10149	Member of the proteasome Regulatory Particle, Non-ATPase-like gene class	Acute lethal or lethal
K11D9.2	CG3725	sarco-endoplasmic reticulum Ca[2+] ATPase homolog	Embryonic lethal or sterile
T20G5.1	CG9012	Clathrin heavy chain	Acute lethal or lethal
T20H4.3	CG5394	Predicted cytoplasmic prolyl-tRNA synthetase (ProRS)	Acute lethal or lethal
T21E12.4	CG7507	Cytoplasmic dynein heavy chain homolog	Acute lethal or lethal
C05C10.3	CG1140	Orthologue to the human gene 3-OXOACID COA TRANSFERASE	Acute lethal or lethal
C09D4.5	CG2746	Ribosomal protein L19, structural constituent of ribosome involved in protein biosynthesis which is localised to the ribosome	Acute lethal or lethal
C09E10.2	CG31140	Orthologue of diacylglycerol kinase involved in movement, egg laying, and synaptic transmission, and is expressed in neurons.	Acute lethal or lethal
C13B9.3	CG14813	Delta subunit of the coatomer (COPI)	Acute lethal or lethal

C14B9.7	CG12775	Large ribosomal subunit L21 protein (RPL-21) involved in protein biosynthesis	Acute lethal or lethal
C15H11.7	CG30382	Type 6 alpha subunit of the 26S proteasome's 20S protease core particle (CP)	Acute lethal or lethal
C17E4.9	CG9261	Protein involved with Na ⁺ /K ⁺ - exchanging ATPase complex	Embryonic lethal or sterile
C17H12.14	CG1088	V-ATPase E subunit	Acute lethal or lethal
C23G10.4	CG11888	Non-ATPase subunit of the 26S proteasome's 19S regulatory particle base subcomplex (RPN-2)	Acute lethal or lethal
C26D10.2	CG7269	Product with helicase activity involved in nuclear mRNA splicing, via spliceosome which is localized to the nucleus	Acute lethal or lethal
C26E6.4	CG3180	RNA polymerase II 140kD subunit (Rpl140), DNA-directed RNA polymerase activity (EC:2.7.7.6) involved in transcription from Pol II promoter which is a component of the DNA-directed RNA polymerase II, core complex	Acute lethal or lethal
C26F1.4	CG15697	Product with function in protein biosynthesis and ubiquitin in protein degradation.	Acute lethal or lethal
C30C11.1	CG12220	Unknown function	Acute lethal or lethal
C30C11.2	CG10484	Member of the proteasome Regulatory Particle, Non-ATPase-like gene class	Acute lethal or lethal
C36A4.2	CG13977	cytochrome P450	Acute lethal or lethal
C37C3.6	CG33103	Orthologous to thrombospondin, papilin and lacunin	Acute lethal or lethal
C37H5.8	CG8542	Member of the Heat Shock Protein gene class	Acute lethal or lethal
C39F7.4	CG3320	Rab-protein 1 involved in cell adhesion	Acute lethal or lethal
C41C4.8	CG2331	Transitional endoplasmic reticulum ATPase TER94, Golgi organization and biogenesis	Growth delay or arrested in growth
C42D8.5	CG8827	ACE-like protein	Acute lethal or lethal
C47E12.5	CG1782	Ubiquitin-activating enzyme, function in an ATP-dependent reaction that activates ubiquitin prior to its conjugation to proteins that will subsequently be degraded by the 26S proteasome.	Acute lethal or lethal
C47E8.5	CG1242	Member of the abnormal DAuer Formation gene class	Acute lethal or lethal
C49H3.11	CG5920	Small ribosomal subunit S2 protein.	Acute lethal or lethal

C52E4.4	CG1341	Member of the proteasome Regulatory Particle, ATPase-like gene class	Acute lethal or lethal
C56C10.3	CG8055	Carrier protein with putatively involved in intracellular protein transport	Growth delay or arrested in growth
CD4.6	CG4904	Type 1 alpha subunit of the 26S proteasome's 20S protease core particle (CP).	Acute lethal or lethal
D1007.12	CG9282	Large ribosomal subunit L24 protein.	Acute lethal or lethal
D1054.2	CG5266	Member of the Proteasome Alpha Subunit gene class	Acute lethal or lethal
D1081.8	CG6905	MYB transforming protein	Acute lethal or lethal
F07D10.1	CG7726	Large ribosomal subunit L11 protein (RPL-11.2) involved in protein biosynthesis.	Acute lethal or lethal
F11C3.3	CG17927	Muscle myosin heavy chain (MHC B)	Acute lethal or lethal
F13B10.2	CG4863	Large ribosomal subunit L3 protein (rpl-3)	Acute lethal or lethal
F16A11.2	CG9987	Methanococcus hypothetical protein 0682 like	Acute lethal or lethal
F20B6.2	CG17369	V-ATPase B subunit	Growth delay or arrested in growth
F23F12.6	CG16916	Triple A ATPase subunit of the 26S proteasome's 19S regulatory particle (RP) base subcomplex (RPT-3)	Acute lethal or lethal
F25H5.4	CG2238	Translation elongation factor 2 (EF-2), a GTP-binding protein involved in protein synthesis	Growth delay or arrested in growth
F26D10.3	CG4264	Member of the Heat Shock Protein gene class	Acute lethal or lethal
F28C6.7	CG6946	Large ribosomal subunit L26 protein (RPL-26) involved in protein biosynthesis	Embryonic lethal or sterile
F28D1.7	CG8415	Small ribosomal subunit S23 protein (RPS-23) involved in protein biosynthesis	Acute lethal or lethal
F29G9.5	CG5289	Member of the proteasome Regulatory Particle, ATPase-like gene class	Acute lethal or lethal
F32H2.5	CG3523	Mitochondrial protein	Acute lethal or lethal
F37C12.11	CG2986	Small ribosomal subunit S21 protein (RPS-21) involved in protein biosynthesis	Acute lethal or lethal
F37C12.4	CG7622	Large ribosomal subunit L36 protein (RPL-36) involved in protein biosynthesis	Acute lethal or lethal

F37C12.9	CG1527	Small ribosomal subunit S14 protein (RPS-14) involved in protein biosynthesis	Acute lethal or lethal
F38E11.5	CG6699	beta' (beta-prime) subunit of the coatomer (COPI) complex	Acute lethal or lethal
F39B2.6	CG10305	Small ribosomal subunit S26 protein (RPS-26) involved in protein biosynthesis	Acute lethal or lethal
F39H11.5	CG12000	Member of the Proteasome Beta Subunit gene class	Acute lethal or lethal
F40F8.10	CG3395	Ribosomal protein S9 (RpS9), structural constituent of ribosome involved in protein biosynthesis which is a component of the cytosolic small ribosomal subunit	Acute lethal or lethal
F42C5.8	CG7808	Small ribosomal subunit S8 protein (RPS-8) involved in protein biosynthesis	Acute lethal or lethal
F49C12.8	CG5378	Member of the proteasome Regulatory Particle, Non-ATPase-like gene class	Acute lethal or lethal
F53A3.3	CG2033	Small ribosomal subunit S15a protein.	Acute lethal or lethal
F53G12.10	CG4897	large ribosomal subunit L7 protein (rpl-7)	Acute lethal or lethal
F54A3.3	CG8977	Unknown function	Acute lethal or lethal
F54E2.3	CG1915	Product with sallimus (sis), myosin-light-chain kinase activity (EC:2.7.1.117) involved in mitotic chromosome condensation which is localized to the nucleus	
F54E7.2	CG11271	Small ribosomal subunit S12 protein (RPS-12) involved in protein biosynthesis	Acute lethal or lethal
F55A11.2	CG4214	Member of the SYNtixin gene class	Acute lethal or lethal
F55A3.3	CG1828	transcription factor	Acute lethal or lethal
F55C10.1	CG11217	Ortholog of calcineurin B, the regulatory subunit of the protein phosphatase 2B	Acute lethal or lethal
F56F3.5	CG2168	rps-1 encodes a small ribosomal subunit S3A protein.	Acute lethal or lethal
F57B9.10	CG10149	Member of the proteasome Regulatory Particle, Non-ATPase-like gene class	Acute lethal or lethal
F58F12.1	CG2968	ATP synthase	Acute lethal or lethal
F59E10.3	CG3948	Zeta subunit of the coatomer (COPI) complex	Acute lethal or lethal
JC8.3	CG3195	Large ribosomal subunit L12 protein (rpl-12)	Acute lethal or lethal
K01G5.4	CG1404	Putative RAN small monomeric GTPase (cell adhesion)	Acute lethal or lethal
K04F10.4	CG18734	Subtilase	Acute lethal or lethal

K05C4.1	CG12323	Member of the Proteasome Beta Subunit gene class	Acute lethal or lethal
K07D4.3	CG18174	Putative proteasome regulatory particle, lid subcomplex, rpn11	Acute lethal or lethal
K11D9.2	CG3725	Sarco-endoplasmic reticulum Ca[2+] ATPase	Embryonic lethal or sterile; Acute lethal or lethal
M03F4.2	CG4027	An actin that is expressed in body wall and vulval muscles and the spermatheca.	Acute lethal or lethal
R06A4.9	CG1109	six WD40 repeats	Acute lethal or lethal
R10E11.1	CG15319	Putative transcriptional cofactor	Acute lethal or lethal
R12E2.3	CG3416	Protein with endopeptidase activity involved in proteolysis and peptidolysis	Acute lethal or lethal
F10C1.2	CG10119	Member of the Intermediate Filament, B gene class	Embryonic lethal or sterile
F35G12.8	CG11397	Homolog of the SMC4 subunit of mitotic condensin	Embryonic lethal or sterile
F53G12.1	CG5771	GTPase homologue	Embryonic lethal or sterile
F54E7.3	CG5055	PDZ domain-containing protein	Embryonic lethal or sterile
H28O16.1	CG3612	ATP synthase	Growth delay or arrested in growth
K12C11.2	CG4494	Member of the SUMO (ubiquitin-related) homolog gene class	Embryonic lethal or sterile
R12E2.3	CG3416	Member of the proteasome Regulatory Particle, Non-ATPase-like gene class	Acute lethal or lethal
R13A5.8	CG6141	Ribosomal protein L9, structural constituent of ribosome involved in protein biosynthesis which is localised to the ribosome	Acute lethal or lethal
T01C3.6	CG4046	rps-16 encodes a small ribosomal subunit S16 protein.	Acute lethal or lethal
T01H3.1	CG7007	proteolipid protein PPA1 like protein	Acute lethal or lethal
T05C12.7	CG5374	Cytosolic chaperonin	Acute lethal or lethal
T05H4.6	CG5605	eukaryotic peptide chain release factor subunit 1	Acute lethal or lethal
T10H9.4	CG17248	N-synaptobrevin; v-SNARE, vesicle-mediated transport, synaptic vesicle	
T14F9.1	CG17332	ATPase subunit	Growth delay or arrested in growth
T20G5.1	CG9012	Claathrin heavy chain	Acute lethal or lethal
T21B10.7	CG7033	t-complex protein 1	Embryonic lethal or sterile
W09B12.1	CG17907	Acetylcholinesterase	
T27F2.1	CG8264	Member of the mammalian SKIP (Ski interacting protein) homolog gene	Acute lethal or lethal

ZC434.5	CG5394	class	predicted mitochondrial glutamyl-tRNA synthetase (GluRS)	Acute lethal or lethal
B0511.6	CG6375		helicase	Embryonic lethal or sterile
DY3.2	CG10119		Nuclear lamin; LMN-1 protein	Growth delay or arrested in growth
R13G10.1	CG11397		homolog of the SMC4 subunit of mitotic condensin	Wild Type
T26E3.7	CG3612		Predicted mitochondrial protein.	Growth delay or arrested in growth
Y113G7A.3	CG1250		GTPase activator, ER to Golgi prot transport, component of the Golgi stack	Acute lethal or lethal
Y43B11AR.4	CG11276		Ribosomal protein S4 (RpS4), structural constituent of ribosome involved in protein biosynthesis which is a component of the cytosolic small ribosomal subunit	Acute lethal or lethal
Y46G5A.4	CG5931		Y46G5A.4 gene	Acute lethal or lethal
Y71F9AL.17	CG7961		Alpha subunit of the coatomer (COPI) complex	Acute lethal or lethal
Y76B12C.7	CG10110		Gene cleavage and polyadenylation specificity factor	Embryonic lethal or sterile
Y37D8A.10	CG1751		Unknown function	Embryonic lethal or sterile
CG7765	C06G3.2		Member of the Kinesin-Like Protein gene class	Embryonic lethal or sterile
CG10922	C44E4.4		RNA-binding protein	Embryonic lethal or sterile
CG4145	F01G12.5		alpha-2 type IV collagen	Embryonic lethal or sterile
CG13391	F28H1.3		apredicted cytoplasmic alanyl-tRNA synthetase (AlaRS)	Growth delay or arrested in growth
CG7765	R05D3.7		Member of the UNCoordinated gene class	Embryonic lethal or sterile
CG7398	R06A4.4		Member of the Importin Beta family gene class	Embryonic lethal or sterile
CG7436	T17E9.2		Unknown function	Embryonic lethal or sterile
CG2666	T25G3.2		putative chitin synthase	Embryonic lethal or sterile
CG17603	W04A8.7		TATA-binding protein associated factor TAF1L (TAFII250)	Embryonic lethal or sterile

Table 1-LD

Target ID	Dm Identifier	SEQ ID NO NA	SEQ ID NO AA	Function (based on Flybase)
LD001	CG11276	1	2	Ribosomal protein S4 (RpS4), structural constituent of ribosome involved in protein biosynthesis which is a component of the cytosolic small ribosomal subunit
LD002	CG8055	3	4	Carrier protein with putatively involved in intracellular protein transport
LD003	CG3395	5	6	Ribosomal protein S9 (RpS9), structural constituent of ribosome involved in protein biosynthesis which is a component of the cytosolic small ribosomal subunit
LD006	CG3180	7	8	RNA polymerase II 140kD subunit (RpII140), DNA-directed RNA polymerase activity (EC:2.7.7.6) involved in transcription from Pol II promoter which is a component of the DNA-directed RNA polymerase II, core complex
LD007	CG7269	9	10	Helicase at 25E (Hel25E), also known in FlyBase as Dbp25F, Hel, l(2)25Eb and l(2)k11511, pre-mRNA splicing factor activity involved in nuclear mRNA splicing, via spliceosome which is localized to the nucleus
LD010	CG1250	11	12	GTPase activator, ER to Golgi prot transport, component of the Golgi stack
LD011	CG1404	13	14	Tutative RAN small monomeric GTPase (cell adhesion)
LD014	CG1088	15	16	V-ATPase E subunit
LD015	CG2331	17	18	Transitional endoplasmic reticulum ATPase TER94, Golgi organization and biogenesis
LD016	CG17369	19	20	V-ATPase B subunit
LD018	CG1915	21	22	Salimus (sis), myosin-light-chain kinase activity (EC:2.7.1.17) involved in mitotic chromosome condensation which is localized to the nucleus
LD027	CG6699	23	24	Beta-coatamer protein, subunit of a multimeric complex that forms a membrane vesicle coat

Table 1-PC

Target ID	Dm Identifier	SEQ ID NO NA	SEQ ID NO AA	Function (based on Flybase)
PC001	CG11276	247	248	Ribosomal protein S4 (RpS4), structural constituent of ribosome involved in protein biosynthesis which is a component of the cytosolic small ribosomal subunit
PC003	CG3395	249	250	Ribosomal protein S9 (RpS9), structural constituent of ribosome involved in protein biosynthesis

					which is a component of the cytosolic small ribosomal subunit
PC005	CG2746	251	252		Ribosomal protein L19, structural constituent of ribosome involved in protein biosynthesis which is localised to the ribosome
PC010	CG1250	253	254		GTPase activator, ER to Golgi prot transport, component of the Golgi stack
PC014	CG1088	255	256		V-ATPase E subunit
PC016	CG17369	257	258		V-ATPase B subunit
PC027	CG6699	259	260		Beta-coatamer protein, subunit of a multimeric complex that forms a membrane vesicle coat

Table 1-EV

Target ID	Dm Identifier	SEQ ID NO NA	SEQ ID NO AA	Function (based on Flybase)
EV005	CG2746	513	514	Ribosomal protein L19, structural constituent of ribosome involved in protein biosynthesis which is localised to the ribosome
EV009	CG9261	515	516	Protein involved with Na ⁺ /K ⁺ - exchanging ATPase complex
EV010	CG1250	517	518	GTPase activator, ER to Golgi prot transport, component of the Golgi stack
EV015	CG2331	519	520	Transitional endoplasmic reticulum ATPase TER94, Golgi organization and biogenesis
EV016	CG17369	521	522	V-ATPase B subunit

Table 1-AG

Target ID	Dm Identifier	SEQ ID NO NA	SEQ ID NO AA	Function (based on Flybase)
AG001	CG11276	601	602	Ribosomal protein S4 (RpS4), structural constituent of ribosome involved in protein biosynthesis which is a component of the cytosolic small ribosomal subunit
AG005	CG2746	603	604	Ribosomal protein L19, structural constituent of ribosome involved in protein biosynthesis which is localised to the ribosome
AG010	CG1250	605	606	GTPase activator, ER to Golgi prot transport, component of the Golgi stack
AG014	CG1088	607	608	V-ATPase E subunit

AG016	CG17369	609	610	V-ATPase B subunit
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Table 1-TC

Target ID	Dm Identifier	SEQ ID NO NA	SEQ ID NO AA	Function (based on Flybase)
TC001	CG11276	793	794	Ribosomal protein S4 (RpS4), structural constituent of ribosome involved in protein biosynthesis which is a component of the cytosolic small ribosomal subunit
TC002	CG8055	795	796	Protein with putatively involved in intracellular protein transport
TC010	CG1250	797	798	GTPase activator, ER to Golgi prot transport, component of the Golgi stack
TC014	CG1088	799	800	V-ATPase E subunit
TC015	CG2331	801	802	Transitional endoplasmic reticulum ATPase TER94, Golgi organization and biogenesis

Table 1-MP

Target ID	Dm Identifier	SEQ ID NO NA	SEQ ID NO AA	Function (based on Flybase)
MP001	CG11276	888	889	Ribosomal protein S4 (RpS4), structural constituent of ribosome involved in protein biosynthesis which is a component of the cytosolic small ribosomal subunit
MP002	CG8055	890	891	Carrier protein with putatively involved in intracellular protein transport
MP010	CG1250	892	893	GTPase activator, ER to Golgi prot transport, component of the Golgi stack
MP016	CG17369	894	895	V-ATPase B subunit
MP027	CG6699	896	897	Beta-coatamer protein, subunit of a multimeric complex that forms a membrane vesicle coat

Table 1-NL

Target ID	Dm Identifier	SEQ ID NO NA	SEQ ID NO AA	Function (based on Flybase)
NL001	CG11276	1071	1072	Ribosomal protein S4 (RpS4), structural constituent of ribosome involved in protein biosynthesis which is a component of the cytosolic small ribosomal subunit

NL002	CG8055	1073	1074	Protein with putatively involved in intracellular protein transport
NL003	CG3395	1075	1076	Ribosomal protein S9 (RpS9), structural constituent of ribosome involved in protein biosynthesis which is a component of the cytosolic small ribosomal subunit
NL004	CG6141	1077	1078	Ribosomal protein L9, structural constituent of ribosome involved in protein biosynthesis which is localised to the ribosome
NL005	CG2746	1079	1080	Ribosomal protein L19, structural constituent of ribosome involved in protein biosynthesis which is localised to the ribosome
NL006	CG3180	1081	1082	RNA polymerase II 140kD subunit (RpII140), DNA-directed RNA polymerase activity (EC:2.7.7.6) involved in transcription from Pol II promoter which is a component of the DNA-directed RNA polymerase II, core complex
NL007	CG7269	1083	1084	Helicase at 25E (Hel25E), also known in FlyBase as Dbp25F, Hel, l(2)25Eb and l(2)k11511, pre-mRNA splicing factor activity involved in nuclear mRNA splicing, via spliceosome which is localized to the nucleus
NL008	CG3416	1085	1086	Protein with endopeptidase activity involved in proteolysis and peptidolysis which is a component of the proteasome regulatory particle, lid subcomplex (sensu Eukarya)
NL009	CG9261	1087	1088	Protein involved with Na ⁺ /K ⁺ - exchanging ATPase complex
NL010	CG1250	1089	1090	GTPase activator, ER to Golgi prot transport, component of the Golgi stack
NL011	CG1404	1091	1092	Putative RAN small monomeric GTPase (cell adhesion)
NL012	CG17248	1093	1094	N-synaptobrevin; v-SNARE, vesicle-mediated transport, synaptic vesicle
NL013	CG18174	1095	1096	Putative proteasome regulatory particle, lid subcomplex, rpn11
NL014	CG1088	1097	1098	V-ATPase E subunit
NL015	CG2331	1099	1100	Transitional endoplasmic reticulum ATPase TER94, Golgi organization and biogenesis
NL016	CG17369	1101	1102	V-ATPase B subunit
NL018	CG1915	1103	1104	Salimus (sls), myosin-light-chain kinase activity (EC:2.7.1.117) involved in mitotic chromosome condensation which is localized to the nucleus
NL019	CG3320	1105	1106	Rab-protein 1 involved in cell adhesion
NL021	CG10110	1107	1108	Gene cleavage and polyadenylation specificity factor

NL022	CG10689	1109	1110	Product with RNA helicase activity (EC:2.7.7.-) involved in nuclear mRNA splicing, via spliceosome which is a component of the spliceosome complex
NL023	CG17907	1111	1112	Acetylcholinesterase
NL027	CG6699	1113	1114	Beta-coatomer protein

Table 1-CS

Target ID	Dm identifier	SEQ ID NO NA	SEQ ID NO AA	Function (based on Flybase)
CS001	CG11276	1682	1683	Ribosomal protein S4 (RpS4), structural constituent of ribosome involved in protein biosynthesis which is a component of the cytosolic small ribosomal subunit
CS002	CG8055	1684	1685	Carrier protein with putatively involved in intracellular protein transport
CS003	CG3395	1686	1687	Ribosomal protein S9 (RpS9), structural constituent of ribosome involved in protein biosynthesis which is a component of the cytosolic small ribosomal subunit
CS006	CG3180	1688	1689	RNA polymerase II 140kD subunit (RpII140), DNA-directed RNA polymerase activity (EC:2.7.7.6) involved in transcription from Pol II promoter which is a component of the DNA-directed RNA polymerase II, core complex
CS007	CG7269	1690	1691	Helicase at 25E (Hel25E), also known in FlyBase as Dbp25F, Hel, I(2)25Eb and I(2)k11511, pre-mRNA splicing factor activity involved in nuclear mRNA splicing, via spliceosome which is localized to the nucleus
CS009	CG9261	1692	1693	Protein involved with Na ⁺ /K ⁺ - exchanging ATPase complex
CS011	CG1404	1694	1695	Tutative RAN small monomeric GTPase (cell adhesion)
CS013	CG18174	1696	1697	Putative proteasome regulatory particle, lid subcomplex, rpn11
CS014	CG1088	1698	1699	V-ATPase E subunit
CS015	CG2331	1700	1701	Transitional endoplasmic reticulum ATPase TER94, Golgi organization and biogenesis
CS016	CG17369	1702	1703	V-ATPase B subunit
CS018	CG1915	1704	1705	Salimus (sls), myosin-light-chain kinase activity (EC:2.7.1.117) involved in mitotic chromosome condensation which is localized to the nucleus

Table 1-PX

Target ID	Dm Identifier	SEQ ID NO NA	SEQ ID NO AA	Function (based on Flybase)
PX001	CG11276	2100	2101	Ribosomal protein S4 (RpS4), structural constituent of ribosome involved in protein biosynthesis which is a component of the cytosolic small ribosomal subunit
PX009	CG9261	2102	2103	Protein involved with Na ⁺ /K ⁺ - exchanging ATPase complex
PX010	CG1250	2104	2105	GTPase activator, ER to Golgi prot transport, component of the Golgi stack
PX015	CG2331	2106	2107	Transitional endoplasmic reticulum ATPase TER94, Golgi organization and biogenesis
PX016	CG17369	2108	2109	V-ATPase B subunit

Table 1-AD

Target ID	Dm Identifier	SEQ ID NO NA	SEQ ID NO AA	Function (based on Flybase)
AD001	CG11276	2364	2365	Ribosomal protein S4 (RpS4), structural constituent of ribosome involved in protein biosynthesis which is a component of the cytosolic small ribosomal subunit
AD002	CG8055	2366	2367	Carrier protein with putatively involved in intracellular protein transport
AD009	CG9261	2368	2369	Protein involved with Na ⁺ /K ⁺ - exchanging ATPase complex
AD015	CG2331	2370	2371	Transitional endoplasmic reticulum ATPase TER94, Golgi organization and biogenesis
AD016	CG17369	2372	2373	V-ATPase B subunit

Table 2-LD

Target ID	Primer Forward 5' → 3'	Primer Reverse 5' → 3'	cDNA Sequence (sense strand) 5' → 3'
LD001	SEQ ID NO: 25 GGCCCCAAGAA GCATTTGAAGC G	SEQ ID NO: 26 TAGCGGATGGT GCGDCCRTCT G	SEQ ID NO: 1 GGCCCCAAGAAGCATTGAAGCGTTTGAATGCCCAAAAGCATGGATGTTGGATAAATTGG GAGGTGTTTTCGCACCTCGCCCATCTACAGGACCTCACAAATTCGAGAGTCTTTGCCCTT GGTGATCTTCCCTACGTAAACCGATTGAAGTATGCTTTGACTTAACAGCGAAGTTACTAAGATTG TTATGCAAAGGTTAATCAAAGTAGATGGAAAAGTGAGGACCGACTCCAATTACCCCTGCTGG GTTATGGATGTTATTACCATTGAAAAAACTGGTGAATTTTCCGACTCATCTATGATGTTAA

				AGGACGATTTGCAGTGCATCGTATTACTGCTGAGGAAGCAAAAGTACAAACTATGCAAAGTC AGGAGGATGCAAACTGGCCCCAAAGGAATTCCTTTCATAGTGACACACGACGGCCGCACC ATCCGCTA
LD002	SEQ ID NO: 27 GAGCGGCCAT GCAAGCVCTBA ARMRRAAG	SEQ ID NO: 28 GCAATGTCATC CATCAKRTCT GCAC	SEQ ID NO: 3 GCAATGTCATCCATCATGTGCGTGACATTGTCCACGTCCAAGTTTTTATGGGCTTTCTTAAG AGCTTCAGCTGCATTTTCATAGATTTCCAATACTGTGGTGTTCTGACTAGCTCCCTCCAGAG CTTCTCGTTGAAGTTCAATAGTAGTTAAAGTGCCACTATTTGCAACTGATTTTTTTCTAATC GCTTCTCCGCTTCAGCGCTTGCAATGGCCGCTC	
LD003	SEQ ID NO: 29 TCGGTCTTCTC GAAGACNTAYG TKAC	SEQ ID NO: 30 CAGGTTCTTCC TCTTKACRCGD CC	SEQ ID NO: 5 CAGGTTCTTCTCTTGACGGCTCCAGGGCGGACCACCCAGGAATGGAGATTTGAGCGAGAA GTCAATATGCTTCTGGGAATCAAGTCTCACAATGAAGCTTGAATATTACGACCTGCTTAC GAACCTGATATGCTTTGACGGACCAGCACAGCATGATGATTTTGAAGCCCC CAACTTGAAACTTGTTGGAGACGTCGTTCCAAGAAATCTTCAATCTTCAAAACCCCAAGA CGTAATCAAGCTTCATACGGGTTTCATCCAACACTCCAATACGCACCAACCGACGAAGAAG AGCATTGCCCTTCAACAACCTGCGCTGATCTTCTCTCCAAGTCAGAAGTTCTCTGGCAG CTTACGGGATTTTGCCAAAGGTATAGTTGACTCGCCACACTTACGTTTGTCTTAAGACCA TATTCTCTATGATTTTCAACTCCTGATCAAGACGTGCTTTTTCATAAGGTGCGCTGGGA	
LD006	SEQ ID NO: 31 GGAGCGAGAC TACAACAAYKA YRGYGGC	SEQ ID NO: 32 CTCGAACTGCT CYTCYTGATCR CC	SEQ ID NO: 7 GGAGCGAGACTACACAACATATGGCTGGCAGGTGTTGGTGGCTTCTGGTGTGGTGAATAC ATCGACACTCTTGAAGAAGAAACTGTCTATGATTGCGATGAATCCTGAGGATCTTCGGCAGG ACAAAGAATATGCTTATTGTACGACCTACACCCACTGCGAAATCCACCCGGCCATGATCTT GGCGTTTGGCGGTCTATTATACCTTTCCCGGATCATAACCCAGAGCCCCAAGGAACACCTAC CAGAGCGCTATGGGTAAAGCAAGCTATGGGGTCTACATTACGAATTTCCACGTGCGGATG GACACCTGGCCACGTGCTATACTACCCGCACAAACCTCTGGTCACTACCAAGTCTATG GAGTATCTGGGTTTCAGAGAATTACCAGCGGGGATCAACAGTATAGTTGCTATTGCTTGT ATACTGGTTATAATCAAGAAGATTCTGTTATTCTGAACGCGTCTGCTGTGGAAGAGGATTT TTCCGATCCGTGTTTTATCGTTCTCTATAAAGATGCCGAATCGAAGCGAATTTGGCGATCAAG AAGAGCAGTTCGAG	
LD007	SEQ ID NO: 33 CCGAAGAAGGA YGTSAAGGGYA C	SEQ ID NO: 34 CGATGCAAGTA GGTGCKGART CYTC	SEQ ID NO: 9 CCGAAGAAGGATGTGAAGGGTACTTACGTATCCATACACAGTTCAGGCTTCAGAGATTTTT TATTGAACCCAGAAATCTAAGAGCTATAGTTGACTGCGGTTTTGAACACCTTCAGAAGTT CAGCAGGAATGTATTCCTCAAGCTGTCAATTGGCATGGACATTTTATGTCAAGCCAAATCTGG TATGGGCAAAACGGCAGTGTGTTGTTCTGGCAGACTGCAACAATTTGAAACCGCGGACAA GTGTTTACGTTTTGGTGATGTGTCACACTCGTGAACCTGGCTTCCAATCAGCAAGAGTA CGAGAGGTTCAAGTAAATATATGCCAGTGTCAAGGTGGGCGTCTTTTCGGAGGAATGCTT	

LD010	SEQ ID NO: 35 CTCTCAAGGAT TCKYTRCARAT GTC	SEQ ID NO: 36 CGCCATTGGGC RATGGTYTCKC C	<p>ATTGCTAACGATGAAGAAGTATTGAAAAACAAATGTCCACACATTGTTGTGGGACGCCTG GGCGTATTTTGGCGCTTGTCAGTCTAGGAAGCTAGTCTCAAGAACCTGAAACACATTTCAT TCTTGATGAGTCGATAAAATGTTAGAACTGTAGAGTGTGATGATGAGGAGACGTCCAGGAAATC TACAGAAACACCCCTCACACCAAGCAAGTGTGATGTTGAGTGCCACACTCAGCAAGAAA TCAGCCCGGTGTCAGAAATTCATGCAAGATCCAATGAGGTGTATGTAGACGATGAAG CCAAATTGACGTTGCACGGATTACAACAGCATTACGTTAACTCAAAGAAAATGAAAAGAAT AAAAAATTATTGAGTTGCTCGATGTTCTCGAATTAATCAGGTGGTCAATTTTGTGAAGTCC GTTCAAAGGTGTGGCTTTGGCACAGTTGCTGACTGAACAGAATTTCCAGCCATAGGAA TTCACAGAGGAATGGACCAGAAAGAGAGTTGTCTCGTATGAGCAGTTCAAAGATTTCCA GAAGAGAATATTGGTAGCTACGAATCTCTTTGGCGTGGCATGGACATTGAAAAGGGTCAAC ATTGCTTCAACTATGATATGCCAGAGGACTCCGACACCTACTTGCATCG</p>
LD010	SEQ ID NO: 35 CTCTCAAGGAT TCKYTRCARAT GTC	SEQ ID NO: 36 CGCCATTGGGC RATGGTYTCKC C	<p>SEQ ID NO: 11</p> <p>CTCTCAAGGATTCGTTGCAGATGCTTTGAGCTTGTGCCCCCGAATGCCTTGATAGGGTT GATTACCTTTGGGAAGATGGTCCAAGTGCACGAACTAGGTACCGAGGGCTGCAGCAAAATC TTACGTTTCCGAGGGACGAAAGACCTCACAGCTAAGCAAGTTCAAGAGATGTTGGAAGTG GGAGAGCCCGCAGTAAGTGTCAACCTGCTCTCAACCAACGAGCAACCCATGAGGCCCT GGAGCACTCCAGCAAGCTCTACGCCACCAGGAAGCAGGTTCTTCAACCCATCTCGAAA TGCACATGAACCTCACTGATCTTATTGGAGAGTTGCAAGAGACCCATGGCCTGTCCACC AAGGCAATGCGCCTTAGATCGACCGGGACAGCTTTATCGATAGCCTTGGTGTGGA GTGCACATACGCCAATACTGGTGCCAGGGTCATGCTATTGTTGGAGGACCTTGCTCTCAA GGCCCTGGTCAAGTCTTGAATGATGATCTGAAGCAACCTATCAGATCTCACCACGACATCC AAAAAGACAATGCCAATACATGAAGAAAGCAATCAAGCACATATGATAATTTAGCGATGAGA GCAGCAACGAATGGCCACTGCGTTGACATATATTCATGCGCTTTGGATCAGACAGGATTGA TGGAGATGAACACAGTGTGTAATTCACAGGGGGACATATGTCATGGCGACTCGTTCAA TTCTCCCTGTTCAAGCAACGTTCCAGCGCATATTTGAAAGATCAGAAAACGAGCTGA AGATGGCATTTAATGGTACTCTGGAGGTCAAGTGTCCAGGGAGTTGAAAATTCAGGCGG GTATTGGATCTTGTTGTTGTTGAATGTGAAGAAATCCTTTGGTTCCGACACCGAAATAGGA ATGGGTAACACGGTCCAGTGGAAATGTGTACGGTAACCTCAAGTACTACCATGGCCTTGT TCTTCGAGGTGTCAAACCAACATCCGCTCCCATACCTCAAGGGGGAAGGGGCTGCATAC AGTTCATCAGGCAATATCAGCATGCTAGTGCCAGAGAGGATCCGAGTAACGACAGTTGC TAGAAACTGGCCGATGCTCCGCTAATATACATCATGTCAGTGTGATTCGATCAGGAG GCAGCCGACGTGATAATGGCAGGATGGCGTTTACAGAGCGGAATCAGACGATAGCCCT GATGTTTTGAGATGGTCGATAGGATGTTGATACGCTGTGCCAGAAATTCGGCCGAATATA ACAAGGACGACCCGAATTCGTTCCGCTTGGCGGAAAACCTCAGCCCTACCCCGCAGTTTCAT GTACCATTTGAGAAGGTCACAGTTCTGCGAGGTGTTTAACAATTTCTCCGACGAAACGTCC TTCTACAGGCACATGCTTATGCGCGAAGACCTCACGCACTGCTGATGATCCAGCCGA TACTCTACAGCTACAGTTTCAATGGACCACCCAGAACCTGTGCTTTTGGATACGAGTTCCATC</p>

LD011	SEQ ID NO: 37 CCCACTTTCAA GTGYGTRYTRG TCGG	SEQ ID NO: 38 GTGGAAGCAG GGCWGGCATK GCRAC	CAACCCGATAGAAATCTGCTCATGGACACGTTCTTCCAGATTCTGATATTCATGGCGGAAAC CATCGCCCAATGGCG SEQ ID NO: 13 GTGGAAGCAGGGCTGGCATGGCGACAAATTTCTAGATTGGGATCACCAATAAGCTTCCTAG CTAGCCATAGGAAGGCTCTCAAGTTGTAGTTAGATTGGCAGAGATATCATAGTACTGC AAATCTCTCTCTATGAAGACAATACTTTTCGCTTTTACTTTTCTGCTTTGATGTCAACCT TGTTCCCGCAAAGTACTATCGGGATATTTTCACAGACTCTGACAAGATCTCTGTGCCAATTT GGTACATTTCTTGATGTAACCTCTGGAAGTTACATCAACATGATAATAGCACACGTCCCTG AATGTAATATCCATACGGAGACCAACAACTTCTCTGACCGGAGTGTCCCATACATTG AACCGAATAGGGCCCTGTTGTATGGAAGACCAAGGATGAGCTTCAACTCCCAAGTAG CTACATATCTTTTTCAAAATTCACCACTCATATGACGTTTCACAAAATGCTGTTTTTCCAGTAC CTCCATCTCCGACCAACACACACTTGAAAGTGGG
LD014	SEQ ID NO: 39 CGCAGATCAAR CAYATGATGGC	SEQ ID NO: 40 CGGATCTCGG GCASMARYTGC	SEQ ID NO: 15 CGCAGATCAAGCATATGATGGCTTTCATTGAACAAGAGGCAACGAAAGGCGAGAAGAAAT CGATGCCAAGGCCGAGGAAGAAATTAATATTGAAAGGGGCGCTTGTTCAGCAACAACGT CTCAAGATTATGGAATATTATGAGAAGAAAGAGAAACAGGTCGAACTCCAGAAAAAATCCA ATCGTCTAACATGTTGAATCAGGCTCGATTGAAAGTATTGAAGTTAGGGAAGATCACGTT CGTACCGTACTAGAGGAGGCGGTAAACGACTTGGTCAGGTCAACAAACGACCCAGGGA TATTTCCCAATCCTGGAAGCCCTCATTTGCGAGGATTATATCAGCTTTTGGAAAGATGT TACCATTCGAGTTCGGCCCGAGGACCGAGAACTGGTCAAAATCCATCATTTCCACCGTCAAG AACAGTATAAAGATGCCACCGGTAAGGACATCCATCTGAAATTTGATGACGAAATCCATCT GTCCCAAGAAACCCAGCGGGGAATCGACCTGCTGGCGCAGAAAAACAAATCAAGATCAG CAATACTATGGAGGCTCGTCTGGAGCTGATTTCCGAGCAACTTCTGCCCGAGATCCG
LD014_F1			SEQ ID NO: 159 TCTAGAATGTTGAATCAGGCTCGATTGAAAGTATTGAAGTTAGGGAAGATCACGTTCTGTA CCGTACTAGAGGAGGCGCGTAAACGACTTGGTCAGGTCAACACGCCCGGG
LD014_F2			SEQ ID NO: 160 TCTAGAAAGATCACGTTGTTACCGTACTAGAGGAGGCGCGTAAACGACTTGGTCAAGGTCA CAACGCCCGGG
LD014_C1			SEQ ID NO: 161 TCTAGAATGTTGAATCAGGCTCGATTGAAAGTATTGAAGTTAGGGAAGATCACGTTCTGTA CCGTACTAGAGGAGGCGCGTAAACGACTTGGTCAGGTCAACAAACGATTTGAATCAGGCT CGATTGAAAGTATTGAAGTTAGGGAAGATCACGTTCTGACCGTACTAGAGGAGGCGCGT AAACGACTTGGTCAAGTCAACAAACGATGTTGAATCAGGCTCGATTGAAAGTATTGAAGTT AGGGAAGATCACGTTCTGTTACCGTACTAGAGGAGGCGCGTAAACGACTTGGTCAAGGTCA

LD014_C2				AACGCCCGGG SEQ ID NO: 162 TCTAGAAAGATCACGTTCGTACCGTACTAGAGGAGGCGGTAAACGACTTGGTCAGGTCA CAAACGAAGATCACGTTCGTACCGTACTAGAGGAGGCGGTAAACGACTTGGTCAGGTCA CAAACGAAGATCACGTTCGTACCGTACTAGAGGAGGCGGTAAACGACTTGGTCAGGTCA CAAACGAAGATCACGTTCGTACCGTACTAGAGGAGGCGGTAAACGACTTGGTCAGGTCA CAAACGAAGATCACGTTCGTACCGTACTAGAGGAGGCGGTAAACGACTTGGTCAGGTCA CAAACGCCCGGG
LD015	SEQ ID NO: 41 CGCCATCCRTC GCTSTTCAAGG C	SEQ ID NO: 42 GCAATGGCATC AAKYTCRTCR TG	SEQ ID NO: 17 GCAATGGCATCAAGTTCATCGATGAAGATGATCGCCGGAGAGTTTTTGTACGCTTCTTCAA AAGCTTTGCGCAAGTTACTCTCAGACTCGCCAGCGAGTTTGCTCATGATCTCCGGCCCGTT TATCAAGAAGAAGAACGCCCCAGTCTCATTAGCCACGGCGGAGCAATCAGGGTCTTACC CGTACCAGGGGGACCACATACAGCAGTATACCCCTAGGGGGCTTCACGCCGATAGCCTTGAA GAGCGATGGATGGCG	
LD016	SEQ ID NO: 43 GACTGTGTCTG GTGTRAACGG WCC	SEQ ID NO: 44 GGAATAGGATG GGTRATRTCGT CG	SEQ ID NO: 19 GGAATAGGATGGGTAATGTCTGTCGTTGGGCATAGTCAATATAGGAATCTGGGTGATGGATC CGTTACGTCTTCAACACGGCCGGCACGTTCATAGATGGTAGCTAAATCGGTGATACATGTA ACCTGGAAACCCACGACGACGACGACCTCTTCTCTGGCAGCAGATACCTCACGCAAGC TTCTGCATACGAAGACATATCTGTCAAGATGACCAAGACGTCTTCTCACATTGGTAAGCC AAGAAATTCGGCAGCTGTCAAAGCCAGACGAGGTGTAATAATCTTCTCAATGGTAGGATCGT TGCCAAATTCAGAACAGGCAGACATTTCCATAGAACCGTTCTCTCGAAATCCTGTTTG AAGAACCTAGCTGTTTCCATGTTAACACCCATAGCAGCGAAACAAATAGCAAAGTTATCTTC ATGATCATCAAGTACAGATTTACCGAATCTTGACTAAACAGCCTGTCTACAGATCTGGG CAGCAATTTCAATTGTGAGGCAGACGAGCTGCAGAGAAATGGGATCTTCTGACCCACGAG CAATGGAGTTTCATCAGCTCAATAGCTGTAATACCCGCTCGGATCATTTCTCAGGATAGATA CGGACCCACGGATTGATTGGTTGACCCCTGGATGCCAAGAAGTCTTCAGCCAAATTTGGG GGACCTTTGTCGATGGGTTTTCTGATCCATTGAAACACGTCCTCAACATATCTTCAGAAAC AGGAGTCTTCAAAATATCTCCTGTGAATTCACAAGCGGTGTTTTGGCGTCGATTCTCTGAT GTGCCCTCGAACACTTGAACCAAGCTTTTGACCCACTGACTTCCAGAACTTGTCGCCGAAAC GTATAGTGCCATCAGCCAGTTTGAGTTGACGATTTTACGATTTTACTTGGGGAACCTTAAACATCT TCGAGGATTACCAGAGGACCGTTACACCCAGACACAGTC	
LD018	SEQ ID NO: 45 CACCTGGTTCA AGRATGGVCAR MG	SEQ ID NO: 46 GTGCATCGGTA CCAHSCHGCR TC	SEQ ID NO: 21 CACCTGGTTCAAGGATGGGCAGCGGATAACGGAGTCGAGAGAAATACGAGAGCACCTTCTC GAACAACCAAGCCCTCCTTGAGGGTAAACAAAGCCAGCTGAGGACTCGGGACACTACAC TTTTTTGGCGGAGAACCCCTCAAGGCTGCATAGTGTATCTGCTTACTTAGCCATAGAACCCTG	

			<p>GTAACCAACCAGGAAGGGTTGATCCACGAGTCCACCCTTCAAGCAGCAACAGACCGAAATG GAGCAAAATCGACACAGCAAGACCTTGGCGCTTAAGTTCGTAGGGTTTGGGGGATAGA GACGTGACCGAGGGAGATGACCCGCTTCGACTCGCGTCACTGGTCTGCTTATCCA GACGTACATGATACATAACCGTTCGACATCACCGACACCAACCAAGATTTTGG TTAACGAATCCGGAAACCATGCCCTGATGATCACCAACCGTTCGAGCAACGACTCAGGAG TAGTGACCTGCGTCGCCAGGAACAAGACGGGAGAAACCTCTTCCAGTCAACCTTAACG TCATCGAAAGGAACAGTAGTCGCGCCCAAGTTCGTGAGAGATTTACCAAGTCAACGT GGCAGAGGAGAACCAAGTGTCTCTGCGCGCTAGAGCTGTTGGACGCCGCTGCCGCGAA TCACTTGGCAGAGGACGGGGCGCCCCCTAGCCAGCGGGCCCCGACGTTCCGATCGCGATT GACGGTGGAGCCTCTACTTTGAATATCTCGAGGGCCCAAGGCCCTCGGATGCTGCATGTTAC CGATGCAC</p>
LD027	<p>SEQ ID NO: 47 CCATGGTGGC GAYAAACCVTA C</p>	<p>SEQ ID NO: 48 GGTATAGATGA ARCARTCDCCV ACCCA</p>	<p>SEQ ID NO: 23 CCATGGTGGCGATAAACCATACCTTGATATCGGGAGCAGACGATCGGTGGTTAAATCTGG GACTATCAAAACAAAACGTTGTCCAAACCTTGGAAAGGACACGCCCCAAACGTAACCGCG GTTGTTCCACCCCTGAACCTACCTGTGGCTCTCACAGGCAGCGAAGATGGTACCGTTAGAG TTTGGCATACGAATACACACAGATTAGAGAAATTTGAAATTTATGGTTCGAGAGAGTGTG GACCATTTGTTGCTTGAAGGTTTGAATATGTTCTCTGGGTATGACGAGGCGAGTATA TTAGTGAAGTTTGAAGAGAGAAACCGGAGTTAGTATGGATGCCAGTGGCGTAAATATA TTTGGCAAGGCACCTCGGAATTACAACAAGCTAATTTGAAGGCGCTGCCAAGGTGGAG AAATAAGAGATGGGAGCGTTTACCTGTCTCTGTAAAGATATGGAGCATGTAAATATA CCCTCAAACAATCCAACATAATCCGAATGGAAGATTCTGTGATGATCGGAGACGCGGAA TATATCATTTACACAGCGATGGCTCTACGGAACAAGGCTTTTGAAGCGCTCAAGAGTTTG TCTGGCTCAGGACTCCAGCGAGTATGCCATTCGCGAGTCTGGTTCCACAATTCGGATATT CAAAACTTCAAAGAAAGGAAGAACTTCAAGTCGGATTTACGCGCGGAAGGAATCTACGGG GGTTTTCTCTTGGGATTAAATCGGTGTCGGTTTAACTTTACGATTGGGAACTTTTGA CTTGGTGAGACGGATTGAAATACAACCGAGGCGGTTTATGGTCTGACAGTGGAAATTA GTCTGTCTCGCAACGGAGGACAGCTACTTCTATCCCTTCTATGATTCGAGCAAGTTTCA AGGCCAGGGAGAACAAATCAAGTCGAGAGGATGGCGTAGAGGCCGCTTTCGATGTGTTGG GGAAATGAACGAGTCTGTCCGAACAGGCTTTGGTCCGAGACTGTTTCACTATACC</p>

Table 2-PC

Target ID	Primer Forward 5' → 3'	Primer Reverse 5' → 3'	cDNA Sequence (sense strand) 5' → 3'
PC001	<p>SEQ ID NO: 261 CATTGAAGCG</p>	<p>SEQ ID NO: 262 CTTCGTGCCCT</p>	<p>SEQ ID NO: 247 CATTGAAGCGTTAGCTGCTCCCAAGCATGGATGTTGGACAAATTTGGGGGTGCTCTCGCCC</p>

	TTWRMYGCGY CC	TGCRATKATR AABACG	CTCGTCCATCCACCGGCGCTCACAAGTTGCGCGAATCCCTGCCCTTAGTGATTTTCCCTTCGTAAAC AGGCTGAAGTATGCCCTTACAAACAGTGAAGTCACTAAAATTGTCATGCAAGGTTGATCAAAAGT TGATGTAAGTGAGGACTGATTAATACCTGCTGGTTTCATGGATGTCATTACTATTAGAGAA GACTGGTGAATTTTCCGCTGATCTATGATGTTAAAGGAAGATTGCTGTGCAACGTTATTACAGC TGAAGAGGCAAAATACAAAGTTGTAAAGTAAGGAGAGTCCAAACTGGTCCCAAGGAATCCCAT TTTTGGTAAACACATGATGCGACAACCATTCGTTACCTGACCCCAACATCAAAAGTGAATGACACA ATTCAAATGGAATTTGCTACATCTAAAATTCTTGACTACATCAAAATTTGAATCTGGCAACCTCTGC ATGATCACGGGGAGG
PC003	SEQ ID NO: 263 TCGGTCTTCTC GAAGACNTAYG TKAC	SEQ ID NO: 264 CCCTGGTTCTT CTTVRRRTTCT TCCTC	SEQ ID NO: 249 CCCTAGACGTCCTTATGAAAAGGCGCTCTGGATCAGGAATTGAAAATTATCGGCGCCTTTGGTT TACGAAACAAACGTAAGTGTGGAGAGTAAAGTACACTTTGGCTAAAATCCGTAAAGCTGCTCGT GAACTGCTACCTTAGAAGAAAAGAGCCCTAAAAGATTGTTGAAGGTAATGCACCTCTACGTCG TTTGGTGCGAATTGGTGTCTGGATGAGAACAGGATGAAGCTTGATTATGTTTGGTCTGAAAA TTGAAGATTTCTTGGAAAAGAGGCTCCAAACTCAGGTGTTCAAACTCTGGTCTGGCAAGTCAATT CATCATGCTAGAGTACTGATTAGGCAGAGACACATCCGGTGGCAAGCAGGTGGTGAACATCC CCTCGTTTCATCGTGGCTGGACTCGCAGAAAGCACATCGACTTCTCCCTGAAGTCGCCCTTCGG GGTGGCGGACCTGGCGGTGTCAA
PC005	SEQ ID NO: 265 TGCATGCGG CAARAARAAGG TBTGG	SEQ ID NO: 266 TCCTGCTTCTT SGYRGCRATW CGYTC	SEQ ID NO: 251 TGCGATGCGGCAAAAAGAGGTGTGGTTGGATCATAATGAAATCAACGAATCGCCAAACACCAA CTCAAGACAAAACATCCGTAAAGTCACTCAAGGATGGTCTTATCATCAAGAGCCAGTGGCAGTAC ACTCTAGGGCGGCTGACGCAAGAACACTGAAGCCAGAAAGGAAGGCAATGTGGATTG GAAAGAGGAAGGTTACGGCAAAATGCCGTATGCCCTCAAAAGGAACTGTGGTGCAGCGCATGC GCGTCTCAGGCGCTCTCAAAAAGTACAGGGAGGCCAAAGAAAATCGACCGCATCTTTACCA CGCCTGTACATGAAGCGAAGGGTAACGTGTTCAAGGAACAAGAGGGTCTTATGGAGTACATC CACAAAGAAGAAGGCAGAGAAGGCCAGGCGCAAGATGCTGTCTGACCAGGCTAACGCCAGGAGA TTGAAGGTGAAGCAGGCCAGGGAACGTAGGGAAGAGCGTATCGCCACCAAGAACGAGCAGG
PC010	SEQ ID NO: 267 CTCTCAAGGAT TCKYTRCARAT GTC	SEQ ID NO: 268 CGCCATTGGG CRATGGTYTCK CC	SEQ ID NO: 253 CTCTCAAGGATCTTTGCAGATGTGCTCAGCCTATTACCGCCCCAACCGGTTGATTGGATTGATC ACGTTCCGGAATAATGGTGCAAGTCCACGAAGTGGTACCGAAGGCTGCAGCAAGTCTGACGTGT TCTGTGGAACGAAAGATCTACCGCCAAAGCAAGTCCAGGAGATTTGGCATTGGAAAGGGTCTC ACCAATCCCCCAACAACAGCCAGGCAACCTGGGCGGCCAGGCGAGAATCCCAAGCTGCCCC TGTAACCGCGGGAGCAGATTCTTGACGCCCCGTGTCAAAATGCGAACTGAACATGACAGATCTG ATCGGGGAGTTGCAGAAAGACCCTTGGCCCCGTACATCAGGGCAAAAGACCTCTTAGATCCACAG GCGCAGCATTTGCCATCGCTGTCGGCTCTTAGAATGCACCTATCCGAATACGGGTGGCAGAAAT CATGATATTCTTAGGAGGACCATGCTCTCAGGGTCCCGCCAGGTGTTGAACGACGATTTGAAG CAGCCCCATCAGGTCCCATCATGACATACACAAGACAATGCCAAGTACATGAAGAAGGCTATCAA

PC014	SEQ ID NO: 269 CGCAGATCAAR CAYATGATGGC	SEQ ID NO: 270 CGGATCTCGG GCASMARYTG C	<p>ACATTACGATCACTTGGCAATGCGAGCTGCCACCAACAGCCATTGTCATCGACATTTACTCCTGCG CCCTGGATCAGACGGGACTGATGGAGATGAAGCAGTGTGCAATTCACCGAGGGCACATGG TCATGGCGATTCTTCAATTCTCTATTCAAACAAACCTTCCAGCGAGTGTCTCAAAGACC CGAAGAACGACCTCAAGATGGCGTTCAACGCCACCTTGAGAGTGAAGTTCAGGAGTTAA AGTCCAAAGGGGCATCGGCTCGTGGTGTCTTGAACGTTAAAGCCCTCTGCTTCCGATACG GAACTAGGCATGGGAATACTGTGCAGTGGAACTTTCACGTTGGCCGAGCTCTACTGTGG CGCTGTTCTTCGAGGTGTTAACCGAGCATTCGGCGCCATACCAAGGAGGCGAGGGCTGCA TCCAGCTCATACCCAGTATCAGCACGCGAGCGGCAAGGAGGATCAGAGTGACACGATTG CTAGAAATTGGGCGGACGCTACTGCCAACATCCACCATATTAGCGTGGCTTCGACCAAGAAGC GGCGCAGTTGTATGGCCCGAATGGCCGTTACAAGCGGAATCGACGAGACTCCCGACGT GCTCAGATGGGTGGACAGGATGTTGATCAGGCTGTGCCAGAAGTTCGAGAGTACAATAAGAC GATCCGAATTCGTTGAGGTTGGGAGAACTTCAGTCTGTATCCGAGTTCATGTACCATTTGAG ACGTCGCGAGTTTCTGAGGTGTTCAATAATCTCCTGATGAACGTCGTTTATAGGCACATGC TGATCGGTGAGGATTTGACTCAGTCTTTGATCATGCCAGCCGATTTGTACAGTTACAGCTTCA ACGGCCCGCCGAGCCTGTGTTGTTGGACACAAAGCTCTATTAGCCGGATAGATCCTGCTCAT GGACACTTTCTCCAGATACTCATTTTCCATGGAGAGACCATTGCCCAATGGCG</p> <p>SEQ ID NO: 255</p> <p>CTGATGTTCAAACAAATCAAACACATGATGGCTTTTCATTGAACAAGAAGCCAAATGAGAAAGCA GAAGAAATTGATGCCAAGCAGAGGAGGAATCAACATTGAAGAGGGCGTTTGGTCCAGCAAC AGAGACTCAAGATCATGAGTACTACGAGAAAAGGAGAAAGTGAAGTTCGAAATTCAAAAGAAAAAT CAGTCTCTAATATGTTGAATCAGGCTCGTTTGAAGTGTCTGAAGTGAAGAGGAGGACCATGTCTCAG AGCAGTCTGGAGGATGCTCGTAAAGTCTTGGTGAAGTAAACCAAGACCAAGGAAATACTCC CAAATTTGGAGAGCCTAATCCTACAGGACTGTTCCAGCTGTTCCGAGAGGAGGTGACGGTCC GCGTGAGACCGCAAGACAGGACCTGGTCAAGTCCATCCTGCCAACGTCGCTGCCAAATACA AGACGCCACCGCAAGACATCCTACTCAAGGTGGAGCATGAGTCGCACCTGTCTCAGGAGAT CACCAGGCGTGGATTGCTCGCTCAGAGAAACAAGATCAAGATCAGCAACACGATGGAGGCT AGGTTGGATCTGATCGCTCA</p>
PC016	SEQ ID NO: 271 GACTGTGCTG GTGTRAACGG WCC	SEQ ID NO: 272 GGAATAGGAT GGGTRATRTC GTCG	<p>GGAATAGGATGGGTGATGTCGTCGTTGGGCATAGTCAAGATGGGATCTGCGTGATGGAGCCG TTGGGCCCCCACCACGACCGGGCGCTCGTAAATGGTGGCCAGATCGGTGTACATGTAACCG GGAAACCCCTACGGCCGGGACCTTCTCTGAGCGGCAGACACCTCACGCAACGCTCCGCG TACGACGACATGTCGGTCAAGATGACCAACGTCGTTCTCGACTGGTAGGCCAAGAAATTCGG CGCCGTGAGAGCCAAACGCGGTGATGATCGCTCGATGTCGTCGATGTCGTTGGCCAAATTCA AGAACAGACACACGTTCTCCATCGAGCCGTTCTCTCGAAGTCTGCTTGAAGAACCCTGGCAGTT TCCATGTTGACACCCATAGCAGCAACACATAGCAAAGTTGCTTTCATGTCATCCAGCACAGA CTTGCCAGGTACTTTGACCAAGCCAGCCTGCCTACAAATCTGGGCTGCAATCTCAATGTTGGGGC AGCCAGCGGGGAGAGAAGATCGGAATCTTCTGCCCTCTGGCGATAGAGTTCATCAGCTCGATGG</p> <p>SEQ ID NO: 257</p>

			CCGTGATCCAGTCTGGATCATTTCTCGGGATAAATACCGGACCAACGGGTGATCGGCTGTCC TTGGATGTCGAGGTAGTCTCAGCCAGGATCGGGGACCTTTATCAATGGGTTTCTGATCCAT TGAAGACAGTCCAGCATATCTTGATGACTGGAGTCTTAGAATATCTCCAGTGAATCACAC ACCGTGTTCTTAGCATCAATACCTGATGCGCTTCAATACCTGAACAACTGCCCTTATCCACTG ACTTCCAAAACCTTGTCAGATCGTAGAGTCCATCTGCCAATTTGAGCTGGACAATTTCAATTGAAT TTTGGAAAACCTTGACATCTCAAGAATGACCAAGTGGTCCGTTACACCCAGACACAGTC
PC027	SEQ ID NO: 273 GGCCCAAGCA CWSYGAAATRC AG	SEQ ID NO: 274 TGTGCCACCC TAGTRCGRTG YTC	SEQ ID NO: 259 GGCCCAAGCAGTGAATACAGCAAGCTAACTTGAAGCACTACCAGAAGGAGCTGAATCAG AGATGGAGAACGTTGCCAGTCACAGTAAAGGACATGGAGCATGCGAGATTTACCCACAACA ATCCAACACAAACCCCAATGGCGGTTGTAGTGGTTGTGGTATGGAGAAATACATAATACAC GGCTATGGCCCTTCGTAACAAAGCAATTTGGTAGCGCTCAAGAAATTTGATGGGCACAGGACTCC AGTGAATATGCCATCCGCAATCCGGATCCACCATTCCGAATCTTCAAGAAATTTCAAAGAAAAA GAATTTCAAGTCCGACTTGGTGCCGAAGGAATCTATGGTGGTTTCTCTTGGGTGTAATCAG TGCTGGCTTAGCTTCTATGACTGGGAACGCTTGAGTTAGTAGGCGCAATGAAATACAGCCT AGAGCTATCTACTGGTCAGATAGTGGCAAGTTGGTATGCCCTGCTACCGAAGATAGCTATTTCTAT ATTGCTCTATGACTCTGACCAAGTCCAGAAAGCTAGAGATAACAACCAAGTTGCCGAAGATGGAG TGGAGGCTGCCCTTGATGTCCTAGGTGAATAAATGAATCCGTAAAGAACAGGCTCTTGGGTAGGA GACTGCTTCATTTACACAAACGCACTCAACCGTATCAACTACTTTGTGGGTGTAATGGTAAC TATTGCACATCTGGACCGTCTCTATATGCTGCTGGCTATGACCTAGAGATGACAGGTTATACT TGGTTGATAAAGAGTAGGAGTAGTCAGCTATCAATGCTATTATCTGCTCAATATCAGACTG CAGTCATGCGACGAGACTTCCCAACGGCTGATCGAGTATGCGCTTCAATTCCAAAAAGAACATCGC ACTAGGGTGGCACA

Table 2-EV

Target ID	Primer Forward 5' → 3'	Primer Reverse 5' → 3'	cDNA Sequence (sense strand) 5' → 3'
EV005	SEQ ID NO: 523 TGCGATGCGG CAARAARAAGG TBTGG	SEQ ID NO: 524 TCCTGCTTCTT SGYRGCRATW CGYTC	SEQ ID NO: 513 TGCGATGCGGCAAGAAGGTTTGGCTGGATCCTAATGAAATAACTGAAATTTGCTAATACA AACTCTAGACAAAACATCCGCAAACTGATTAAGATGGTCTTATTATTAAGAGCCCTGTCCGG GTGCATTCTCGTGACGCTGACGCAAAAATACTGAAGCCCGCAGGAAAGGTCGTCAATTGTG GATTTGGTAAAGGAAAGGAATGCAATGCTAGGATGCCAGAAAGGAATTTATGGATTCAA CGTATGAGAGTTCTCAGAAGGTTATTGAAGAAATATAGGAAAGCTAAGAAAATTTGATAGGCA TTTATACCATGCTTTATATATGAAGCTAAGGGAAATGTATTCAGAATAAGAGAGTAATGAT GGACTATATCCATAAAAAGGCGGAGAAAGCACGTCACAAAGATGCTCAATGATCAAGCT GATGAAGGAGGCTGAAAGTCAAAAGAGGCACGTAAGCGACGTGAAGAGCGGTATCGCTACG

EV009	SEQ ID NO: 525 GGCCCGTGGT CAGAAYATYWA YAAC	SEQ ID NO: 526 GCAGCCACG CYYTGCACTC	AAGAAGCAGGA SEQ ID NO: 515 CCAACTCTCGATCCAAGCATTCCAAAATACAGGACTGAAGAATCTATAATAGGAACAACCC AGGAATGGGTTTTAGGCCAATGCCCGACAAACGAAAGAAAGTACCCTGATTTGGTTACAG GGTTCTAATAAACAACAACTACGAAAATGGAATCTCTCTCATATTTAGACAAGTAT TACACTCCGGGAAAAATAGAAAAGGGAATATCCAGTAAAGCGCTGTTACATACGGAGAAAA ATTGATTAGGGACAAGTATGTAGTAGTGAGGAAATGGAGCCGTGCACCCCGGAA AATCAATTTGATTACCTCAGAAATGGCCCTTGATATTTCTGAAGCTGAACAGGATATATGGA TGGGAACCGGAGTACTACAACGATCCAAATGATCTCCAGATGATATGCCGCAGCAGTTGA AGGACCATATACGTTATAATATCACCAATCCAGTGGAGAGAAATACCGTCTGGGTAAACATGC GCAGTGAAAATCCGGCAGACGTGGAGTACTTGGCCCTGTGAAGTATTACCCATCTTTCC AGGATTCCCGGTTACTATTTCCATATTTGAATTCGAAGGGTACCTAAGTCCATTATTGG CGGTACAATTCAAGAGACCGGTGCTGTGTTGTTATAAATATCGAGTGCAAAAGCGTGGCT GC
EV010	SEQ ID NO: 527 CGGCTGACGT GGAAYGKTGG CC	SEQ ID NO: 528 CGGCGTATTCT CCRAAYTTCTG GC	SEQ ID NO: 517 CTGGCGGCCACATGGTCATGGGTGATTCAATTAACCTTTCACCTTTTCAACAAACATTTCAAC GAGTATTTTCGAAAGATTCCAATGGAGACTTGAGATGTCTTCAACGCCATATTAGAAGTG AAGTGTCTTAGAGAACTTAAAGTACAAGGAGGTATAGTCCCTTGCTCTCTCTAAATGTCAA AAATCCTCTTGTTCTGATTAGAAATAGGCATGGTAACACAGTTCAGTGGAACCTGTGTA GCTTAAGTCCAAGCCTACGGTGGCTTATTTTCGAAAGTGTAAATCAGCATGCAGCACCC ATTCTCAAGGGGACGTGGATGCATTCAGTTTACTCAATATCAGCATTCAGTGGTCA GAAAAAATAAGGGTAACATAAATAGCAAGAAATGGCGGATGCCACTGCAATATTCACC ATATTAGCGCTGGCTTTGACGAACAACTCGGCTGTTTAAATGGCGAGGATCGCTGTATAT AGAGCAGAACTGATGAGATTCAGATGTTCTCAGATGGGTGACAGAATGTTGATACGATT GTGTCAGAAATTTGGAGAAATAACAAGATGACACCAACAGCTTCAGGCTCAGTGAAACT TCAGCTTATATCCACAGTTTATGTATCATCTACGTGCTTCCCAATTTCTACAAGTGTTCATTA TTCACCAGATGAAACTTCATTTCTATAGGCACATGTTGATAGGGGAAGATCGCAATCAG
EV015	SEQ ID NO: 529 CGCTGTCGAR GCRAARATGG	SEQ ID NO: 530 CGATCAAAAGC GWCCRAAVCG ACG	SEQ ID NO: 519 CGCCATCCGTCGCTGTTCAAGGCGATCGGCGTTAAGCCTCCAAGGGGTATTCTCCTTTACG GGCTCCCGGCACGGGAAACCGCTGATCGCCAGGCGGTGCCAACGAACTGGTGCGT TCTTCTTCTCATCAATGGGCCGAGATTATGAGCAAGCTGGCCGAGAAATCCGAGAGCAA TCTTAGAAAGGCTTTTGAAGAGGCTGATAAAACTCTCTGCAATCATCTTTATCGACGAAT AGAGCAATCGTCCCAAGCGGAGAGAACTCATGTTGAGTAGAGACGATCGTCTC CCAACGTGTTGACTTTGATGGACGGCATGAAGAAAAGTTCCCATGTGATCGTGCGCGCC ACGAACAGGCCCAATTCATCGACCTGACCCCTGACAGCGTTTCGCCGATTCGACACGAGAGA TCGACATCGGTATCCCCGACGCTACTGGAAGATTAGAAGTACTCAGAAATACACACCAAAAAAC

EV016	SEQ ID NO: 531 GTTCACCGGC GAYATYCTGCG	SEQ ID NO: 532 CGGCATAGTC AGAATSGGRAT CTG	ATGAAATTGGCTGACGATGTAGATTGGAAACAGATTGCCGCAGAGACTCACGGTTCATGTAG GTGCTGACTTGCTTCTTTGTGCTCAGAGCTGCCCTTGAACAAATAGAGAAAAATGGAC CTCATCGACTTAGATGAGCAGATCGATGCCGAAGTCCTAAATCTCTGGCAGTTACCAT GGAGAACTTCGGTTACGCCATGTCTAAGAGCAGTCCGAGCGCTTTGCCGCGAAACCGTCGT SEQ ID NO: 521 GACTGTGCTGTGTGAACGGACCGTTGGTGATCCTTGATAGTGTAAAGTTTCCAAAAATTTA ACGAAATTGTACAGCTCAAGTTATCAGATGGAACAGTTAGGTCTGGACAAGTTTGGAAAGTC AGTGGACAGAAAGCGGTTGTCCAAGTTTTTGAAGGCACCTCCGGAATTGATGCTAAAAACA CTTTATGTGAATTTACAGGAGATATCTTAAGAACTCCAGTGTCTGAAGATATGTTGGTCTGT GTGTTAATGGATCTGAAAGCCTATCGATAAAGGCCGCCAATCTTAGCTGAAGATTTTCT TGACATTCAGGTCAACTATAATCCTTGGTCTCGTATCTATCCAGAAGAAATGATCCAGA CTGGTATTTCTGCGATTGATGTGAATCCATTGCCAGAGGACAAAAGATTCCTCAATTTTCT CTGCAGCTGGTTTACCCCAATGAATCGCTGCTCAATCTGTAGACAAGCTGGTCTGTGTC AAAATCCAGGGAAATCTGCTTAGATGATCATGAAGACAACTTTGTCTATCGTTTTCGCCGC TATGGGTGCTCAATATGAAACAGCCAGATTCTTCAAGCAAGATTTGAAGAGAATGGCTCTA TGGAAATGTGTGCTATTTTGAACCTGGCCAAATGATCCTACCATTTGAAGAGAATTAACAC CCGTTTGACTTAAACAGCGGCTGAATTTATGGCATATCAATGTGAGAAGCATGTGTTAGTC ATATTGACTGACATGTCATCTTATGCTGAGGCTTTGCGTGAGGTATCTGCTGCT
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Table 2-AG

Target ID	Primer Forward 5' → 3'	Primer Reverse 5' → 3'	cDNA Sequence (sense strand) 5' → 3'
AG001	SEQ ID NO: 611 CATTGAAGCG TTTWRMYGCYC C	SEQ ID NO: 612 CGCTTGTCCTC GCTCCTCNGC RAT	SEQ ID NO: 601 CATTGAAGCGTTTGTGCTGCCCCCAAAGCATGGATGTTGGACAAAATTGGGGGTGTGTTGCCCC CCAGGCCCTCCACCGGGCCACACAAGCTCAGGGAGTCCCCTCCATTAGTGATTTTCTTGGTAA CAGGTTGAAGTACGCCCTGACAACTGTGAGGTGACCAAGATCGTTATGCAGAGACTTATTAAG GTCGACGGCAAAGTCAGGACTGATCTAACTATCTGCTGATTCTGATGGATGATCACCATTGA AAAACTGGTGAATCTTCCGTTTGATCTATGATGTTAAGGGAAGATTCACTATTCACAGATCAC TGCTGAAGAAGCAAAATACAAATTGTGCAAGTCCGCAAGGTGCAAAACCGGACCAAAAGGTATTC CATTCTTGGTCAACCCAGATGGTAGGACCATAGGTACCTGACCCCAATGATCAAGGTAAACGAC ACCATCCAACCTGAAATCGCCACCTCAAAGATCTGGACTTATCAAAATTCGAATCCGGCAACTT GTGCATGATCACCGGAGGAGAAATTTGGGTAGAGTGGGAACCGTAGTGAACAGGGAAAGGCA TCCGGGATCATTCGATATTGTCCACATTAGGACCGCTAATGATCACGTGTTCCGCCACTAGATTAA ACAACGTATTCTGTCATCGGTAAGGAAGCAAGCTTTCGTGTCCTGCCAAGGGGCAAGGGAGT GAAACTGTCCATCGCTG

AG005	SEQ ID NO: 613 GGTCTGGTTGG ATCCHAATGAA ATCAAYGA	SEQ ID NO: 614 TCCTGCTTCTT SGYRGCRATW CGYTC	SEQ ID NO: 603 GGTCTGGTGGATCCAAATGAAATCAATGAGATTGCCAACACCAACTCGAGGCAAAACATCCGTA AATTGATCAAGGATGTTTATCATTAAGAAACCGGTGGCAGTGCACTCTAGGCTCGTGTCCGT AAAAACACAGAAGCTCGCAGGAAGGAGGCACTGCGTTTCGGTAAGAGGAAAGGTACAGCG AACGCTCGTATGCCTCAAAGGAACTATGGATCCAAAGGATGCGTGTCTTGAAGCGTCTCCTGA AAAAATACAGGGAAGCCAAAAGATCGACAGGCATCTGTACCACGCCCTGTACATGAAGGCCAA GGTAACGTGTTCAAGAACAGAGAGTTGATGGAATACATCCACAAGAAAGGCTGAGAAG GCCGTGCCAAGATGTTGGCCGACCAAGCTAACGCCAGAAAGGCAAAAGGTGAAACAAGTCCCCG TGAGAGGAGGGAAGAGCGTATCGCCCGCGAAGAAGCAGGA
AG010	SEQ ID NO: 615 CTGGCGGCCCA CATGSTBATGG	SEQ ID NO: 616 CGCCATTGGG CRATGTYTCK CC	SEQ ID NO: 605 CTGGCGGCCACATGCTTATGGAGACTCTTTCAATTGCTGTTGTTCAACAACAACTTTCCAAAGG GTGTTCCGGAAGGACCAGATGGACATTTGAAGATGGCTTCAACGGTACTTTGGAGGTGAAGT GCTTAGGGAAATTAAGTTCAAGGCGGTATTGGCTCATGCGTGCCTAAATGTAAAAAGTCCCT TTGGTAGCGGACACGGAATAGCATGGAAACACCGTGCAATGGAAGATGTGCACCTTCAACC CTAGCACGACGATGGCGCTGTTTTTCGAGGTGGTCAATCAGCATTCGCCCCCATTCCTCAAGG TGGTAGAGGATGTATACAGTTTATACACAATATCAGCACTCGAGTGCCCAAGGAGGATAAGGG TGACGACGATAGCGAGAAATTTGGCGGACGCATCGCGAATATTCACCATCAGCGCGGTTT CGATCAGGAACGTGCCGCGGTGATTGCCCCGATGCTGTTTATAGAGCGGAGACCGATGA GAGTCCCGATGTTTTAAGATGGTCTGATCGGATGCTGATTCGTTTGTCAAAAGTTTGGAGAA ATAACAAAGATGACCAGGCATCCTTCAGATTAGGAGAAATTTAGCTTATACCCGCAATTCTATGT ACCACTTAAGCGGATCCAGTTTTTCAAGTGTCAACAATTCACCTGACGAAACGTCGTTTACAG GGCATATGCTTATGAGGGAAGATTTGACACAGTCCCTGATAATGATTAGCCGATCTTGTACAGT TACAGTTTTAATGTTCTCCGGAGCCGTTTTTGTGGACACCAAGCTCAATACAACCGGACAGAA TCTGCTTATGGACACGTTTTTCCAGATATTGATTTCCATGGAGAAACCATTGCCCCAATGGCG
AG014	SEQ ID NO: 617 CGCAGATCAAR CAYATGATGGC	SEQ ID NO: 618 GAACTTGCGG TTGABGTTSCG DCC	SEQ ID NO: 607 CGCAGATCAAGCATATGATGGCTTCAATTGAGCAAGAGGCTAATGAAAAGGCCGAGGAAATTGA TGCCAAGGCGGAAGAAGAAATTTAAACATTGAAAAGGGCGCCCTTGTGCAACAACAAGATTGAAG ATCATGGAATACTATGAGAAGAGGAGAAAGCAAGTCGAACCTACAAGAAATTCATCTCCAA CATGCTGAACCAAGCCCGTCTTAAGGTTCTGAAAGTCCGCGAAGATCATGTTAGAGCTGTATTGG ATGAGGCTCGCAAGAAGCTTGGTGAAGTCACCAAGGATCAAGGCAAAATATGCCAGATTCTGGA ATCTTTGATCCTTCAGGGACTCTACCAGCTTTTCGAGGCAACCGTGACCGTACCGTCCGCCCA CAAGACAGAACTTAGTCCAATCAGTGTGCCAACCTGCAACCAAAATCCGTGACGTCCACCG GCCGAGATGTACACCTGTCCATCGATGACGAACTCAACTGTCCGAATCCGTAACCGCGGAAT CGAATTTTGTGCAAAACAAAACAAATTAAGGTTCTGCAACACCCCTGGAGGACGCTTGGACCTGA TTTCGCAACAGTTGGTTCCGCAAAATCCGTAAACGCCCTTGTTCGGACGCAACATCAACCGCAAGTTC
AG016	SEQ ID NO: 619	SEQ ID NO: 620	SEQ ID NO: 609

GTGTCGGAGG ATATGYTGGY CG	GGAATAGGAT GGGTRATRTC GTCG	GTGTCGGAGGATGTTGGCCGAGTGTCAACGGATCAGGAAACCCATTGACAAAAGGTCCTC CAATCTTAGCCGAAGATTTCTGGACATCCAAAGTCAACCCATCAACCCATGGTCGCGTATCTAC CCGGAAGAAATGATCCAGACCGGTATCTCCGCCATCGACGTGATGAACCTCCATCGCGCGTGGG CAAAAATCCCAATTTCTCCGCGCGGTTTACCGCACAAACGAAATCGCGCCCAATCTGTAG ACAGCCGGTTAGTCAAACTGCCGGGCAATCGGTAACTGACGATCAGGAGCAATTTGGCC ATCGTGTTCGCCCATGGGTGTCAACATGAAACCGCCGTTCTTCAAGCAGGACTTCGAAG AAACGGTTCATGGAGAACGTGTCTCTTCTTGAATTTGGCCAAAGATCCCAACATCGAGAGA ATCATACGCCCGTTGGCTCTGACCGCCCGAATTTTGGCTTATCAATCGAGAAACACGT GCTGGTTATCTTAACGTATGTCTTCTTACGCCGAGGCTTTCGTTGAAGTATCGCGCCGACAG AAGAAGTACCCGGACGTCTGGTTCGCCGTTACATGTACACCGATTTGGCCACCATTTACGA AAGAGCCGGTCGCGTTGAGGTAGAAACGGTTCATCACCACAGATCCCATCTTGACTATGCCG AACGACGACATCACCCATCCTATTCC
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Table 2-TC

Target ID	Primer Forward 5' → 3'	Primer Reverse 5' → 3'	cDNA Sequence (sense strand) 5' → 3'
TC001	SEQ ID NO: 803 GGCCCCAAGA AGCATTTGAAG CG	SEQ ID NO: 804 CGCTTGTCCTC GCTCCTCNGC RAT	SEQ ID NO: 793 GGCCCCAAGCATTTGAAGCGTCTCAATGCGCCCCAAGCATGGATGTTGGATAAACTG GGGGGTGTGTTGCCCTCCACGGCCCCCACAAGCTACGGGAGTCGCTACC TTTGGTTATCTTCTCGAAACAGGCTGAAGTATGCCCTTGACCACTCAGAAGTGACGAA GATTGTTATGCAAGATTGATTAAAGTTGACGGAAAGTTAGGACAGACCCCAACTACCCC GCGGGTTTCATGGATGTTGTGACTATTGAGAAACTGGGAAATCTTCCGCTTGATTTATG ATGTTAAGGGAAGGTTCAATCCATCGCATTAATGAGAGAGAGGCAATATAAATTTGTG CAAAGTGAAGAAAGTACAGACAGGCCCAAGGGCATTCCTTCTTGGTACCCGCGGACG GACGCACTATCAGATACCCAGACCCCATGATCAAAAGTGAATGACACCATTCATTTGGAGAT TGCCACTTCGAAAATTTGATTTTATCAAAATTTGAGTCCGGTAATTTGTGTATGATTACTG GAGGTCGTAACCTTGGGCGGTGTCGGTACAGTGGTGAGCCCGAGAACGTCACCCAGGTTCC TTCGACATCGTTCATATTAGGATGCAAAATGGGCACACC
TC002	SEQ ID NO: 805 CAGGAGTTCCT GGARRMBAAR ATMGA	SEQ ID NO: 806 GCAATGTCTATC CATCAKRTCT GTAC	SEQ ID NO: 795 CAGGAGTTCCTGGAGGCTAAATCGACCAGAGATCCTCACAGCGAAGAAAACCGCGTC GAAAACAACGAGCGCCATCCAGGCCATCAAGAGGAAGAAACGCTACGAAAAGCAGC TCCAGCAGATCGATGGCACCCCTCAGCACCATCGAGATCGAGCGGAGGCCCTCGAGGG GGCCAAACACCAACAGCCGCTACTCAAAACGATGAAAACGACGCGGACGCCCTCAAAAA TGCCCCACCTCAACATGGATGTTGATGAGGTACATGACATGATGGATGACATTGC
TC010	SEQ ID NO: 807	SEQ ID NO: 808	SEQ ID NO: 797

TC014	<p>GCATTCTGCGC TGGGTCGATCG</p> <p>SEQ ID NO: 809 GAGAAAGCCG ARGARATYGAT GC</p> <p>SEQ ID NO: 810 GAAC TTGCGG TTGABGTTSCG DCC</p> <p>TGCCGGAAGT TCTC RTAYTK GGC</p> <p>AAAAATCGGCGAATACAACAAGAGCAGACCCTAACAGTTTCGGTTTGAGTGAAAACTTCAGT CTCTATCCCAATTCATGTACCATTTGCGCCGCTCCCAATTCCTCCAAGTTTCAACAAC CCCCAGACGAGACCTCGTTCTACCGCCACATGCTGATGCGGGAGGACCTCACCCAAAGT CTCATTATGATCCAGCCGATTTGTACAGTTATAGTTTCAACGCCCCCTGAACCCGTCG TCCTCGACACTAGTTCATTCAACCCGATCGGATCCTTCTCATGGACACATTTTCCAAAT TTGATTTTCCACGGTGAGACAAATCGCCCAATGGAGGAACCTCAAGTACCAGGACATGCC GAATAGGAGAACTTCGGCA</p> <p>SEQ ID NO: 799 GAGAAAGCCGGAAGAAATCGATGCGAAAGCTGAGGAGGAGTTTAACTTGAAAAAGGGCG CCTGTGTCACAACACAGCGCTTGAAGATCATGGAATATTACGAGAAAGAGAAACCGGT GGAATTGACAGAAAGAAATTCAGTCGTCAACATGCTGAACCAAGCCCGTTTGAAGTATTA AAAGTGGTGAAGACCAACGTCACAAATGTGCTGGATGACGCCCGCAACGCTCGGGCA AATCACCAATGACCAGCGGAGATATTCACAACCTTTTGAGTCTCTTATCCTCCAGAGTCTC TACCAGTACTTGGGAATCAGTGATGAGTTGTTGAGAACAAATATAGTGGTGAGAGTCAGG CAACAGGACAGGAGTATAATCCAGGCGCATCTCCAGTTGTTGCGACGAAATACAGGGAC GCCACTGGTAAAGACGTTTCATCTTAAATCGACGATGAGAGCCACTTGCCATCCGAAACC ACCGGAGGAGTGGTTTGTATGCGCAAAAGGGTAAATCAAGATTGACAACACCTTGGAG GCTCGTTGGATTAAATGACACAGCAACTTGTGCCAGAAATTCGTACGGCCTTGTGTTGGAC GCAACATCAACCGCAAGTTC</p>
TC015	<p>SEQ ID NO: 811 GGATGAAC TAC AGCTBTTCGGH GG</p> <p>SEQ ID NO: 812 CGATCAAAGC GWCCRAAVCG ACG</p> <p>SEQ ID NO: 801 GGATGAAC TACAGCTGTTCCGTGGCGATACAGTGTGCTGAAAGGGAAGCGCGGAAAG AGACCGTCTGCATTGTGCTGCCGACGAAAC TCCCGATGAGAAAGATCCGGATGAAC AGGATCGTCAGGAATAATCTACGGGTTAGGCTCTCTGACGTCGTCTGGATCCAGCCCTGT CCGACGTCAATACGGAAGAGGATCCACGTTTGGCCATCGATGACACGGTCGAAGG GCTCGTCGGAATCTCTTCGAGGTGACTTAAACCATAC TCCCTCGAAGCTTATCGACCA ATCCACAAAGCGACGTTTTCATCGTCCGTGGTGCGATGCGAGCCGTTGAATCAAAGTG GTGGAACGGAAACCGTCACCATATTGTATCGTCCCCCGATACCGTCATCCATTGTGAC GGCATCCGATCAAACGAGAAAGAGAGGAGGAAGCCTTGAACGCCGTCGGCTACGACGA TATCGGCGGTTGTCGCAACAACTCGCACAAATCAAAGAAATGTCGAAATACCTCTACG CCACCCGTCGCTCTTCAAGGCCATTGGCGTGAACCCACACGTTGATCCTCTTGTACGG ACCTCCAGGTACCGGTAAACCTTAAATCGCATGTCAGTGCCCAACGAAACCGGCTTT CTTCTCTTAAATCAACGGTCCCGAAATTAAGTAAATAGCCCGGGAATCCGAAAGTAAT CTAAGGAAAGCGTTCGAAGAAGCCGATAAAAC TACCCGGCTATTAATTTTCATCGATGAAT TGGACGCGATTGCACCGAAACGTGAAAAACCCGCGGAAGTCGAACGCCGAATTGTC TCGCAATTGTTAACACTGATGGACGGCATGAAGAAAAGCTCGCATGTTATCGTATGGCG GCCACAAATCGCCCGAACTCAATCGATCCGGCTTTCGGTCGGTCCGCTTGTGATCG</p>

Table 2-MP

Target ID	Primer Forward 5' → 3'	Primer Reverse 5' → 3'	cDNA Sequence (sense strand) 5' → 3'
MP001	SEQ ID NO: 898 GGCCCCAAGAA GCATTTGAAGC G	SEQ ID NO: 899 CGCTTGTCCTC GCTCCTCNGC RAT	SEQ ID NO: 888 GGCCCCAAGAACATTGAAGCGTTAAACGCAACCCAAAGCATGGATGTGGACAAATCGGG GGGTGCTTCGCTCCACGTCACAGCACCGGTCCACACAACTTCGTGAATCACTACCGTTATT GATCTTCTGGTAATCGTTGAAGTATGCACCTTACTGGTCCGAAGTACCAAGATTGTCTAT GCAAAGATTAAATCAAGGTTGATGGCAAAGTCCGTAACGACCTTAATTATCCAGCCGGTTTTAT GGATGTTATATCTATCCAAAGACCAAGTGAAGTATGATTTAGATTGATCTATGATGTGAAGGTGCG TTTCACCATCCACAGAAATTAATCTCTGAAGAGCAAAATACAAGTTGTGTAAAGTAAAGAGGGT ACAACTGGACCCAAAGGTGTCCTATTTTAACTACTCATGATGCGCTACTATTCCGTACCCC TGACCCCTAACATCAAGGTTAATGACACTATTAGATACGATATTCATCATCTAAAATTTTGGAT CATATCCGTTTTGAACTGGAACCTTGTCATGATACTGGAGTCCCAATTTAGGGCGTGTT GGTATTGTTACCAACAGGGAAGACATCCAGGATCTTTGATATTGTTACATTAAGGATGCA AATGAACATATTTTGTACCCCGGATGAACAAATGTTTTATTATTGAAAGGTCAAAAGAACT ACATTTCTCTACCAAGGAGTAAGGGAGTTAAATTGACTAT
MP002	SEQ ID NO: 900 GAGTTCTTTA GTAAAGTATTC GGTGG	SEQ ID NO: 901 GCAATGTCATC CATCAKRTCT GTAC	SEQ ID NO: 890 GAGTTCTTTAGTAAAGTATTCGGTGGCAAAAGGAAGAGAGGACCATCAACCCGAAGATG CGATACAAAAGCTTCGATCCACTGAAGAGATGCTGATAAAGAAACAAGAAATTTTAGAAAAA AAATTGAACAAGAGTAGCGATAGCCAAAAAATGTTACAACATAAAGAGAGTGCATTGC AAGCATTGAAGCGTAAGAAACGGTACGAACAACAAATTAGCCCAATTTGATGGTACCATTAA CTATTGAACAACAGCGGGAGGCATTAGAAGGTGCCAACACAAATACAGCAGTATTGACTACC ATGAAAACTGCAGCAGATGCACCTTAATCAGCTCATCAAAACATGAATGTAGATGATGTACAT GATCTGATGGATGACATTGC
MP010	SEQ ID NO: 902 GTGGCTGCATA CAGTTCATTAC GCAG	SEQ ID NO: 903 CGCGGCTGCT CCATGAAYASY TG	SEQ ID NO: 892 GTGGCTGCATACAGTTCAATTAGCGCAGTATCAACATTCAGTGGCTATAAACGAATTAGAGTCA CCACATTAGCTAGGAATTGGCAGACCCCTGTTCAGAAATATGATGCATGTTAGTGTGCTGCAATTG ATCAAGAAGCATCTGCCGTTTAAATGGCTCGTATGTTAGTAGTGAACCGTGTGAACTGAGGATA GTCCAGATGTGATGCGTTGGCTGATCGTACGCTTATACGCTTGTGTCAAAATTTGGTGATT ATCAAAAAGATGATCCAAATAGTTTCCGATTGCCAGAAACCTTCAGTTTATATCCACAGTTTCA GTATCAATTTAAGAAGGCTCAATTTTACAAAGTTTTTAAATAAGTCTGATGAACATCATATT ATAGGCACATGTTGATGCGTGAAGATGTTACCCAAAGTTTAAATCATGATACAGCCCAATTTCTGT ATAGCTATAGTTTTAATGGTAGCCAGAACCTGTACTTTTGGATACCCAGTAGTATTCAACCTGA TAAATATTATTGATGGACACATTTTTCCATATTTTATGATATTCATGGAGAGACTATTGCTCAAT

MP016	SEQ ID NO: 904 GTGTCGGAGG ATATGYTGGY CG	SEQ ID NO: 905 GGAATAGGAT GGGTRATRTC GTCG	GGAGAGCAATGGATTATCAAAATAGACCAGAGTAGTAACCTCAAGCAGTTGCTTCAAGCCC CCGTTGATGATGCTCAGGAAATCTCAAACCTCGATCCCAATGCCTCGGTATATTGACACAG AACAAGGTGGTAGTCAGGCAAGATTTTACTATGCAAAAGTAAACCCATCTCAAACACATAATAA TATGATGCTTATGGAGGGTGATGGTGAGCACCAAGTTTGGACAGATGATGTAAGCTTGACG CTGTTGATGGAGCAGCCGCG
		SEQ ID NO: 894	GTGTCGGAGGATATGTTGGCCGCGTTTCAATGGCAGTGGAAAGCCGATAGATAAAGGACC TCCTATTTTGGCTGAAGATTATTTGGATATTGAAGGCCAACCTATTATCCATCTCCAGAACA TATCCTCAAGAAATGATTCAAACTGGTATTTCAAGCTATTGATATCATGAACCTATTGCTCGTG GACAAAAATCCAAATATTTTCACTGCAGGTTTACCACATATGAGATTGCTGCTCAAAATTTG TAGACAAGCTGGTCTCGTTAAAAAACCTGGTAAATCAGTTCTTGACGATCATGAAGACAAATTTT GCTATAGTATTTGCTGCTATGGGTGTTAATATGGAACAGCCAGATTCTTTAAACAAGATTTTG AGGAAATGGTTCAATGGAGAAATGTTGTTGTTCTTGAATTTAGCTAATGATCCTACTATTGA GCGTATCATTACACCACGCTTGCCTTAACTGCTGCTGAATTTTAGCTTACCAATGTGAAAAG CATGCTTAGTTATTTAACTGACATGAGTTTCATATGCTGAAGCTTTAAGAGAAGTTTCTGCTG CTCGTGAAGAAGTACCTGGCGTCTGGTTTCCCTGGTTACATGTACACCCGATTAGCTACAA TTTATGAACGTGCTGGCGGTGAGAAGGAAATGGTTCTATCACACAAATACCTATTTTAA CTATGCCCTAACGACGACATCACCCATCCTATTCC
MP027	SEQ ID NO: 906 CGCCGATTACC AAAACAARACB TG	SEQ ID NO: 907 GGGATACTGT CACAAYTCDG CRCC	SEQ ID NO: 896 CGCCGATTACCAAAACAAGACGTGTGTTCCAGACATTAGAAGGCCATGCTCAAAATATTTCTGC TCGTTTGTTCATCCAGAACTTCCCATCGTGTAACTGGCTCAGAAGATGGTACCGTCAGAA TTTGGCATTCTGGTACTTATCGATTAGAATCATCAATTAACCTATGGTTAGAACGTGTATGGAC AATCTGTTGCTTACGGGATCTAATAATGATGCTCTAGGTTATGATGAAGGAAGTATAATGGT TAAAGTTGGTCGTGAAGAGCCAGCAATGTCAATGGATGTTTCATGGGGTAAATTTGTTGGG CACGTCATAGTGAATTCACAAGCTAACCTTAAAGCCGATGCTTCAAGCAGAAGGAGCCGAAA TCAAAGATGGTGAACGTTTACCAATACAAGTTAAGACATGGGTAGCTGTGAAATTTATCCAC AGTCAATATCTCATAATCCGAATGGTAGATTTTATAGTAGTATGTGGTATGGAGAGTATATTAT ATATACATCAATGGCTTTGCGTAATAAAGCAATTTGGCTCCGCTCAGGATTTTGTATGGTCTCT GATTCTGAGTATGCCATTAGAGAAAATTTCTTACAATCAAGTTTTTAAAAATTTTAAAGAAAA AAAGCTTTTAAACCAGAAGGTGGAGCAGATGGTATTTTGGAGGTATTTGTAGGTGTGAA ATCTGTTACTGGGTGGCTTTATATGATTGGGAAAATGGTAACCTAGTTTCGAAGAATTGAGAC ACAACTAAACATGATTTTGGTCAGAGTCTGGAGAAATAGTATGCTTGGCCACAGATGAAGC ATACTTTATTTTACGTTTGGACGTCATGTAATGTAAGTCTGCAAGAGCATCCAATTTATGAAGCT GCTAGTCTGATGGTCTTGAAGATGCCCTTTGAGATTTTAGGAGAAGTTCAAGAAGTTGTAAAA ACTGGTCTATGGGTGGTGGTATGCTTTTATTTACACCAATGGAGTAAATCGTATCAACTATTATG TTGGTGGTGAAGTTGTGACAGTATCCC

Table 2-NL

Target ID	Primer Forward 5' → 3'	Primer Reverse 5' → 3'	cDNA Sequence (sense strand) 5' → 3'
NL001	SEQ ID NO: 1117 GAAATCATGGAT GTTGGACAAATT GG	SEQ ID NO: 1118 ACTGAGCTTCACAC CCTTGCCC	SEQ ID NO: 1071 GAAATCATGGATGTTGGACAAATTGGGTGGTGTATGCACCCCGACCCAGCACAGG TCCACACAAGCTGCGAGAATCTCTCCACTTGTGTCATATTTTGGCGTAATCGGCTCAAG TACGCTTTAACTAAGTGAAGTGAAGAAATTTGTATGCAGCGTCTCATCAAGGTTG ACGGCAAAGTGAGGACTGACCCCAACTATCCTGCAGGTTTTATGGACGTTGTTCAAAT CGAAAGACAAACGAGTTCTTCCGTTTGTATGATGTTAAAGGGACGTTTCACCATC CACAGGATCACAGCTGAAGAAGCTAAGTACAAGCTGTGCAAAAGTGAAGAGGGTTTCAG ACAGGACCCCAAGGGCATTCATTTTGACCACTCACGATGGACGCCACATCAGGTAT CCAGACCCCTTGTTAAAGTCAATGACACCATCCAATTGGACATTTGCCACATCCAATA TCATGGACTTCATCAGATTGCACTCTGGTAACCTGTGTATGATCACTGGAGGTCGTAA CTTGGGTCGTGGGCACGTGCTGAACAGGGAGCGACACCCCGGGTCTTTCCGACA TCGTGCACATCAAGGACGTGTTGGGACACACTTTTGCCACTAGGTTGAACAACGTTTT CATCATCGGCAAGGGTAGTAAAGCATACGTGTCTCTGCCCAGGGCAAGGGTGTGAA GCTCAGT
NL002	SEQ ID NO: 1119 GATGAAAAGGG CCCTACAACTG GC	SEQ ID NO: 1120 CTGATCCACATCCA TGTGTTGATGAG	SEQ ID NO: 1073 GATGAAAAGGGCCCTACAACCTGGCGAAGCCATTGAGAACTACGCGAAACAGAGGAA ATGCTGATAAAGAAACAAGACTTTTGTAGAAAAGAAATTTGAAGTTGAAATTTGGAGTTGC CAGGAAGATGGAACAAACAAACAAAGAGCCGCGATCCAGGCACTCAAAAGGAAAGAA GAGGTATGAAAAGCAATTGCAGCAGATCGATGGAACGTTATCAACAAATTGAGATGCA GAGAGAGGCCCTCGAAGGAGGCCAACACGAATACGGCCGTACTGCAAACTATGAAGA ACGCAGCAGATGCTCTCAAAGCGGCTCATCAACACATGGATGTGGATCAG
NL003	SEQ ID NO: 1121 TCCGCGTCGTC CTTACGAGAAG GC	SEQ ID NO: 1122 TTGACGCGACCAG GTCGGCCAC	SEQ ID NO: 1075 TCCGCGTCGTCCTTACGAGAAGGCACGTCCTCGAACAGGAGTTGAAGATCATCGGAGA GTATGGACTCCGTAACAAGCGTGAGGTGTGGAGAGTCAATACGCCCTGGCCAAAGAT TCGTAAGGCCGCTCGTGAGCTGTTGACTCTGGAAGAGAGGAGCCAGAACCGTTTGT TGAAGGTAACGCCCTGCTGCGTCCCTGGTGGCTATTGGAGTGTGGACGAAAGGAA GAATGAAGCTCGATTACGCTTGGGTTTAAATTTGAAGATTTCTTGAACGTCGCT ACAGACTCAGGTGTACAACTCGGTTTGGCCAAAGTCCATCCATCAGCCCGCTGTACT CATCAGACAAAGACATATCAGAGTGGCAACAAAGTAGTGAACATTCGAGCTTTGTG GTGCGCCCTGGACTCGCAGAAGCACATTGACTTCTCGCTGAAGTCGCCGTTTCGGCGG TGCCCGACCTGGTCGCGTCAA
NL004	SEQ ID NO: 1123	SEQ ID NO: 1124	SEQ ID NO: 1077

	TGAAGGTGGAG AARGTTYGGM WCMAAG	GTCGTCTTCTCDGA HACRTAVAGACC	AAGGAGTTGGCTGTAAGAACTGTCTGCTCTCACATCGAAACATGCTGAAGGGA GTCACAAAGGATTCTGTACAAGATGCGTGCCGTGTACGCCCATTTCCCCATCAAC TGTGTACGACCGAGAACAACTCTGTGATCGAGGTGCGTAACCTCTCTGGGCGAGAAG TACATCCGACGGGTGAGGATGGCGCCCGCGTCACTGTTACCAACTCGACAAAGCA GAAGGACGAGCTCATCGTGAAGGAACAGCATAGAGGACGTGTCAAGATCAGCTG CCCTCATCCAACAGTCAACAACAGTGAAGAACAGGATATTCGTAATTTCTTGAC
NL005	SEQ ID NO: 1125 GGTCTGGTTGG ATCCHAATGAAA TCAAYGA	SEQ ID NO: 1126 TCCTGCTTCTTSGY RGCRA TWCGYTC	SEQ ID NO: 1079 TTGGATCCCAATGAAATAAATGAAATCGCAAAACACAAAATTCACGTCAAAGCATCAGGA AGCTGATCAAAAGACGGTCTTATCATCAAGAAACCGGTTGCAGTACATTACCGTGCTCG CGTTCTGTAACAACTGAAGCCAGGAGGAAAGGAGACATTTGGCTTTGGTAAGAG GAAAGGTACAGCCCAACGCCCTGATGCCACAAAAGGTTCTATGGGTGAATCGTATGCG TGCTTTGAGAAGACTGTTGAAAAAATACAGACAAGATAAGAAAAATCGACAGGCATCTG TACCATCACCTTTACATGAAGGCTAAGGTTAAGTATTCAGAAACAAGCGTGTATTGA TGGAGTTCAATCATGAAGAAAGGCGCGAGAAAGCAAGATGAAGATGTTGAACGACC AGGCTGAAGCTCGCAGACAAAAGGTCAAGGAGGCCAAGAACGCGAAGGGAA
NL006	SEQ ID NO: 1127 GGAGCGAGACT ACAACAAYKAYR GYTGGC	SEQ ID NO: 1128 GAGATCTTCTGCAC RTTKACVGCATC	SEQ ID NO: 1081 AAGTGCTTGTGTCAGTGGTGTGGTGAGTACATTGACACCCCTGGAGGAGGAGACG ACCATGATAGCATGTGCGGGATGACCTGCGTCAGGACAAAGAGTATGCCACTACTGT ACCACCTACAGCACTGCGAGATCCACCCGGCCATGATACCTGGTGTGCGCCTCT ATTATCCCTTCCCGATCACAAACCAAGTCCCAGGAACACCTATCAGAGCGCTATGG GGAACAGGCGATGGCGGTACATCAACCTCCACGTCGGAATGGACACGCTG GCTCACGTGCTGTTCTACCCGACAAAGCCACTGGTCAACCTCGCTCCATGGAGTAC CTGCGCTTCAGGGAGCTTCTGCGGGCATCAACTCTGGTCGCCATCGCCTGCTAC ACTGGATACAACCCAGGAGGACAGTGTCAATCTCAACGCCCTCCGCTGTCGAGCGCGG ATTCTCAGATCGGTTTTCTCCGATCTTACAAGATGCAGAAATCGAAGCGTATTGGC GACCAAGAGGAGCAATTCGAGAAGCCCAACAGACAGACGTGTCAAGGAATGAGGAA TGCCATTTATGACAAATTGGACGATGATGGCATCATTTGCTCCCGGTCTGAGAGTGTCT GGTGACGATGTGGTTATTGGCAAAACCATACACTGCCCGATAATGATGACGAGCTG GAAGGTACAACAAGAGGTTACGGAAGAGAGATGCCAGTACTTTCCTGCGTAACAGT GAGACGGGAATCGTCGACCAAGTCATTTAACTTGAACCTGAGGGTTACAAGTTTC TGCAAAATTCGATCAGGTCTGTGCGTATCCCGAGATGGCGATAAGTTCCGCTTCC CGACATGGCCAAAAGGACGTTGGAATACAGTATCGTCAAGAGGACATGCCCTTTT ACAAGCGAGGGAATCGCACCGGATATTATCAATCCTCACGCTATCCCATCTCGTA TGACAAATTGGCCATTTAAATTGAATGTCTCCAAGGAAAGGTGTCGTGCAACAAGGGCG AGATAGGTGACGCGACGCCGCTTCAAC
NL007	SEQ ID NO: 1129	SEQ ID NO: 1130	SEQ ID NO: 1083

	CGGTGTCCATT ACAGYTCCGG	CGATGCAAGTAGG TGTCRGARTCYTC	TTTCAGAGATTCTCTGAAACCTGAAATTTTGAGAGCAATCCTTGACTGTGGTTTTG AACATCCATCTGAAGTACAACATGAATGCATTCCTCAAGCTGTACTTGAATGGACAT ATTGTGTCAGCGAAATCCGGTATGGGAAACTGCTGTATTTGTGTGGCGACATTA CAGCAAAATTGAACCAACTGACAACCAAGTCAAGTGTATTTGGTGTATGTGTATACCAGAG AGCTTGCAATCCAAATCAGCAAGAGTATGAACGATTTCGAAATGTATGCCAAATAT CAAGGTTGGAGTTTCTTCGCGGACTGCCGATTCAGAGGATGAGGAGACGTTGAA ATTGAACGTGCTCCATCATCGTGGTTGGAACACCCGGAGAAATTTGGCGTTGTACG CAACAAGAAGCTGGACCTCAAGCATCTCAAGCACTTTGCTTGACGAATGTGACAAA ATGTTGGAACGTTAGATATGCGAAGAGATGTCAGGAAATATTCGAAACACGCCG CACAGCAACAAGTCAATGATGTTCAAGTCAAGTCTCAGCAAGAAATTCGTCCAGTCT GCAAGAAATTCATGCAAGATCCGATGGAAGTGACGTGTGATGACGAGGCCAAGCTGA CGCTCACGGCTGCAGCAGCACTATGTCAAACTCAAGAAACCGAAAGAAACAAAA AGTTATTTGAATTACTTGACATACITGAATTCACCCAGGTGTTATATTTGTGAAGTCA GTGAGCGCTGCATGCCCTATCGCAACTCCTAACAGAGCAAACTTCCTGCAGTG GCTATTCACCGTGGCATGACACAAGAAGAACGATTGAAGAAATATCAAGAGTTCAAAG AGTTCCCTAAAGCGAAATTTGGTAGCAACGAATCTGTTTGGCAGAGGAATGGATATTGA GAGAGTCAACATTTGATTCAACTATGACATGCCT
NL008	SEQ ID NO: 1131 GTGGTGATCA CTTYAAYCGKAT G	SEQ ID NO: 1132 GCGCATTTGATCGT TBGTYTTCAC	SEQ ID NO: 1085 GGAAGGATAGAAACCAGAAACGAGTTGTTGGTGTCTTTTGGGATGCTGGAGACCT GGAGGTGATAGATGTTTCAACAGTTTTGCAGTTCATTTGATGAGGACGACAAAG AAAAGAAATGTTGGTCTTAGACCATGATTACTTGGAAACATGTTCCGGGATGTTCAA GAAAGTTAATGCTAGAGAAAGGTTGTGGTTGGTACCATCTGACCCAAACTCCA CCAAAACGATGTTGCAATCAATGAGTTGATTGTCGTTACTGTCCAACTGTGCTTTA GTCATAATCGATGCCAAGCCTAAAGATTTGGTCTACCTACAGAGGCATACAGAGTC GTTGAAGAAATCCATGATGATGGATCGCCAAACATCAAAACATTTGAACATGTGATGA GTGAGATTGGGCGAGAGAGGCTGAGGAGATTGGCGTTGAACATCTGTTGAGAGAC ATCAAGATACAACAGTCGGGTCACTGTCACAGCGCGTCAAAATCAGCTGATGGGC TTGAAGGGCTTGATCTGCAATTACAGGATATGCGAGATATTTGAATCAGGTTGTGCG AAGGAAAGTTGCCAATGAACCATCAATCGTTTACCAACTGCAAGACATCTTCAACCT TCTACCCGATATCGGCCACGGCAATTTTGTAGACTCGCTCTAC
NL009	SEQ ID NO: 1133 GGCCCGTGGTC AGAAYATYWAYA AC	SEQ ID NO: 1134 CCGCCAAAGGACT SARRTADCCCTC	SEQ ID NO: 1087 TGCGACTATGATCGACCGCCGGGACGCGGTGAGGTGTCGACGTCGACGTCAGAA CTGGTTTCCCTGCACCTCTGAGAACAAATTTCAACTACCATCAATCGAGCCCTTGTT TTTCTCAAACCTGAACAAGATAATTGGTTGGCAACCGGAGTACTACAATGAGACTGAAG GCTTCCAGATAATATGCCAGGTGACCTCAAGCGACACATTTGCCCAACAGAGAGTA TCACAAGCTGTTTATGCAACAATCTGGATAACTTGGCAAGGAGAGGGTCTCTAGA

NL010	SEQ ID NO: 1135 CGGCTGACGTG GAAYGKTGGC C	SEQ ID NO: 1136 TGCCGGAAGTTCTC RTAYCKGGC	<p>CAAGGAGAATGCAGGGGAGATCCAGTACATCCCTAGACAGGGATTTCGGGGCTACTT CTACCCCTTACACTAATGCC</p> <p>SEQ ID NO: 1089 (amino terminus)</p> <p>GTCCAGTCGACTGGAAGCCACCAGGCTTGTTGTTCCCGTTGGATGTCTGTATCAACC TTTGAAGGAGAGACCTGATCTACCGCTGTACAGTACGATCCAGTTCCTTTGTACTAGG AATACTTGCTGCTCAATTCTGAATCCATTGTCGAAGTGAATATCGAGCAAGCTAT GGTCTGCAACTTTTGTCCAGAGGAATCTTCCGCCCTCAATATGCAAGTATTTT GGAGCAGCATCAACCAGCAGAACTGATACCTTCATTTCCACCATCGAATACATCATT ACAGAGCGCAACGATGCCCGCATGTCGTGCTGGTGGACACATGTCTGGA CGACGAGGAGCTGGGAGCTTTGAAGGACTCACTGCAGATGTGCTGCTGCTGC CGCCCAATGCATCTCGGTCTCATCACGTTCCGCAAAATGGTCAGGTGCACGAGC TTGGCTGCGACGGCTGCTCGAAGAGCTACGTGTTCCGTGGCGTGAAGGACCTGACT GCCAAGCAGATCCAGGACATGTTGGCATTTGGCAATGGCAAGATGGCCGCGCTCCACAGCC CATGCAACAGCGCATTCGGCGCGCTCCCTCCGACCTGTCAACAGATTCTTCA GCCTGTCGGAAGTGCATATGAGTTAACTGATCTGCTGGGGAATTGCAAGAGA TCCATGGAATGTGGCTCAGGGCAAGAGACCTCTCCGATCTACTGGAGTTGCATTGTC CATTGCAGTTGGTCTGCTCGAGTGCACA</p> <p>SEQ ID NO: 1115 (carboxy terminus)</p> <p>CGTTGAACGTGAAAGGCTCGTGTGTCTCAGACACTGACATTGGCTTGGCGGCACT CTCAATGGAAATGTGCGCTTCACTCCACACACAACCTTGTCATTCTTCGAAAGT TGTCAAACAGCAGCAGCCCAATCCACAGGAGGAAGAGGATGCATCCAAATTCAT TACGCAATACCAACATTCAGTGGCCAGAGGATACGTGTCACCACTCGCTCG AACTGGGCAGATGCGAGCACCAACCTGGCACACATCAGTCCCGGCTTCGACCAAG AGCAGGAGCCGTGCTGATGGCCCGCATGGTCGTGATCGCGCCGAGACTGACGAT GGACCTGACGTGATGCGCTGGCTGACCGCATGCTCATCCGTCTCTGTGAGAGGTT GGTGAATACAGTAAGGATGACCTTAACAGTTTCGTCCTCCAGAGAACTTCACACTTT ATCCGAGTTTCATGACCATCTGCGTCGATCCCAATTTCTGCAAGTGTTCACCAACAG TCCTGATGAAACATCTTACTACAGGCACATTTCTTATGCGAGAGGATCTGACTCAGAGT TTGATTATGATCCAGCCGATTTGTACAGCTACAGCTTCAATGGTCCCCCGGAGCCAG TGCTGCTCGACACAGCAGTATTCAACCCGACAGAACTCTATTGATGGACACATTTT CCAAATTCATTTTCCATGGAGAGACGATTGCTCAATGGCGATCTCTGGGCTACCCAG GACAT</p>
NL011	SEQ ID NO: 1137 CCCACTTTCAAG TGYGTRYTRGTC GG	SEQ ID NO: 1138 CGCTCTCTCTCGAT CTGYDSCTGCC	<p>SEQ ID NO: 1091</p> <p>AGATGGTGGTACCCGGCAAAACTACATTTGTCAAACGACATCTTACCGGAGAAATTTGAA AAGAAAGTATGTTGCCACCCCTTGGAGTTGAAGTTCAAGTTACCCCTTGTATTTCAACAAACA GAGGTGTATTAGGTTCAATGTGTGGACACACAGCTGGCCAGGAAAGTTTCGGGTGGA</p>

			CTTCGTGATGGATATTACATTACAGGGACAATGCGCCATCATTTATGTTGACGTAACGT CAAGAGTCACCTACAAGAACGTTCCAACTGGCACAGAGATTAGTGAGGGTTTGCG AAACATTCCATTGTACTATGCGGCAACAAAGTAGACATCAAGGACAGAAAGTCAA GGCCAAAGAGCATAGTCTCCATAGGAAGAAACCTTCAGTACTACGACATCAGTGC GAAAGCAACTACAATTCGAGAAGCCGTTCTGTGGTTGGCAAAGAAGCTGATCGG TGACCCCAACCTGGAGTTGTCGCCATGCCCGCCCTCTCCACCCGAGGTCACAAT GGACCCCCCAAT
NL012	SEQ ID NO: 1139 GCAGGCGCAGG TBGABGARGT	SEQ ID NO: 1140 GAATTCCTCTTSA GYTTBCCVGC	SEQ ID NO: 1093 GCAGCAGACGAGGACAGGAGGAGGTTGTCGATATAATGAAAAACAAACGTTGA GAAAGTATTGGAGAGGGATCAAAAACATATCAGAAATTGGATGATCGAGCAGATGCTCTA CAGCAAGGCGCTTCACAGTTTGAACAGCAAGCTGGCAAACTCAAGAGGAAATTC
NL013	SEQ ID NO: 1141 CAGATGCGCCC GTBGTDGAYAC	SEQ ID NO: 1142 GCCCTTGACAGAYT GDATVGGATC	SEQ ID NO: 1095 CGCAGAGCAAGTCTACATCTCTCACTGGCCCTATTGAAAAATGCTTAAGCACGGTCGC GCCGGTGTCCCATGGAAGTTATGGCCCTAATGCTGGCGAAATTTGTAGACGACTAC ACTGTGCGTGTCAATTGATGATTCTGCTATGCCACAGAGTGGAACGGGAGTGAGTGTG GAGGCTGTAGACCCGGTGTCCAAAGCGAAGATGTTGGACATGCTAAAGCAGACAGG ACGCCCCGAGATGGTGGCTGTACCACCTCGACCCCGGCTTCGGCTGCTGG CTGTGCGGTGTGACATCAACACGACGAGGAGGCTTCGAGCAACTATCCAAGAGAGC CGTTGCCGTGCTCGTC
NL014	SEQ ID NO: 1143 CGCAGATCAAR CAYATGATGGC	SEQ ID NO: 1144 GAACTTGCGGTGA BGTSCGDCC	SEQ ID NO: 1097 TTTCATTGAGCAAGAAGCCCAATGAGAAAGCCGAAGAGATCGATGCCAAGGCCGAGGA AGAATTCACATTTGAAAAGGGAAGGCTCGTACAGCACACGCGCTTAAAATCATGGA GTACTATGACAGGAAAGAGAGCAGGTTGAGCTCCAGAAAAAATCCAATCGTCAAA CATGCTGAACCAAGCGCTCTGAAGGCACTGAAGGTGCGCGAAGATCACGTGAGAA GTGTGCTCGAAGATCCAGAAAACGCTCTGGAGAAGTAACCAGAAACCCAGCCAAAGT ACAAGGAAGTCTCCAGTATCTAATTGTCCAAAGGACTCCTGCAGCTGCTAGAAATCAA CGTAGTACTGCGGTGCGGAGGCTGACGTGAGTCTGATCGAGGGCATTGTTGGCT CATGCGCAGAGCAGTACGCGAAGATGACCGGCAAGAGGTGGTGAAGCTGGAC GCTGACAACTTCTGGCCCGCGAGACGTGTGGAGGCGTCGAGTTGTTCCGCCGCAA CGGCCGATCAAGATCCCCAACACCCCTCGAGTCCAGGCTCGACCTCATCTCCCAGCA ACTTGTGCCCCGAGATTAGAGTCGCGCTCTTT
NL015	SEQ ID NO: 1145 GCCGCAAGGAG ACBGTVTGC	SEQ ID NO: 1146 GTCCGTGGGAYTC RGCHGCAATC	SEQ ID NO: 1099 ATTGTGCTGTCTGACGAGACATGTCCGTTGAAAAGATCCGCAATGAATCGAGTGGTC AGGAAGAATCTCGAGTGGCTGTCCGACATGTCTCGATCCAGCCTTGCCCGAGAC GTCAAGTATGAAAAGCGTATCCATGTGCTGCCCATTTGATGATACCGTTGAGGGTCTTA

NL016	SEQ ID NO: 1147 GTTACCCGGCG AYATYCTGCG	SEQ ID NO: 1148 CGGCATAGTCAGA ATSGGRATCTG	CAGGAAATCTGTTGGAAGTGATTGAAGCCATACITTCCTGGAAGCATACAGGCCAAT TCACAAGGATGATGCATTGTTGCGGAGGATGAGAGCGGTCGAATCAAGGT GGTTGAAACAGATCCATCGCCCTACTGCTGCGGAGGATGAGAGCGGTCATCCATTG TGAGGAGACCCCATCAAACTGAGGATGAGGATGAGGAGGATGAGGAGGATGAGGAGGAT ACGACGACATTGGAGGCTGCAGAAAGCAGCTGGCGGAGATCAAGAGAGATGGTGGAG TTGCCGCTGAGACATCCAGTCTGTTCAAGGCGATCGGCGTGAAGCCGCCACGAGG CATCCTGCTGACGGACACCGGGAACCGGAAGACGTTGATAGCGCGCGCGCTCG CCAACGAAACGGCGCTTCTTCTCTCATCAACGACCCGAGATTATGAGCAAT TGCCGCGGAGTGGAGAGTAACCTGCGCAAGCTTTCGAGGAAGCGGACAAAAC GCACCGGCCATCATCTTCATCGATGAGCTGACGCAATCGCGCCAAAACCGGAGAA GACGCACGGCGAGTGGAGCGACGATCGTGCAGCTGCTGACGCTGATGGAC GGTCTCAAGCAGAGCTCGACGATGATGTCATGCGCGCCACCAATCGGCCCAACTC GATCGATGCCGCGCTTAGCGCTTGGCGCTTGGCGCTTGGATCGGAAATCGACATTGGCAT TCCCGATGCCACCGGCTGCTCGAGGTGCTGCGCATCCACACCAAGAACATGAAGTT GGCTGATGACGTCGATTGGAAACA
NL017	SEQ ID NO: 1149 GCTCCGCTTACA THCARCCNGAR GG	SEQ ID NO: 1150 GTGCATCGGTACC AHSCHGCRTC	SEQ ID NO: 1101 GAGCCAGTATCAGAAGACATGCTTGGTGTGTTTCAACGGAAGTGGTAAGCCCAT CGACAAAGGACCTCCCATCTTCTGAGGATATCTCGACATTCGAAGTCAACCCATC AATCCTGGTGGTATCTATCCGAGGAAATGATCCAGACTGGAATTCAGCCATCG ACGTATGAACTGATTGCTGCTGCGGCAAGAAATCCCATCTTTTCAGCTGCCGCTCT ACCTCACAACGAAATGCTGCTCAATCTGTAGACAGGCTGGTCTTGTCAAATGCCA GGAAAGTCAGTTCTCGATGACTCTGAGGACAACTTTGCTATTGTTTCGCGAGCCATGG GAGTCAACATGGAACCTGCTCGATTCTTCAACAGGATTCGAGGAGAACGGCTCTAT GGAGAACGTGTCCTGTTCTTGAACCTGGCGAACGCCGACGATCGAGCGTATCAT CACACACGCTGCGCTGACGGCGCGCGAGTTCTGGCCCTACCAAGTCCGAGAGC ACGTGCTGTCATCCTCACCGACATGAGCTCCTACGCGGAGCGCTGCCGAGAGGTG TCCGCGCGCGGAGGAGGTGCCGCGCGCTGCTGGTTTCCCGGTTACATGTACAC CGATCTGGCCACCATCTACGAGCGCGCGGAGTGCAGGGTCCGCAACGGCTCCA TCACG
NL018	SEQ ID NO: 1151 GCTCCGCTTACA THCARCCNGAR GG	SEQ ID NO: 1152 GTGCATCGGTACC AHSCHGCRTC	SEQ ID NO: 1103 TATGCAATGCTGTGCCACGCCACAAATAGAAAGCACACACAGTTTATTCGATCC GAGAAACAACTACTCGAATGATTACCACTTGAAGGAGGACTTCAAGTAGACA CTTTCGAATACCGTCTTCTGCGGAGGTGCTGTCGCGAATCTCTGATCAGAACTA CTTGACGAGGCGGACATGCAGATGTCGACGGTGGTGGACCGAGCATTTGGTCCCC CCTCGCGCCACACATCCAGCAGAGCGCGCAACTCAAAATCCAGGAGGCGCGC GATCGCGCTTTTCCATCAAGCTCAGCGCCCAACCCCAAGCTCGGCTGGTCTGTTT AAGAACGGTCAAGCGCATCGGTGACGCGCAGAAACACAGGCTCTACTCCATCAG

			<p>ACGCCACGGCTCAAGGTCAACAAAGTCAGCGCTCAAGACTCCGGCCACTACACGCT GCTTGCTGAAAAATCCGCAAGGATGTACTGTGCTCCTCAGCTTACCTAGCTGTCGAATCA GCTGGCACTCAAGATACAGGATACAGTGAGCAATACAGCAGCAAGAGGTGGAGAC GACAGAGCGGTGGACAGCAAGATGCTGGCAGCAACTTTGCTCGCGTCCCGG CCGATCGCGACGCGAGCGAAGCAAGATGACCGGTTTACTGCCCGTACCGGG CCGACCTACCCGGACGTGGCTGGTTTCATCAACGGCCAACAGGTGGCTGACGACG CCAGCACAAGATCCTCGTCAACGAGTCTGGCAACCACTCGCTCATGATCACCGGG TCACTCGCTTGACACGAGTGGTGGCTGTATTGCCCGCAACAAAGCTGGCGAA ACCTCATTCAGTGCAACTTGAATGTGATCGAGAAAGAACTGGTTGGCGCCGAAA TTTGTGGAGAGATTCGCACAAGTGAATGTGAAGGAGGTGAGCCGGTTGTCTGAG CGCACGCGCTTGGCACACCTGTTCCAAGATAACATGGCAGAAAGGACGGCGCCC CGATCCAGTCGGACCGAGCGTGAGTCTGTTTGTGGACGGAGGTGCGACCGCCTG GACATCCCGTACGCGAAGCGCTCG</p>
NL019	<p>SEQ ID NO: 1151 GTCCTGTCTGCT GCTVMGWTTYG C</p>	<p>SEQ ID NO: 1152 CCTTGATCTCHGC MGCCATBGTC</p>	<p>SEQ ID NO: 1105 CGATGACACATACACAGAAAGTTACATCAGTACCATTGGTGTAGATTTAAAAATTAGAA CAATAGATCTCGATGGAACCACTAAAGCTTTCAGATTTGGACACGGCCGGCCAGG AGCGGTTCCGACCATCACATCGAGCTACTACCGGGGCCACCGCATCTTGTG GTACGAGTGCACCCAGCAGAGTCTGTTCAACAACCTCAACACAGTGGCTCGAGGA GATTACCGCTACCGCTGTGATAATGTCAACAACCTGCTCGCGCAACAAAGTGTGA TCAGACCAACAACAAAGGTGCTGACTATACACAGGCTAAGGAATACGCCGACCACT GGCATTCGGTTCTCTGGAGACGTGGCGGAAGAACGCCGACCAATGTGGAGCAGGCGT TCAT</p>
NL021	<p>SEQ ID NO: 1153 CTCAATCAGAGC GTYCCHCCRTAY GG</p>	<p>SEQ ID NO: 1154 GGAATTGCCSAGV CGDGADCC</p>	<p>SEQ ID NO: 1107 CGTCAGTCTCAATTCTGTACCGATATCAGCACCACGTTCAATCTCAAGCCACAAGAG AACGTGAAGATAACGCTTGAGGCGCACAGGCTGTTTCATTTACACGAAACGACTT GTGATCTCACTGAAGGAGGAGAACTCTATGTTCACTCTCTATTCGATAGTATGC GCAGTGTGAGGAGTTTTCATCTGGAGAAAGCTGCTGCCAGTGTCTTGAATCTGTTG CTGTGTTGTGAGGAGAACTATCTGTTCCCTTGTCCCGTCTTGGAACTCACTGTTG CTCAGGTTTACTGAGAAGGAATTGAACCTGATTGAGCCGAGGGCCATCGAAAGCTCA CAGTCCAGAAATCCGGCCAAAGAAAGAAAGCTGGATACCTTTGGAGATTGGATGGCA TCTGACGTCACCTGAAATACCGACCTGGATGAAGTGAAGTGTATGGCAGTGAACA CAAACCTCTATGCAAAATTGCATCCTACATATTC</p>
NL022	<p>SEQ ID NO: 1155 GCGTGCTCAAG TAYATGACBGAY GG</p>	<p>SEQ ID NO: 1156 CCAGTTCATGCTTR TANGCCANGC</p>	<p>SEQ ID NO: 1109 TACATTGCACAGAGAATTCCTTTCCGAGCCAGATCTGCAATCTTACAGTGTATGATA ATTGATGAAGCTCACGAGAGGACGTTGCACACTGATATACTGTTCCGTTTGTGTA GATGTCGCCCGGATTACAGACCTGACTTGAAGCTGCTCATATCAAGCGCCACACTGGAT</p>

NL023	SEQ ID NO: 1157 CCGGAGCTTCT CTCAGGAACGC	SEQ ID NO: 1158 GAAAGCACACGCT GTTGCTCTGG	GGTCAGAAATCTCCGAGTTTTTCGACGATGCACCCATCTTCAGGATTCGGGGCCGT AGATTTCCGGTGACATCTACTACACAAAGCGCCGAGGCTGACTACGTGGACGCA TGTCGTTTTTCGATCCTGCAGATCCAGCCACTCAGCCGCTGGAGACATCCTGGTC TTCCTCACCGGTACGAGGAGATCGAAACCTGCCAGGAGCTGCTGCAGGACAGAGT GCGCAGGCTTGGCCTCGTATCAAGGAGCTGCTCATATTGCCGCTATTCCAACCT ACCCAGTGATATGCAGGCAAGATTTTCTGCCACTCCACCAATGCTAGAAAGGTA GTATTGCCACAAATATTGCAGAAACCTCAATTGACCATCGACAAATAATCTACGTGA TTGATCCTGGTTTTGTAAGCAGAAATAACTCAATCAAGGACTGGAATGGAATCGCT TGTGTAGTGCCTGTTTCAAGGCATCGGCCAATCAGCGAGCAGGCGGGGGGAC GGGTGGCGCGCGCAAGTGCTTCGCTCTGTACACG
	SEQ ID NO: 1157 CCGGAGCTTCT CTCAGGAACGC	SEQ ID NO: 1158 GAAAGCACACGCT GTTGCTCTGG	SEQ ID NO: 1111 CCGGAGCTTCTCTCAGGAACGCCACGACGAGGAAATGAAGGAATCCTCGGGTCGCA TGCATCACAGCGATCCTCTAATCGTCGAGACTCATAGCGGTACGTGAGAGGAATCT CGAAGACCGTCTCGGACGGGAGTCCACGTGTTACCGGATTCGGTTTTCGAAA CCTCCATCGGTCCGTTCCGATTCCGTAACCCGTTCCCGTCCGACCCGTGGCACGG CGTTCTGGATCGACCCGCTTCCCAACAGCTGTACAGGAACGGTACGAGTATTT CCCGGCTTCGAGGAGAGGAAATGTGGAATCCGAATCCGAATTTGTCGGAAGATTG TCTGATTTGAACATATGGTGCCGACCGTTGAGAAATCCGACACAGAGCCAAACAG CGAGGAATAAACCAAGAGCGAAGGTGCCGTGCTGATCTGGATCTACGGCGGG GTTACATGAGCGGCACAGCTACACTGGACGTGTACGATGCTGACATGGTGGCCGCC ACGAGTGACGTATCGTCGCTCCATGCAGTACCGAGTGGTGCGTTCGGCTTCCTC TACCTCGCACAGGACTTGCTCGAGGACGAGGAGCGCGCGGCAACATGGGGC TCTGGACACAGGCCCTTGCCATCCGCTGGCTCAAGGACAAACATTGCCGCTTCGGA GGCGATCCCGAACTCATGACGCTCTTTGGCGAGTCGGCTGGGGTGATCTGTAAG CATCCACTTGGTATCACCGATAACTCGCGGCTAGCGCGTCTGGCATCATGCAGTC AGGAACGATGAACGCACCGTGAGCTTCATGACGCGGAAACGCGACCGAAATCG CCAAGACGCTCATTGACGACTGCGGTGCAACTCGTCTGCTGACCGACGCTCCC AGTCGCGTATGTCCTGTATGCGATCAGTCAGGCAAGATCATCTCCGTGCAGCAA TGGAACAGCTACTCCGGCATTCGCGACTCCGCTCGACCCACCATCGACGGCAT TTCCTGCCAAACATCCCCTCGATCTGCTCAAGGAAGGCGACTTCAGGACACTGAA ATACTCATCGGCAGTAATCAGGATGAGGTACCTACTCATATTGTACGATTCATCG ACTTCTTCCAAAAGACGGGCCGAGTTTTCGAAAGATAAGTTCTTAGACATCAT CAACACAAATTTCAAGAAATAGCGAAATTTGAGAGGGAAGCTATCATATTCAGTAC ACAGATTGGGAGCATGTTATGGATGTTATCTGAACCCAGAAATGATCGGAGATGTG GTTGGTATTACTTCTCATCTGTCCGACAAATCATTCGACAGGCAATTCGACAGAGC ATGGAAGAAAGGTGTTACTATTCTTCACCCAGAGAACCAAGTTTATGGGG CGAGTGGATGGGAGTCATGCATGGAGATGAAATAGAAATACGTTTTTGGTCATCCTC

			AACATGTCGCTGCAATTCAATGCTAGGAAAGGATCTCAGTCTCGAAATATGCAA GCTTACTCTAGGTTTGCAATGACAGGTAAACCAGTGCCTGATGACGTGAATTGGCCTA TCTACTCCAAGGACACGCGCAGTATTACATTTTCAATGCGGAGACTTCGGGCACAG GCAGAGGACCCAGAGACAACAGCGTGTGCTTTG
NL027	SEQ ID NO: 1159 GCCGATCGTKYT VACKGGCTC	SEQ ID NO: 1160 GGTATAGATGAARC ARTDCCVACCCA	SEQ ID NO: 1113 AGAAGACGGCACGGTGCCTATTTGGCACTCGGGCACCTACAGGGTGGAGTCTCTCGC TGAATTATGGCCTCGAAAGAGTGTGACCAATTTGCTGCATGCGAGGATCCAACAATG TGGCTCTTGGCTACGACGAAGGCAGCATAATGTTGAAGTGGTGGGAGGAGCGG GCCATCTCGATGATGTGAACGGTGAGAAATTGTGTGGCGGCCACTCGGAGAT ACAACAGGTC AACCTCAAGGCCATGCCGAGGGCGTCAAATCAAAGATGGCGAAC GACTGCCGGTCCGCTTAAGGATATGGCAGCTGTGAAATATATCCGCAGACCATCG CTCATAATCCCAACGGCAGATTCCTAGTCTTTTGTGGAGATGGAGAGTACATAATTCA CACATCAATGGTGTCTAAGAAATAAGGCGTTTGGCTCGGCCCAAGAGTTCAATTTGGGG ACAGGACTCGTCCGAGTATGCTATCAGAGAAGGAACATCCACTGTCAAAGTATTCAAA AACTTCAAAGAAAGAAATCATTCAAGCCAGAAATTTGGTGTGAGAGCATAATTCGGCG GCTACCTGCTGGAGTTTGTCTGTTGCTGGACTGGCGTGTACGACTGGGAGACCC TGGAGCTGGTGGCTCGCATCGAGATCCAAACGAAACAGTGTACTGGTGGAGAGT GGGAGCTGGTGGCGTGGCGTGGCACTGATGACTCTTGTGCTCCGCTACGACGC ACAGGCCGTGCTCGCTGCACGCGACGCCGCTGACGACGCTGTACGCCGCGACGGC GTCGAGGATGCTTCGAGGTCTTGGTGAAGTGCACGAAACTGTAAAAACTGGATTG

Table 2-CS

Target ID	Primer Forward 5' → 3'	Primer Reverse 5' → 3'	cDNA Sequence (sense strand) 5' → 3'
CS001	SEQ ID NO: 1706 CATTGAAGCGT TTWRMYGCYCC	SEQ ID NO: 1707 CTTCGTGCCCTT GCCRATKATRAA BACG	SEQ ID NO: 1682 TAAAGCATGGATGTTGGACAAACTGGGTGGCGTGTACGCGCGCGCGCGTGCACCGG CCCCACAAGTTGCGCGAGTGCCTGCCGTGGTGATCTTCCTCAGGAACCGGCTCAA GTACGCGCTCACCGGAAATGAAGTGTCTAAGATTGTAAAGCAGCGACTTATCAAAGTTG ACGGCAAAGTCAGGACAGACCCACATATCCCGTGGATTTATGGATGTTGTTCCATT GAAAAGACAAATGAGCTGTTCCGTCTATATATATGATGTCAAAGGCGAGATTTACTATTAC CGTATTACTCTGTGAGGAGCTAAATACAAGCTGTCAAGGTGCGGCGCGTGGCGACG GGCCCCAAGAACGTGCCTTACCTGGTGACCCACGACGAGCACCGGTGCGATACCCC GACCCACTCATCAAGTCAACGACTCCATCCAGCTCGACATCGCCACCTCCAAGATCA TGGACTTCATCAAGTTTGAATCTGGTAACTATGTATGATCACGGGAGGCGGTAACCTTG GGCGCGTGGGCACCATCGTGTCCCGGAGCGACATCCCGGGTCTTCGACATCGTG

CS002	SEQ ID NO: 1708 GAGTTCTTTAG TAAAGTATTCGG TGG	SEQ ID NO: 1709 GCAATGTCATCC ATCAKRTCRTGTA C	CATATACGGGACTCCACCGGACATACCTTCGCTACCAGATTGAACAACGTTGTTTCATAAT CGGCAAGGGGCACGAAG SEQ ID NO: 1684 GAGTTCTTTAGTAAAGTATTCGGTGGCAAGAAGGAGGAGAGGGTCCATCAACACAC GAAGCTATACAGAAATTACGCGAAACGGAAGAGTTATTGCAGAAAGAAACAAGAGTTTCT AGAGCGAAAGATCGACACTGAATTACAAACGGCGAGAAACATGGCACAAAGAATAAG AGAGTGCCTATTGCGCACTGAAGCGCAAGAAGCTTATGAAAGCAGCTTACCCAGA TTGATGGCAGCTTACCCAAATTGAGGCCCAAGGAGCGCTAGAAGAGCTAACAC CAATACACAGGTGCTTAACACTATGCGAGATGCTGCTACCGCTATGAGACTCGCCAC AAGGATATCGATGTAGACAAGGTACACGATCTGATGGATGACATTGC
CS003	SEQ ID NO: 1710 CAGGAGTTGAR RATHATYGGHSA RTA	SEQ ID NO: 1711 CAGGTTCTTCT CTTKACRCGDCC	SEQ ID NO: 1686 TGGTCTCCGAACAAGCGTGAGGTGGAGGGTGAAGTACACGCTGGCCAGGATCCG TAAGCTGCCCGTGAGCTGCTCACACTCGAGGAGAAAGACCCCTAAGAGGTTATTCGAA GGTAATGCTCTCCTTCGTCGCTGGTGAGGATCGGTGTTGGATGAGAAAGCAGATGA AGCTCGATTATGTACTCGGTCTGAAGATTGAGGACTTCTTGGAAACGTCGTCTCCAGACT CAGGTGTTCAAGGCTGGTCTAGCTAAGTCTATCCATCATGCCGTTATCTTATCAGACA GAGGCACATCCGTGCCGAAGCAAGTTGTGAACATCCCTTCGTTTCATCGTCCGGCTG GACTCTGGCAAGCACATTGACTTCTCGCTGAAGTCTCCGTCGGCGGCGGCCGCGCG
CS006	SEQ ID NO: 1712 ACCTGCCAAGG AATGMGVAAYG C	SEQ ID NO: 1713 GAGATCTTCTGC ACRTTKACVGCAT C	SEQ ID NO: 1688 ACCTGCCAAGGAATGAGGAACGCTTTGTATGACAAATTGGATGATGGTATAATTGC ACCAGGGATTCGTATCTGTTGACGATGATGTCATTGGAAAACTATAACTTTGCCAG AAAACGATGATGAGCTGGAAGGAACATCAAGACGATACAGTAAGAGAGATGCCTCTAC ATTCTTGGAAACAGTGAACCTGGTATTGTTGACCAAGTTATGCTTACACTTAACAGCG AAGGATACAAATTTGTAAATACGTGTGAGATCTGTGAGAATCCACAAATTGGAGAC AAATTTGCTTCTCGTCATGGTCAAAAAGGGACTTGTGGTATTCAATATAGGCAAGAAGA TATGCCCTTTCACCTTGTGAAGGATTGACACCAGATATTATCATCAATCCACATGCTATCCC CTCTCGTATGACAAATTGGTCACTTGATTGAATGATTCAAGGTAAGGTCTCCTCAATAA AGGTGAAATAGGTGATGCTACACCATTTAACGATGCTGTCAACGTGCAGAAGATCTC
CS007	SEQ ID NO: 1714 CGGTGTCCATT ACAGYTCCGG	SEQ ID NO: 1715 CGATGCAAGTAG GTGTCKGARTCY TC	SEQ ID NO: 1690 TTTCAGAGATTTCTTGTGGAACACAGAGATTTTGGGGCTATCGTCGATTGCGGTTTCG AGCACCTTCAGAAAGTTCAACATGAATGATTCCTCCCAAGCTGTTTGGGAATGGATATT CTTTGTCAAAGCTAAATCCGGAATGGGAAAAACCGCCGTTATTTGTTAGCAACTGC AACAGCTAGAACCCTCAGAAAACCATGTTTACGTATTAGTAATGTGCCATACAAAGGAA CTCGCTTCCAAATAGCAAGGAATATGAGAGGTTCTCTAAATATATGGCTGGTGTAG AGTATCTGATTTCTTGGTGGATGCCAATTCAGAAAGATGAAGAAGTATTGAAGACAG

			<p>CCTGCCGCACATCGTTGGTACTCCTGGCAGAAATTAGCATTTGGTTAACAAAG AAACTGAATTTAAACACCTGAAACACATTCATCCTGGATGAATGTGACAAAATGCTTGAA TCTTAGACATGAGACGTGATGTCAGGAAATATTCAGGAACACCCCTCACGGTAAGC AGGTATGATGTTTTCTGCAACATTGAGTAAGGAGATCAGACCAGCTGTGAAGAAATTT ATGCAAGATCCTATGGAAGTTTATGTGGATGATGAAGCTAAACTTACATTGCACGGTTT GCAGCAACATTATGTTAAACTCAAGGAAATGAAAGAAATGAAGTTATTTGAACTTTT GGATGACTGGAGTTCAACCAAGTTGTATATTTGTAAAGTCAGTGCAGCGCTGCATAG CTCTGCACAGCTGCTGACAGACCACAACTTCCCAGCTATTGGTATACACCGAAATATG ACTCAAGATGAGCGTCTCTCCCGCTATCAGCAGTTCAAGATTTCCAGAAGAGGATCCT TGTTGCGACAAATCTTTTGGACGGGTATGGACATTGAAAGAGTCAACATAGTCTTCA ATTATGACATGCCG</p>
CS009	<p>SEQ ID NO: 1716 CCTCGTTGCCAT YTGWTKTG</p>	<p>SEQ ID NO: 1717 CTGGATTCTCTC CCTCGCAMGAHA CC</p>	<p>SEQ ID NO: 1692</p> <p>CCTCGTTGCCATTTGATTTGGACGTTTCTGCAGCGGCTGGACTCACGGGAGCCCCATG TGGCAGCTGGACGAGAGCATCATCGGCACCAACCCCGGCTCGGCTTCCGGCCACG CCGCCAGAGGTGCGCAGCAGCGTCTGTTAAGGGCAACGCCCAACAGCCAA CAATTCTGGTGCAAGAACTCCAACTTTCTAACCGGTACAAACGAGACGGTAAGA AAGCAGGAGCAGGCCAGAACATCCACAACCTGATTTCAAACTGCCCTCTCCGGCCGG TAAGGTGTCGACGTGGACATCAGCGCTGGAGTCCCTGTGTAGAGGACAAGCACATTT GGATACCACAAAGTCCAGCCCTGCACTTCTCTCAAACTCAACAAGATCTTCGGCTGGA GGCCGCACTTCTACAACAGCTCCGACAGCTGCCCACTGACATGCCCGACGACTTGAA GGAGCACATCAGGAATATGACAGCGTACGATAAGAAATATCTAAACATGGTATGGGTGT CTTGCGAGGGAGAGATCCAG</p>
CS011	<p>SEQ ID NO: 1718 GGCTCCGGCAA GACVACMTTYGT C</p>	<p>SEQ ID NO: 1719 GTGGAAGCAGGG CWGGCATKGCRA C</p>	<p>SEQ ID NO: 1694</p> <p>GGCTCCGGCAAAGCAGACCTTTGTCAAACGACACTTGACTGGAGAGTTCGAGAAAAGAT ATGTGCCACATTAGGTGTCGAGGTGCATCCCTTAGTATCCACACAAATAGAGGCCCT ATAAGGTTTAATGTATGGTACTGCTGCCAAGAAAAGTTTGGTCTCCGAGATG GTTACTATATCCAAAGTCAATGTCCATCATGTTCCGATGTAACGTCCTGTCACC TACAAAATGTACCCAACTGGCACAGAGATTTAGTCCGAGTCTGTGAAGGCATTCCAAAT TGTTCTTTGTGGCAACAAAGTAGATATCAAGGACAGAAAAGTCAAAGCAAAAACATTTG TTTTCCACAGAAAAAGAACCTTCAGTATTATGACATCTCTGCCAAGTCAAACTACAAT TCGAGAAACCTTCCCTCTGTTAGCGAGAAAAGTTGATCGGTGATGGTAACCTAGAGTTT GTCGCCATGCAGCCCTGCTTCCAC</p>
CS013	<p>SEQ ID NO: 1720 GGATCGTCTGC TAMGWYTWGGA GG</p>	<p>SEQ ID NO: 1721 CTATGGTGCCA GCATSGCGC</p>	<p>SEQ ID NO: 1696</p> <p>CAGATGCGCCCGTTGTTGATACTGCCGAACAGGTATACATCTCGTCTTTGGCCCTGTT GAAAGATGTTAAACACGGCGCGCGGTGTTCCAATGGAAGTTATGGACATTATGTTA GGTGAATTTGTTGATGATTACACGGTGCCTGTCATAGACGTATTTGCCATGCCTCAAC</p>

CS014	SEQ ID NO: 1722 ATGGCACTGAG CGAYGCHGATG	SEQ ID NO: 1723 GAACTTGCGGTT GABGTTSCGDCC	TGGCACAGGAGTGTGGTTGAAGCTGTAGATCCTGTCTTCCAAGCAAGATGTTGGAT ATGTTGAAGCAAACTGGACGACCTGAGATGGTAGTGGATGGTACCACCTCGCATCCTG GCTTTGGATGTTGGTTATCTGGAGTCGACATTAACTACAGCAGTCTTTCCAAGCTTTG TCTGAACGTGCTGTAGCTGTAGTGGTTGATCCCATTCAGTCTGTCAAGGGC SEQ ID NO: 1698 TTCAAAAGCAGATCAAGCATATGATGGCCTTCATCGAACAAAGAGGCTAATGAAAAGGCC GAGGAAATCGATGCAAGGCCGAGGAGGAGTTCAACATTGAAAAGGCCGCTGGTG CAGCAGCAGCGGCTCAAGATCATGGAATACGAAAGAGAAAGAGAAACAAGTGGAAAC TCCAGAAAAGATCCAACTCTCGAACATGCTGAATCAAGCCCGTCTGAAGGTGCTCAAA GTGCGTGAGACCACTACGCAACGTTCTCGACGAGGCTCGCAAGCGCCTGGCTGAG GTGCCAAAGACGTGAACTTACACAGATCTGCTGGTCACGCTCGTACCAAGCCC TATTCAGCTCATGGAACCCACAGTAACAGTTTCGCTTAGGACGCGACGCTCCTCTT AGTACAGTCCATATTGGCAAGGCACAGCAGGATTACAAAGCAAGATCAAGAAAGGAC GTTCAATTGAAGATCGACACCGGAAATTCCTGCCCGCGATACCTGTGCGGAGTGG AACTTATTGCTGTAGAGGGCGTATTAGATCAGCAACACCTCTGGAGTCTCGTCTGGA GCTGATAGCCCAACTGTTGCCCGAAATACGTACCGCATTTGTC SEQ ID NO: 1700 ATCGTGCTTTCAGACGATAACTGCCCCGATGAGAAGATCCGCATGAACCCGCGTCGTGC GAAACAACCTTGC GTACGCTGTGAGACATAGTCTCCATAGCGCTTGTCCATCGGT CAATATTGGGAAACGGGTACATATATGCCATTGATGATCTGTGAGGGTTTGACTG GAAATTTATTCGAAGTCTACTTGAACCATACITTCATGGAAGCTTATCGGCCATCCATC GCGATGACACATTCATGTTCCGCGGGGATGAGGCTGTTGAATCAAAGTGGTGA GACTGATCCGTGCGGTATTGCTGCTGCTCCGACACAGTATACACTGCGAAGGA GACCTATCAAACGAGAGGAAGAAAGAAAGCCCTAAACGCCGTAGGTACGACGAC ATCGGTGGCTGCTGTAACAGCTCGCTCAGATCAAGAGATGGTCGAGTTGCCTCTAA GGCATCCGTGCTGTTCAAGGCAATTGGTGAAGCCCGCACGTGGAATCCTCATGTA TGGCCGCGCTGGTACCGGCAAACTCTCATTGCTCGGGCAGTGGCTAATGAAACTGGT GCATTCCTCTTCTGATCAACGGGCGGAGATCATGTCCAACTCGCGGGGAGTCCG AATCGAACCTTCGCAAGGCATTCGAGGAAGCGGACAAAGAACTCCCGGCTAATCTT CATCGATGAACCTGGATGCCATCGCACCAAGAGGAGAGAACTCACGGTGAAGTGA GCGTCGATTGTGTCGCAACTACTTACTCTTATGATGGAATGAAGAACTCATCGCACG TGATCGTAATGGCCGCCCAACCGTCCGAAATTCGATCGACCCGCGGCTA SEQ ID NO: 1702 AGGATGGAAGCGGGGATACGTTTGAGCATCTCCTTTGGGGAAGATACGGAGCAGCTGC CAGCCGATGTCAGCGACTCGAATACTGTGCGGTTCTCGTAGTTGCCCTGTGTGATGA AGTTCTTCTCGAACTTGGTGAGGAACTCGAGGTAGAGCAGATCGTGGGTGTAGGGC
CS015	SEQ ID NO: 1724 GCCGCAAGGAG ACBGTVTGC	SEQ ID NO: 1725 CGATCAAAAGCGW CCRAAVCGACG	ATCGTGCTTTCAGACGATAACTGCCCCGATGAGAAGATCCGCATGAACCCGCGTCGTGC GAAACAACCTTGC GTACGCTGTGAGACATAGTCTCCATAGCGCTTGTCCATCGGT CAATATTGGGAAACGGGTACATATATGCCATTGATGATCTGTGAGGGTTTGACTG GAAATTTATTCGAAGTCTACTTGAACCATACITTCATGGAAGCTTATCGGCCATCCATC GCGATGACACATTCATGTTCCGCGGGGATGAGGCTGTTGAATCAAAGTGGTGA GACTGATCCGTGCGGTATTGCTGCTGCTCCGACACAGTATACACTGCGAAGGA GACCTATCAAACGAGAGGAAGAAAGAAAGCCCTAAACGCCGTAGGTACGACGAC ATCGGTGGCTGCTGTAACAGCTCGCTCAGATCAAGAGATGGTCGAGTTGCCTCTAA GGCATCCGTGCTGTTCAAGGCAATTGGTGAAGCCCGCACGTGGAATCCTCATGTA TGGCCGCGCTGGTACCGGCAAACTCTCATTGCTCGGGCAGTGGCTAATGAAACTGGT GCATTCCTCTTCTGATCAACGGGCGGAGATCATGTCCAACTCGCGGGGAGTCCG AATCGAACCTTCGCAAGGCATTCGAGGAAGCGGACAAAGAACTCCCGGCTAATCTT CATCGATGAACCTGGATGCCATCGCACCAAGAGGAGAGAACTCACGGTGAAGTGA GCGTCGATTGTGTCGCAACTACTTACTCTTATGATGGAATGAAGAACTCATCGCACG TGATCGTAATGGCCGCCCAACCGTCCGAAATTCGATCGACCCGCGGCTA SEQ ID NO: 1702 AGGATGGAAGCGGGGATACGTTTGAGCATCTCCTTTGGGGAAGATACGGAGCAGCTGC CAGCCGATGTCAGCGACTCGAATACTGTGCGGTTCTCGTAGTTGCCCTGTGTGATGA AGTTCTTCTCGAACTTGGTGAGGAACTCGAGGTAGAGCAGATCGTGGGTGTAGGGC
CS016	SEQ ID NO: 1726 GTTCAACCGCG AYATYCTGCG	SEQ ID NO: 1727 GTCGCGCAGGTA GAAATCKGC	AGGATGGAAGCGGGGATACGTTTGAGCATCTCCTTTGGGGAAGATACGGAGCAGCTGC CAGCCGATGTCAGCGACTCGAATACTGTGCGGTTCTCGTAGTTGCCCTGTGTGATGA AGTTCTTCTCGAACTTGGTGAGGAACTCGAGGTAGAGCAGATCGTGGGTGTAGGGC

CS018	SEQ ID NO: 1728 GCTCCGTCTACA THCARCCNGAR GG	SEQ ID NO: 1729 GTGCATCGGTAC CAHSCHGCRTC	<p>TTCTCACCGACGACAGCCTTCATGGCCTGCACGTCCTACCGATGGCGTAGCAGGCG TACAGCTGGTTGAAACATCAGAGTGGTCTTCGGGTCATTCCTCACCGATGGCAG ACTTCATGAGACGACAGGAGGAGGACGACGTTTACAGCGGGTAGATCTGTCTGTT GTGGAGCTGACGGTCTACGTAGATCTGCTCCCTAGTACGCGGTTAAATCGGGA ATAGGATGGTGATGTCGTCGTTGGGCATAGTCAAGATGGGATCTGCGTGATGATC CGTTTCTACCTCTACACGCCCGCTCTCTCGTAGATGGTGCCAAATCGGTGTACAT GTAACCTGGAAACACGTCGTCGGGCACCTCTCACGGGCGGACACTTCACG CAGAGCCTCCGGTACGAAGACATGTAGTCAAGATTACCAGCAGTGTCTCTCACAC TGGTAGGCCAAGAACTCAGCAGCAGTCAAGGCCAAACGTTGATGATCTCTCAA TAGTGGGATCGTTGGCCAGATTCAAGAACAGGCACACGTTCTCCATGGAGCCGTTCTC CTCGAAGTCTGCTTGAAGAACCAGGCGGCTCTCCATGTTACACCCATGGCGCGAAG ACGATGGCAAGTTGTCTCGTGTCTCCAGCACAGATTGCCGGGATCTTTACAA GACCGCTTGCCCTACAGATCTGGCGGCAATTTCTGTTGTGGCAGACCCGAGCCG AGAAATGGGGATCTTTGCCCGGAGCAATGGAGTTCTACGTCGATAGCGGAGAT ACAGTCTGGATCAITTTCTCAGGGTAGATCGGGACAGGGTTGATGGCTGTCCC TGGATGTCCAAAAGTCTTCAGCAAGGATTGGGGACCTTTGTCAATGGGTTTTCCAGA GCCGTTGAATACGCGACCCAAACATGTCCTCGGAGACAGGGGTGC</p>
	SEQ ID NO: 1704 GCTCCGTCTACATTCAGCCGGAAGCGTCCCTGTACCTGCTCAGCAATCCCAACAGCA GCAGAGTTACGCCACGTACGAGAGCGTGAACACAAATCTACGGCAGCAAGG GTACACCACTTCGGAACAGACCAAGCAGACACAGAGGTGGCGTACACCAACGGTTCC GACTACTCTTCCACGGACGACTTAAAGTGGATACGTTCCGAATACAGACTCCCTCCGAG AAGTTTCGTTCAGGGAATCCATCACGAAGCGGTACATTGGCGAGACAGACATTTCAGAT CAGCACGGAGGTCGACAAAGTCTCTCGGTGTGGTGACCCCTCTAAGATAGCACAAAG CCTAGGAATTCGAAGCTGAGGAGGGAGCCGACGCTCAGTTTCAAGTGCAGCTGTCTG GGTAACCCCGCGCCACGGGTGTCATGTTCAAGAACGGGAGGATAGTCAACTCG AACAAACACGAAATCGTCACGACACATAATCAAAACATACCTAGGTAAGAAACACACA AAAGTCTGATACTGGCAACTACACGTTGTTGGCTGAAAATCTAACGGATGCGTCGTCA CATCGGCATACCTGGCCGTGGAGTCGCCTCAAGAACTTACGGCCAAAGATCAATAATC ACAATACATAATGGACAATCAGCAACACAGCTGTAGAAGAAAGATAGAAGTTAATGAAA AAGCTCTCGCTCCGCAATTCGTAAGAGTCTGCCAAGACCGGATGTAAACGGAGGGAA AATGACGCGATTCCATTGCCCGTACGGGCGAGACCTTACCCAGAAATCACGTTGTTTC ATTACGGATAGACAAATTCGAGACGATTATWATAGATAAGTAAACGAATCGTGT AATCATGCACCTTATGATTACAACGTCGATCTCAGTATAGTGGCGTAGTATGTATATA GCACGCAACAAGACCGCGAACTTCGTTTTCAGTGTAGGCTGAACGTATAGAGAAGG AGCAAGTGGTGGTCTCCCAAAATTCGTGGAGCGGTTACGACGCTCAACGTGCGCGAGG CGAGCCCCGTGCAGCTGCACGCGCGCGCGCTGGCACGCTACGCCACGCATCACA		

			TGGCAGAAGGACGGCGTTCAAGTTATACCCAATCCAGAGCTACGAATAATACCGAAG GTGGGCGCTCGACGCTGGACATCCCTCGAGCCAAGGCGTCTGGACGCGGGATGGTAC CGATGCAC
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Table 2-PX

Target ID	Primer Forward 5' → 3'	Primer Reverse 5' → 3'	cDNA Sequence (sense strand) 5' → 3'
PX001	SEQ ID NO: 2110 GGCCCCAAGAAG CATTTGAAGCG	SEQ ID NO: 2111 CTTCGTGCCCTTGC CRATKATRAABACG	SEQ ID NO: 2100 GGCCCCAAGAAGCATTTGAAGCGCCTGAACGCGCCGCGCGCATGGATGCTGGA CAAGCTCGGCGCGGTGTACGCGCCGCGGCCAGCACGGGCCCGCACAAAGCTG CGGAGTGCCCTGCCGCTCGTCACTTCTGCAACCGCTCAAGTACGCGCTCAG CGGCAACGAGGTGCTGAAGATCGTGAAGCAGCGCCTCATCAAGGTGGACGGCA AGTCCGCAACCGACCCACCTACCGGCTGGATTGATGGATGTTGTGCGATTG AAAAGACCAATGAGCTGTTCCGCTGATCTACGATGTGAAGGACGCTTCACCAT CCACCGCATCACTCCGAGGAGGCCAAGTACAAGCTGTGCAAGGTGAAGCGCG TGCGACGGGCCCCAAGAAGTGCCTGATATCGTACGCACAAACGCGCCGACG CTGGCTACCCGACCCGCTCATCAAGTCAACGACTCCATCCAGCTCGACATC GCCACCTGCAAGATCATGGACATCATCAAGTTGACTAGGTAACCTGTGCATGA TCACGGGAGGGCGTAACTTGGGCGGAGTGGGACCATCGTGTCCCGGAGAGG CACCCCGGAGCTTCGACATCGTCCACATCAAGGACACCAACCGGACACACCTTC GCCACCGAGTTGAACAACGTGTTTCATCATCGGCAAGGGCACGGAAG
PX009	SEQ ID NO: 2112 GCACGTTGATCTG GTACARRGGMAC C	SEQ ID NO: 2113 GCAGCCCAAGCYYT GCACTC	SEQ ID NO: 2102 GCACGTTGATCTGGTACAAAGGAACCGGTTACGACAGCTACAAGTATTGGGAGA ACCAGCTCATTGACTTTTGTCAAGTATACAAGAAGAGGTGACAGACGCGGTGC TGGTCAGAACATCTTCAACTGTACTCCGCAACCCGCCCCACACGCGCAAGGT GTGCGACGTGGACATCCGCGCTGGAGCCCTGCATTGATGAGAACCACTTCTC TTTCCACAAGTCTTCGCTTGCATCTTCTTGAAGCTGAATAAGATCTACGGCTGG CGTCCAGAGTTCTACAACGACACGGCTAACCTGCCTGAAGCCATGCCCGTGGAC TTGCAGACCCACATTGTAACATTACTGCCCTCAACAGAGACTATGCCGAACATGG TGTGGGTGTCGTCCACGGCGAGACGCCGCGGACAGGAGAGAACATCGGGCC GGTGGCTACCTGCCCTACCCGGGCTTCCCGGGTACTTCTACCCGTACGAGAA CGCCGAGGGGTATCTGAGCCCGCTGGTCCCGTGCATTGAGAGGCGCGGAGGA CCGGCATAGTGATCAACATCGAGTGCAAAGCGTGGGCTGC
PX010	SEQ ID NO: 2114 GTGGCTGCATAGA	SEQ ID NO: 2115 CGCGGCTGCTCCAT	SEQ ID NO: 2104 GTGGCTGCATACAGTTCATTACGCAGTACCAGCACTCTAGTGGAACAACGTCGCG

	GTTCAATTAGCGAG	GAAYASYTG	<p>TTCGGGTACCACTGTCCGGCGCAATTGGGGGACGACGACGCCCAACTTACAC CACATATCGCGGGCTTCGACCAGGAGGCGGGCGGTGGTATGCGCGGC TGGTGGTGTACCGCGGAGCAGGAGACGGGCGGCGGCGGTGCTGCGCTGGCT CGACCGCATGCTCATACGCTGTGCCAGAAGTTCGGCGAGTACGCGAAGGACG ACCCGAACAGCTTCGCTGTGCGAGAATTCAGCTGTACCCGCAAGTTTCATGT ACCACCTGCGCGCTCGAGTTCCTGCAGGTTCACAACTACCCCAATCCCTCATCAT CCACCTTCTACAGACACATGCTGATGCGCGAAGACCTGACCCAAATCCCTCATCAT GATCCAGCGCATCCTACTCGTACAGCTTCGGAGGCGCGCGCAACCCGCTGCT GTTAGACACAGCTCCATCCAGCCCGACCGCATCTGCTCATGGACACCTTCTT CCAGATCCTCATCTACCATGGAGAGACAAATGGCGCAATGGCGGCTCTCCGCTA CCAAGACATGGCTGAGTACGAGAACTTCAAGCAGCTGCTGCGAGCGCGCGTGG ACGACGCGCAGGAGATCCTGCAGACCAGGTTCCCGTCCCGGTACATTGATA CAGAGCACGGCGCTCACAGGCCGCTTCTTCTTCCAAAGTGAATCCCTCTC AGACTCACAACAACATGTACGCGTATGGCGGGCGATGCCGATACCATCAGCGG ACGGTGGCGCCCCCGTGTGACGGATGACGTGCTGCTGCAAGTGTTCATGGAG CAGCGCGCG</p>
PX015	SEQ ID NO: 2116 GCCGCAAGGAGA CBGTVTGC	SEQ ID NO: 2117 GCAATGGCATCAAK YTCRTCRATG	<p>SEQ ID NO: 2106</p> <p>GCCGCAAGGAGACCGGTGTGCAATTGTGCTGTCCGACGACAACTGCCCGGACGAG AAGATCCGCATGAACCGCTGCTCGGAACAACCTGCGAGTGCCTGTGAGAC ATTGTGCCATCGCTCCTGCCCGTCAGTGAAGTACGGCAAGAGAGTTTCATATTC TGCCATTGATGACTCTGTTGAGGGTTGACTGGAACCTGTTCGAAAGTCTACCT GAAGCCGTACTTCATGAGGCGTACCGGCGCATCCACCGCGACGACACGTTTCAT GGTGGCGCGCGCATGCGCGCGCTCGAGTTCAAGGTGTTGAGAGACCGACCCCT CGCCTACTGCATGCTGGCCCCCGACACGCTCATTGTTGAGGGAGAGCGCA TTAAACGCGAGGAAGAAGAGGAGGCTCTCAACGCGCTCGGCTACGACGACATC GGCGGGTCCCGCAAGCAGCTGGCGCAGATCAAGAGAGATGGTGAGCTGCCGCT GCGCCACCCCTCGCTGTTCAAGGCCATCGGGGTCAAGCCGCGCGGGGGATAC TGATGTACGGGCCCCCGGACGGGAAGACCTTGATCGCTAGGGCTGTCGCT AATGAGACGGGCGCATCTTCTTCTCTCATCAACGCGCGCGAGATCATGTGAAA CTCGCCGGTGAATCCGAGTCAACCTGCGCAAGGCGTTCGAGGAGGCGGACAA GAACTCTCCGGCCATCATCTCATTTGATGAACCTTGATGCCATTGC</p> <p>SEQ ID NO: 2108</p> <p>GTTCAACGGCGATATTCTGCGACGCGCGCTCTCTGAGGACATGCTGGGTCGTAT TTTCAACGGCTCCGGCAAGCCCATCGACAAGGGGCGCCCGATCCTGGCCGAGG AGTACCTGGACATCCAGGGGACGCCCATCAACCCGTGGTCCCGTATCTACCCGG AGGAGATGATCCAGACTGGTATCTCCGCTATCGAGCTGATGAACCTCCATCGCCC GTGGTCAGAAGATCCCATCTTCTCCGCGCGCGGTCTGCCCCACAAACGAGATTG</p>
PX016	SEQ ID NO: 2118 GTTACCGGCGGAY ATYCTGCG	SEQ ID NO: 2119 CATCTCCTTGGGGA AGATACGCAGC	

			CTGCTCAGATCTGTAGGCAGGCTGGTCTTGTCAAGGTCCTCCCGGAAATCCGTGT TGGACGACCACGAAGACAACCTTCGCCATCGTGTTCGCCGCCATGGAGTCAACA TGGAGACCGCCAGGTTCTTCAAGCAGGACTTCGAGGAGAACGGTTCATGGAGA ACGTCTGTCTGTTCTTGAACTTGGCCAATGACCCGACCAATTGAGAGATTATCAC GCCGAGGTTGGCGTGAATGACCGACATGCTTCCGAGTCTTGGCCTACCAAGTCCGAGAACA CGTGTGGTAATCTTGACCGACATGCTTCAATACCGGAGGCTCTTCGTGAAGTG TCAGCCGCCCGTGAGGAGGTGCCCGGACGACGTGGTTTCCAGGTTACATGTA CACGGATTTGGCCACAATCTACGAGCGCGCGGCGGAGTCGAGGGCCGCAACG GCTCCATACGCAGATCCCATCTGACCATGCCAACGACGACATCACCCACC CCATCCCGACTTGACCGGTACATCACTGAGGACAGATCTACGTGGACCGTC AGCTGCACAACAGGCAGATCTACCCGCCGTGAATGTCTCCCGTCCGTATCTC GTCTCATGAAGTCGCCCATCGGAGAGGGCATGACAGGAAGGACCACTCCGAC GTGTCCAACCAACTGTACGCGTGTACGCCATCGGCAAGGAGCGTGCAGGCGAT GAAGGCGGTGTGGCGGAGGAGGCGCTCACGCCGACGACCTGCTCTACCTCG AGTTCCCTACCAAGTTCGAGAAGAACTTCATCACACAGGGAAGCTACGAGAACC GCACAGTGTTCGAGTCGCTGGACATCGGCTGGCAGCCCCCTGCGTATCTTCCCCA AGGAGATG
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Table 2-AD

Target ID	Primer Forward 5' → 3'	Primer Reverse 5' → 3'	cDNA Sequence (sense strand) 5' → 3'
AD001	SEQ ID NO: 2374 GGCCCCAAGAAGCA TTTGAAGCG	SEQ ID NO: 2375 CGCTTGTCCCG CTCCTCNGCRA T	SEQ ID NO: 2364 GGCCCCAAGAAGCATTTGAAGCGTTTAAATGCTCTAAAGCATGGATGTTGGACAA ACTCGGAGGAGTATTCGCTCCTCGCCCAAGTACTGGCCCCACAAATTCGCTGAA TGTTCACCTTTGGTGAATTTCTTCGCAATCGGCTCAAGTATGCTCTGACGAACTGT GAAGTAACGAAGATTGTTATGCAGCGACTTATCAAGTTGACGGCAAGGTGCGAAC CGATCCGAATTATCCCGCTGGTTTCATGGATGTTGCACCATTGAGAAGACTGGAG AGTTCTTCAGGCTGGTGTATGATGTGAAGGCGGTTTCACAATTCACAGAAATTAGT GCAGAAGAAGCCAAAGTACAAGCTCTGCAAGGTGAGGAGAGTCAAACTGGGCCAA AAGGTATTCATCTTGGTGACCCATGATGGCCGTACTATCCGTTATCCTGACCCA GTCATTAAAGTTAATGACTCAATCCAATTGGATATTGCCACTTGTAAATCATGGAC CACATCAGATTTGAATCTGGCAACCTGTGTATGATTACTGGTGACGTAACCTGGG TCGAGTGGGACTGTTGTGAGTCGAGAAGCTCACCCAGGCTCGTTTGATATTGTT CATATCAAGGATACCCCAAGGACATACCTTTGCCAAGATTGAATATGATTATCATC ATTGGAAAAGCTACAAAGCCTTACATTTTCATTTGCCAAAGGGTAAGGGTGTGAAATT GAGTATCGCCGAGGAGCGGACAAAGCG

AD002	SEQ ID NO: 2376 GAGTTTCTTTAGTAA AGTATTCGGTGG	SEQ ID NO: 2377 GCAATGTCATCC ATCAKRTCRTGT AC	SEQ ID NO: 2366 GAGTTTCTTTAGTAAAGTATTGGTGGGAAGAAAGATGGAAAGGCTCCGACCACCTG GTGAGGCCATTGAGAACTCAGAGAAACAGAGAAATGTTAATCAAAAAGCAGGAA TTTTTAGAGAAGAAATCGAACAGAAATCAATGTTGCAAGAAAAATGGAACGAAA AATAAGCGAGCTGCTATTCAGGCTCTGAAAAGGAAAAAGAGGTATGAAAAACAATT GCAGCAAAATTGATGGCACCTTATCCACAATTGAAATGCAAGAGAGAGCTTTGGAGG GTGCTAATACTAATACAGCTGTATTACAAACAATGAAATCAGCAGCAGATGCCCTTA AAGCAGCTCATCAGCACATGGATGTGGACAAGGTACATGACCTGATGGATGACATT GC
AD009	SEQ ID NO: 2378 GAGTCCTAGCCGCV YTSGTKGC	SEQ ID NO: 2379 CTGGATTCTCTC CCTCGCAMGAH ACC	SEQ ID NO: 2368 GAGTCCTAGCCGCTTGGTTCAGTATGTTTATGGTCTTCTCCAGACACTGGAT CCTCGTATCCCACTGGCAGTTAGATTCTTCTATCATTTGGCACATCACCTGGCCT AGGTTCCGGCCAAATCCAGAAAGTAGCAATGTAGAGTCAACTCTCATCTGGTACC GTGGAACAGATCGTGATGACTTCGTCAGTGGACAGACACCTTGATGAATTTCTT GCTGTACAAAGACTCCTGGTCTGACCCCTGGTCGAGGTGAGAACATCCACAAC GTGACTATGATAAGCCGCCAAAGAAAGGCCAAGTTTGCAATGTGGACATCAAGAA TGGCATCCCTGCATTCAAGAGAACTCACTACAACACCACAAGAGCTCTCCATGCAT ATTCAATCAAGCTCAACAGATCTACAATGGATCCCTGAATACATAATGAGAGTAC GAAATTCCTGAGCAGATGCCAGAAAGACCTGAAGCAGTACATCCACAACCTGGAG AGTAACAACCTCGAGGGAGATGAACACGGTGTGGGTGTCGTCCGAGGGAGAGAA CCAG
AD015	SEQ ID NO: 2380 GGATGAACTACAGC TBTTCCGHGG	SEQ ID NO: 2381 GTCCGTGGGAY TCRGCHGCAAT C	SEQ ID NO: 2370 GGATGAACTACAGCTTTCCGAGGAGATACAGTTCTTTAAAGGAAAAAGGAGGA AAGAACTGTATGCATAGTGTATCAGATGATACATGCTCTGATGGAAAAATAAGAA TGAATAGAGTTGTACGCAACAATTTACGTGTTCTGTTGTGATGTTGTATCTGTAC AACCTTGCTCTGATGTTAAGTATGAAAAAGGATACATGATACCAATTGATGATA CAGTTGAAGGACTAACCGGGAATTTGTTGAGGTGTACTTAAACCGTACTTTCTC GAAGCATACCGACCCATTACAAAGATGATGCGTTATTGTTCTGGTGGTATGCG AGCAGTAGAATTCAAAGTAGTGGAAACAGATCCTTCAACATATTGATTGTTGCTCC TGATACTGTTATTCACCTGTGAAGGTGATCCCAATAAACCGTGAAGAGGAAGAAAG CATTAATGCTGTTGTTATGATGACATGGGGGTGCGGAAACAGCTAGCACAG ATCAAGGAAATGTTGGAATGCCATTACGGCACCCAGCTCTTTAAGGCTATTGG TGTTAAGCCACCGAGGGAATACCTGCTGATGACCCCTGGAACCTGGTAAACCC CTCATGCGCAGGGCTGTGGCTAATGAACTGGTGCATCTCTTTTAAATAAATGGT CCTGAAATATGAGCAAGCTTGCTGGTGAATCTGAAAGCAACTTACGTAAGGCATT TGAAGAAGCTGATAAGAAATGCTCCGGCAATTATTTATTGATGAACCTAGATGCAAT

			TGCCCCATAAAGAGAAAAAATCATGGAGAGGTGGAACGTCGCATAGTTTCACAAC TACTAACTTTAATGGATGGTCTGAAGCAAAAGTTACATGTTATTGTTATGGCTGCCA CAATAGACCCAACTCTATTGATGGTGCCTTGGCCGCTTTGGCAGATTGATAGG GAAATTGATATTGGTATACCAGATGCCACTGGTCGCTTGAATTTCTTCGTATCCAT ACTAAGAATATGAAGTTAGCTGATGATGTTGATTGGAAACAGATTGCAGCCGAATC CCACGGGAC
AD016	SEQ ID NO: 2382 GTTCAACCGGGCGAYA TYCTGCG	SEQ ID NO: 2383 GGAATAGGATG GGTRATRTCGT CG	SEQ ID NO: 2372 GTTCAACCGGGGATATTCTGCGCGTGCCCGTGTCGAGGAGACATGCTGGGCCGCAC CTTCAACGGCAGCGGCATCCCCATCGACGGCGGCCCGCCCATCGTCGCAGAGAC CTACCTCGACGTCAGGGCATGCCGATTAATCTCAACCGCGCATCTACCCGGAA GAAATGATCCAGACGGGATCTCGACCATCGACGTGATGACGTCCATCGCGCGAG GGCAGAAGATCCCCATCTCTCGGGCGAGGCTGCCACACAGAGATCGCTG CGCAGATCTGCCGACAGGGGGCTGGTGACGACACAGGAGAACAGGACGACT TCGCCATCGTGTTCGCGCGATGGCGTCAACATGGAGACGGCGCTTCTTCAA GCGCGAGTTCGCGCAGACGGGCGGTGCAACGTGGTGTCTCAACCTGGC CAACGACCCCAACCATCGAGCGCATCATACCCGCGCTCGCGTCAACCGTGGC CGAGTTCTTGGCTACAGTGCAACAAGCACGCTCGTCATCATGACCGACATG ACCTCTACGCGGAGCGCTGCGGAGGTGAGCGCGCGCGGAGGAGGTTCC TGGGCGAAGAGGCTTCCAGGCTACATGATACCCGATCTCCACCATCTACGAG CGCGTGGCCGTGTGCAAGGCGCGCCCGCTCCATCACTCAGATCCCCCATCCTG ACGATGCCCCAACGACGACATCACCCTATTC

Table 3-LD

Target ID	cDNA SEQ ID NO	Corresponding amino acid sequence of cDNA clone
LD001	1	SEQ ID NO: 2 (frame +1) GPKKHLRLNAPKAWMLDKLGGVFAPRPSTGPHKLRESPLVIFLRNRLKYALTNSEVTKIVMQRLIKVDGKVRTD SNYPAGFMDVITIEKTGEFFRLIYDVKGRAFVHRITAEAAKYKLCVKRRMQTGPKGIPFIVTHDGRTR
LD002	3	SEQ ID NO: 4 (frame -3) AMQALKRKRLEKNQLQIDGTLTIELQREALEGASTNTTVLESMKNAEALKKAHKNLDVDNVHDMDDI
LD003	5	SEQ ID NO: 6 (frame -2) PRRPYEKARLDQELKIIGEYGLRNKREWVRVKYTLAKIRKAARELLTLEEKDQRRLEFEGNALLRRLVRIGVLDETRM KLDYVLGLKIEDFLERRLQTQVFKLGLAKSIHARVLVRQRHVRKQVWNIPSFVRLDSQKHIDFSLKSPFGGGRP GRVKRKNL

LD006	7	SEQ ID NO: 8 (frame +1) HNYGWQVLVASGVVEYIDTLEEETVMIAMPEDLRQDKEYAYCTTYTHCEIHPAMILGVCAIIPFDHNQSPRNT YQSAMGKQAMGVYITNFHVMDTLAHVLYPHKPLVTTRSMEYLRFRELPAGINSVAIACYTGYNQEDSVILNAS AVERGFRSVFYRSYKDAESKRIGDQEEQFE
LD007	9	SEQ ID NO: 10 (frame +1) PKKDVKGTYVSIHSSGFRDILLKPEILRAIVDCGFEHPSEVQHECIPQAVIGMDILCOAKSGMGKTAVFVLATLQQL EPADNVVYVLVMCHTRELAFQISKEYERFSKYMPSKVGVFVGGMPIANDEEVLKNKCPHIVVGTGPRILALVKSR KLVLKNLKHFIIDECCKMILELDMRRDVQEYRNTPTHTKQVMFSAATLSKEIRPVCKKFMQDPMVEVYDDDEAKLTL HGLQQHYVVKLENENKKNKLFELLDVLEFNQVWIFVKSQVQRCVALAQLL TEQNFPAIGHRGMDQKERLSRYEQFKD FQKRILVATNLFGRGMDIERVNIVFYDMPEDSDTYLH
LD010	11	SEQ ID NO: 12 (frame +1) VKCSRELKIQGGIGSCVSLNVKNPLVSDTEIGMGNTVQWKMCTVTPSTTMALFFEVNQHSAPIQGGRGCIQFIT QYQHASGQKRIRVTTVARNWADASANIHHVSAGFDQEAAMVIMARMAMAVYRAESDDSPDVLRWVDRMLRLCQKF GEYNKDDPNFRLGENFSLYPQFMYHLRRSQFLQVFNNSPDTSFYRHMLMREDLTQSLIMIQLPILYSYSFNGPP EPVLLDTSSIQPDRILLMDTFFQILIFHGETIAQW
LD011	13	SEQ ID NO: 14 (frame -1) PTFKCVLVGDGGTGKTTFKVRHMTGEFEKRYVATLGVVHPLVFHTNRGPIRFNVWDTAGQEKFGGLRDGYVIQ GQCAIMFDVTSRVTYKNVPNWHRDLVRVCENIPVLCGNKVDIKDRKVAKSIVFHRKKNLQYYDISAKSNYNFEK PFLWLARKLIGDPNLEFVAMPALLP
LD014	15	SEQ ID NO: 16 (frame +3) QIKHMAFIEQEA NEKAEEDIDAKAEFEENIEKGRLVQQQRLKIMEYKEKQVELQKKIQSSNMLNQARLKVLV REDHVRTVLEEARKRLQVTDQGGYSQILESLILQGLYQLFEKDVTRVRPQDREL VKSIPTVTNKKYKDATGKDI HLKIDDEIHLQSQETTGGIDLLAQKNKIKISNTMEARLEISQQLLPEI
LD015	17	SEQ ID NO: 18 (frame -1) RHPSLFKAIGVKPPRGILLYGPPGTGKTLIARAVANETGAFFFLINGPEIMSKLAGESSENLKKAFAEEADKNSPAIFI DELDAI
LD016	19	SEQ ID NO: 20 (frame -2) TVSGVNGPLVILEDVKFPKYNEIVQLKLADGTIRSGQVLEVSGSKAVQVFEGTSGIDAKNTACEFTGDILRTPVSE DMLGRVFNNGSGKPIDKGPPIAEEDFLDIQQGPINPWSRIYPEEMIQGTITAVMNSIARGQKPIFSAAGLPHNEIAA QICRQAGLVKIPGKSVLDDHEDNFAIVFAAMGVNMETARFFKQDFEENGSMENVCLFLNANDPTIERIITPRALT AAEFLAYQCEKHVLVILTDMSSYAEALREVSAAREEVPGRRGFGPYMYTDLATYERAGRVEGRNGSITQIPILTMP NDDITHPI

LD018	21	SEQ ID NO: 22 (frame +2) TWFKDGGQRTESQKYESTFSNNQASLRVKQAQSEDSGHYTLAENPQGCIVSSAYLAIEPVTTQEGLIHSTFKQQ QTEMEQIDTSKTLAPNFVRVCGDRDVTGKMTFRDCRVTGRYPDVTWYINGRQVTDHNNHKLIVNESGNHALM ITTVSRNDSGVVTCVARNKTGETSFQCNLNVIEKEQVAPKFEVERFTTVNVAEGEPVSLRARAVGTPVPRITWQR DGAPLASGPDVRIAIDGGASTLNISRAKASDAAWYRC
LD027	23	SEQ ID NO: 24 (frame +1) HGGDKPYLISGADDRLLVKIWDYQNKTCVQTLEGHAQNVTA VCFHPELPVALTGSEGDGTVRWHTNTHRLNCLN YGFERVWTTICLKGSNNVSLGYDEGSILVKVGREPAVSMDSGGKIWARHSELQQANLKAPEGGEIRDGERL PVSVKDMGACEIYPQTIQHNPNGRFVVCVGDGEYIYTAMALRNKAFGSAQEFVWAQDSSEYAIRESGSTIRIFKN FKERNFKSDFSAGIEYGGFLGKSVSGLTFYDWETLDLVRRIEIQPRAVYWSDSGKLVCLATEDSYFILSYDSEQ VQKARENQVAEDGVEAAFDVLGEMNESVRTGLWVGDCFIYT

Table 3-PC

Target ID	cDNA SEQ ID NO	Corresponding amino acid sequence of cDNA clone
PC001	247	SEQ ID NO: 248 (frame +1) AWMLDKGGVFAPRPSTGPHKLRESPLVFLRNRLKYALTNSEVTKIVMQRLIKVDGKVRTDSNYPAGFMDVITIE KTGEFFRLIYDVKGGRFAVHRITAEAEAKYKLCVKRRVQTGPKGIPFLVTHDGRITIRYDPDNKVNNDTIQMEIATSKILDY IKFES
PC003	249	SEQ ID NO: 250 (frame: +2) PRRYPYEKARLDQELKIIGAFGLRNKREVVRVKYTLAKIRKAAARELLTLEEKEPKRLFEGNALLRRLVRIGVLDENRM KLDYVLGLKIEDFLERRLQTQVFKSGLAKSIHHARVLRQRHVRKQVVNIPSFVRLDSQKHIDFSLKSPFGGGGRP GRV
PC005	251	SEQ ID NO: 252 (frame +3) PNEINEIANTNSRQNIIRKLIKDGIIKKPVAVHSRARVRKNTTEARRKGRHCGFGKRKGTANARMPQKELWVQRM VLRRLKKYREAKKIDRHLHYHALYMKAKGNVFRNKRVLMEYIHKKAEKAKAKMLSDQANARRLKVQKARERRE
PC010	253	SEQ ID NO: 254 (frame +3) LKDSLQMSLSLLPPNALIGLITFGKMVQVHELGTGCSKSYVFCGTDLTAKQVQEMLGIGKSPNPQQPGQPG RPGQNPAAPVPPGSRFLQPVSKCDMNLTDIGELQDPWPVHQGRPLRSTGAALSIAVGLLLECTYPNTGGRI MIFLGPCSQGPGQVNLDDLKQPIRSHDHIKDNKAKYMKKAIKHYDHLAMRAATNSHCIDIYSCALDQGTGLMEMK QCCNSTGGHMVMGDSFNSSLFKQTFQRVFSKDPKNDLMAFNATLEVKCSRELKVQGGIGSCVSLNVKSPVSD TELMGNTVQWKLCTLAPSSVALFFEVNVQHSAPIQGGRGCIQLITQYHASGQRRIRVTTIARNWADATANI HISAGFDQEAATAVVMARMAGYKAESDETPDVLRWVDRMLRLCQKFGEYNKDDPNFRLGENFSLYPQFMYHLR

		RSQFLQVFNNSPDETSFYRHMLMREDLTQSLIMIQILYSYSFNGPPEPVLLDTSSIQPDRIILLMDTFFQILIFHGETI AQW
PC014	255	SEQ ID NO: 256 (frame +3) DVQKQIKHMMAFIEQEAKEAEEEFNIEKGRLVQQQLKIMEYYEKKQVLELQKKIQSSNNMLNQARLK VLKVRREDHVRAVLEDAKSLGEVTKDQKYSQILESLUQLFQLFEKEVTVRVRPQDRDLVRSILPNVAAYKDA TGKDILLKVDDSHLSQEITGGVDLLAQKNKIKISNTMEARLDLIA
PC016	257	SEQ ID NO: 258 (frame +2) LVILEDVKFPKFNIEIVQLKLAGTLRSGQVLEVSGSKAVQVFEFGTSGIDAKNTVCEFTGDILRTPVSEDMLGRVFN GSGKPIDKGPPIAEEDYLDIQGPINPWSRIYPEEMIQTGITADVMNSIARGQKPIFSAAGLPHNEIAAQICRQAGL VKVPGKSVLDDHEDNFAIVFAAMGVNMETARFFKQDFEENGSMENVCLFLNANDPTIERIITPRALTAAEFLAYQ CEKHVLVILDTMSSYAEALREVSAAAREEVPGRRGFGYMYTDLATIERAGRVEGRNGSITQIPILTMP
PC027	259	SEQ ID NO: 260 (frame +1) QANLKVLPGEAGIERDGERLPVTVKDMGACEIYPQTIQHNPNGRFVWCGDGEYIYTAMALRNKAFGSAQEFVWA QDSSEYAIRESGSTIRIFKNFKKFKSDFGAEGYGGFLGVKSVSGLAFYDWETLELVRRIEIQPRAIYWSDSG KLVCLATEDSYFILSYSDSQVQKARDNNQVAEDGVEAAFDVLGEINESVRTGLWVGDCFIYTNVNRINYFVGGEL VTIAHLDRPLYVLGYVPRDDRLLYLDKELGVVSYXIAICTRISDCSHATRLPNG*SSIAFNSK

Table 3-EV

Target ID	cDNA SEQ ID NO	Corresponding amino acid sequence of cDNA clone
EV005	513	SEQ ID NO: 514 (frame +3) RCGKKKWWLDPNEITEIANTNSRQNIKLIKDGIIKPPAVHSRVRKNTAARRKGRHCGFGKRKGTANARMPRK ELWQRMRLVRLLLKKYREAKKIDRHLHYHALYMKAKGNVFNKRVMMMDYIHKKAEKARTKMLNDQADARRLKVKE ARKRREERIATKKQ
EV009	515	SEQ ID NO: 516 (frame +1) PTLDPSIPKYRTEESIIGTNPGMGFRMPDPNNEESTLIWLQGSNKTNYEKWKMNLLSYLDKYYPGKIEKGNIPVKRC SYGEKLIRGQVCDVDVRKWEPTPENHFDYLRNAPCIFLKNRIYGEPEYNDPNLDDMPQQLKDHIRYNTNP VERNTVWVTGAGENPADVEYLGPKVYYPFSGQFPGYFFPYLNSEGYSPLLAQFKRPVSGIVNIECKAWA
EV010	517	SEQ ID NO: 518 (frame +3) GGHMVMGDSFNSSLFKQTFQRVFSKDSNGDLKMSFNAILEVKCSRELKVQGGIGPCVSLNVKNPLVSDLEIGMGNT VQWKLCSLSPSTTVALLFFEVNQHAAPIQGGRGCIQFITQYQHSSGQKKIRVTTIARNWADATANIHHISAGFDEQT AAVLARIAVYRAETDESSDVLRWVDRMLRLCQKFGEYNKDDTNSFRLSEFSLYPQFMYHLRRSQFLQVFNNSP DETSFYRHMLMREDRNG

EV015	519	SEQ ID NO: 520 (frame +1) RHPSLFAIGVKPPRGILLYGPPGTGKTLIARAVANETGAFFFLINGPEIMSKLAGESNLKAFEEADKNSPAIFIDE LDAIPKREKTHGEVERRIVSQLTLMDGMKSSHVIVMAATNRPNSIDPALRRFGRFDREIDIGIPDATGRLEVLRIHT KNMKLADDDVDLEQIAAETHGHVGADLASLCSAALQQIREKMDLIDLDDDEQIDAEVLNSLAVTMENFRYAMSKSSPSA LRETV
EV016	521	SEQ ID NO: 522 (frame +2) TVSGVNGPLVILDSVKFPKFNIEVQLKLSDGTVRSGQVLEVGSKAVVQVFEGTSGIDAKNTLCEFTGDILRTPVSED MLGRVFNCGSKPIDKGPPIAEDFLDIQGPINPWSRIYPEEMIQTGISAIDVMNSIARGQKPIFSAAGLPHNEIAAQIC RQAGLVKIPGKSVLDDHEDNFAIVFAAMGVNMETARFFKQDFEENGSMENVCLFLNLANPTIERITPRLTLTAAEFM AYQCEKHVLVILTDMSSYAEALREVSAA

Table 3-AG

Target ID	cDNA SEQ ID NO	Corresponding amino acid sequence of cDNA clone
AG001	601	SEQ ID NO: 602 (frame +1) HLKRFAAPKAWMLDKLGGVFAPRPSTGPHKLRESPLVIFLRNLKYALTNCEVTKVMQRLIKVDGKVRTDPNYPAG FMDVITIEKTGEFFRLYDVKGFRTHITAEAAKYKCKVKVQTGPKGIPFLVTHDGRITRYPDPMIKVNNDTQLEIATS KILDFIKFESGNLCMITGGRNLGRVGTVNRERHPSGFDIVHIRDANDHVFATRLNNVFGKSKAFVSLPRGKGVK LSIA
AG005	603	SEQ ID NO: 604 (frame +2) VWLDPNEINEIANTNSRQNIKLIKDGIIKKPVAVHSRARRVRKNTARRKGRHCGFGKRKGTANARMPQKELWIQR MRVLRRLKKYREAKKIDRHL YHAL YMKAKGNVFKNKRVLMEYIHKKKAERAKAMLADQANARRQKVQVP*EEG RAYRREEAG
AG010	605	SEQ ID NO: 606 (frame +3) GGHMLMGDSFNSSLFKQTFQRFVAKDQNGHLKMAFNGTLVKCSRELKVQGGIGSCVSLNVKSPVLVADTEIGMGN TVQWKMCFTFNPSTTMALFFEVNQHSAPIQGGRGCIQFITQYQHSSGQRRIRVTTIARNWADASANIHHISAGFDQ ERAAVIMARMAMAVYRAETDESPDVLRWVDRMLRLCQKFGYKDDQASFRLENFSLYPQFMYHLRRSQFLQVFNN SPDETSFYRHHMLMREDLTQSLMIQPILYSYSFNGPPEPVLLDTSSIQPDRILLMDTFFQILIFHGETIAQW
AG014	607	SEQ ID NO: 608 (frame +3) QIKHMMAFIEQEA NEKAEIEIDAKAEFEENIEKGRLVQQQRLKIMEYEEKQVLELQKKIQSSNMLNQARLKVLRRE DHVRVAVLDEARKKLGEVTRDQGYAQILESILQGLYQLFEANVTVRVPQDRTLVQSVLPTIATKYRDTVTRDVLHS IDDETQLSESVTGGIELLCKQNKIKVCNTLEARLDLISQQLVPQIRNALFRNINRKF
AG016	609	SEQ ID NO: 610 (frame +1)

		VSEDMGRVFN GSGKPIDKGPPIAEFLDIQGPINPWSRIYPEEMIQTGISAIDVMNSIARGQKIPFSAAGLPHNEIA AQICRQAGLVKLPKGSVIDDHEDNFAIVFAAMGVNMETARFFKQDFEENGSMENVCLFLNLANPTIERITPRALTA AEFLAYQCEKHVLVILTDMSSYAEALREVSAAREEVPGRRGFGYMYTDLATYERAGRVEGRNGSITQIPILTMPND DITHPI
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Table 3-TC

Target ID	cDNA SEQ ID NO	Corresponding amino acid sequence of cDNA clone
TC001	793	SEQ ID NO: 794 (frame +1) GPKKHLKRLNAPKAWMLDKLGGVFAPRPSTGPHKLRSLPLVFLRNLKYALTNSEVTKIVMQRLIKVDGKVRTD PNYPAGFMDVVTEIKTGEFFRLYDVVKGRFTIHRITGEEAKYKLCVKVQGTGPKGIPFLVTRDGRITRYPDPMIKVN DTIQLEIATSKILDIFIKFESGNLCMITGGRNLGRVGTVVSRRERHPGSDIVHIKDANGHTFATRLNNVFIIGKSKPYV SLPRGKGVKLSI
TC002	795	SEQ ID NO: 796 (frame +1) QEFLEAKIDQELTAKKNASKNKRAAIAIKRKKRYEKQLQIQIDGTLSTIEMQREALEGANTNTAVLKTMKNAADAL KNAHLNMDVDEVHDMDDI
TC010	797	SEQ ID NO: 798 (frame +3) PELVFGHVLVLEVPPLGDCLTVENQNLEKCVHEKDPGLNGTSVEEDGFRGAVETITVQNRLDHNETHLGEVLPH QHVAVERGLVWGVVENLEELGAAQMVHELGIETEVFTQTETVRVVFVFAEF
TC014	799	SEQ ID NO: 800 (frame +1) EKAEEIDAKAEFEFNIEKGRVLVQQRLKIMEYYEKKPKVELQKIQSSNMLNQARLKVLRKVEDHVNVLDDARK RLGEITNDQARYSQLLESILQSLYQYLGISDEL FENNIVVRVRRQQDRSIQILPWATKYRDATGKDVHLKIDDES HLPSETTGGVLYAQKGKIKIDNTLEARLDLIAQQLVPEIRTALEGRNINRKF
TC015	801	SEQ ID NO: 802 (frame +2) DELQFRGDTVLLKGKRRKETVCIVLADENCPDEKIRMNRIVRNLRVRLSDVWVIQPCPDVKYGRKRIHVLPIDDTV EGLVGNLFVYLPKYFLEAYRPIHKGDVFIVRGGMRAVEFKVWETEPSPYCVIAPDVIHCDGDPKIKREEEEALNA VGYDDIGGCRKQLAQIKEMVELPLRHPSLFKAIGVKPPRGILLYGPPTGKTLIARAVANETGAFFFLINGPEIMSKL AGESESNLRKAFEEADKNSPAIFIIDELDAIAPKREKTHGEVERRIVSQLLTMDGMKKSSHVIVMAATNRPNISIDPA LRRFGRFD

Table 3-MP

Target ID	cDNA SEQ ID NO	Corresponding amino acid sequence of cDNA clone
MP001	888	SEQ ID NO: 889 (frame +1) GPKKHLKRLNAPKAWMLDKSGGVFAPRPSTGPHKLRESPLILFLNRLKYALTGAETKIVMQRLIKVDGKVRTDPN YPAGFMDVISIQKTSEHFRLIYDVKGRTIHRITPEEAKYKLVKRVQTGPKGVFPLTTHDGRITRYPDPNIKVNDRIR YDIASSKILDHIRFETGNLCMITGGRNLGRVGNTRERHPGSDIVHIKDANEHIFATRMNNVFIIGKGQKNYISLPRSK GVKLT
MP002	890	SEQ ID NO: 891 (frame +2) SFFSKVFGGKKEEGPSTEDAIQKLRSSTEMLIKKQEFLEKIEQEVIAKKNGTTNKRAALQALKRKKRYEQQLAQID GTMLTIEQQREALLEGANTNTAVLTTMKTAADALKSAHQNMNVDDVHDLMDDI
MP010	892	SEQ ID NO: 893 (frame +3) GCIOFITQYQHSSGKYKRIRVTTLARNWADPQNMHVSAAFDQEAASAVLMARMVWVNRATEDSPDVMRWADRTL RLCQKFGDYQKDDPNFRLPENFSLYPQFMYHLRRSQFLQVFNNSPDETSYYRHMLMREDVTQSLMIQIPILYSYSF NGRPEPVLLDTSSIQPKILLMDTFFHILIFHGETIAQWRAMDYQNRPEYSNLKQLLQAPVDDAQEILKTRFPMPRYID TEQGGSQARFLLCKVNPSTHNNMYAYGG*WWSTSFDR*CKLAHVHGAAA
MP016	894	SEQ ID NO: 895 (frame +1) VSEDMGRVFNFGSGKPIDKGPPILAEDYLDIEGQPINPYSRTYPQEMIQTGISAIMNSIARGQKPIFSAAGLPHNEIA AQICRQAGLVKKPGKSVLDDHEDNFAIVFAAMGVNMETARFFKQDFFENGSGMENVCFLNLANPTIERIITPRALT AAEFLAYQCEKHVLVILDTMSSYAEALREVSAAREEVPGRRGFGYMYTDLATYERAGRVEGRNGSITQIPILTMPN DDITHPI
MP027	896	SEQ ID NO: 897 (frame +3) PITKTRRVFRH*KAMLKIFLLVCFHPPELPIVLTGSEDGTVRIWHSHTYRLESSLNYGLERVWTTICLRGSNNVALGYDE GSIMVKVGREEPAMSDVHGGKIVWARHSEIQQANLKAMLAEGAEIKDGERLPIQVKDMGSCSEIYQSSISHNPNG RFLVWCGDGEYIYTSMALRNKAFGSAQDFVWSSDSEYAIRENSSTIKVFNKFKKSKFPEGGADGIFGGYLLGVKS VTGLALYDWENGNLVRRIETQPKHVFWSSEGLVCLATDEAYFILRFDVNVLSAARASNYEAAASPDGLEDFAFEILGEV QEVVKTGLWVGDCFIYTNNGVNRINYVVGGEVTVTS

Table 3-NL

Target ID	cDNA SEQ ID NO	Corresponding amino acid sequence of cDNA clone
NL001	1071	SEQ ID NO: 1072 (frame +2) KSWMLDKLGGVYAPRSTGPHKLRSLPLVFLNRRLKYALTNCEVKKVMQRLIKVDGKVRTDPNYPAGFMDVWQIEK TNEFFRLIYDVKGFRTHIRITAEAAKYKLCVKRVQTPGKGIPELTHDGRITRYPDPLVKVNDTIQLDIATSKIMDFRDS GNLCMITGGRNLGRVGTWNRERHPGSDIVHIKDVLTGHTFATRLNNVFIIGKSKAYVSLPKGKGKLS
NL002	1073	SEQ ID NO: 1074 (frame +1) DEKGP TTGEAIQKLRETEEMLIKQDFLEKKIEVEIGVARKNGTKNKRAAIQALKRKKRYEKQLQIDGTLSTIEMQREAL EGANTNTAVLQTMKNAADALKAHQHMDVDQ
NL003	1075	SEQ ID NO: 1076 (frame +2) PRPYEKARLEQELKIIGEYGLRNKREVWRVKYALAKIRKAAARELLTLEEKDQKRLFEGNALLRRLVRIGVLDEGRMKLD YVLGLKIEDLELRLQTQVYKGLAKSIHARVLRQRHI RVRKQVWNIPSFVRLDSQKHIDFSLKSPFGGGRPRGV
NL004	1077	SEQ ID NO: 1078 (frame +1) KELAAVRTVCSHIENMLKGVTKGFLYKMRVYAHFPINCVTENNNSVIEVRNFLGEKYIRRVRMAGVTVTNSTKQKDEL IVEGNSIEDVSRSAALIQSSTTVKNKDIRKFLD
NL005	1079	SEQ ID NO: 1080 (frame +1) LDPNEINEIANTNSRQIRKLKDGIIKKPVAHVSRARVRKNTAARRKGRHCGFGKRKGTANARMPQKVLWVNRMRVL RRLKKYRQDKKIDRHL YHHL YMKAKGNVFNKRVLMFEFIH KKKAEKARMKMLNDQAEARRQKVKEAKRRE
NL006	1081	SEQ ID NO: 1082 (frame +3) VLVSSGVVEYIDTLEETTMIAMSPDDL RQDKEYAYCTTYTHCEIHPAMILGVCASIIPFDHNQSPRNTYQSAMGKQAM GVYITNFHVRMDTLAHVLFYPHKPLVTTRSMEYLRFRREL PAGINSVVAIACYTGYNQEDSVILNASAVERGFFRSVFFRS YKDAESKRIGDQEEQFEKPTRQTCCQGMRAIYDKLDDGGIAPGLRVSGDDVVGKTTILPDNDDELEGTTKRFTKRDS TFLRNSETGIVDQVMLTLNSEGKFKIRVRSVRIPQIGDKFASRHGQKGTCTGCIQYRQEDMPFTSEGIAPDIINPHAIPSR MTIGHLIECLQGKVSSNKGEIGDTPFN
NL007	1083	SEQ ID NO: 1084 (frame +2) FRDFLLKPEILRAILDCGFEHPSEVQHECIPQAVLGMDILCQAKSGMGKTAVFVLATLQQIEPTDNQVSVLVMCHTREL FQISKEYERFSKMPNIVKGVFFGGLPIQRDEETLKNCPHIVGTPGRILALVRNKKLDLHLKHFVLDECDKMLELDM RRDVQEIRNTPHSKQVMMFSATLSKEIRPVCKFMQDPMVEVYDDAKLTLHGLQQHYVYKLNENEKNKLFELLDILE FNQVVFVKSQVQRCMALSQLL TEQNFPVAIHRGMTQEERLKKYQEFKEFLKRILVATNLFGRGMDIERVNVFNVDMP
NL008	1085	SEQ ID NO: 1086 (frame +1) GRIENQKRWGVLLGCWRPGGVLDVSNFAVPFDEDDKEKNVWFLDHDYLENMFMGFKKNAREKVVGWYHTGPKL

NL009	1087	HQNDVAINELIRRYCPNCVLVIIDAKPKDGLPTEAYRWEEIHDDGSPTSKTFEHVMSEIGAEAEVEHLLRDIKDTT VGSLSQRVTNQLMGLKGLHLQLQDMRDYLNQVVEGKLPNMNHQIVYQLQDIFNLLPDIGHGNFVDSLY SEQ ID NO: 1088 (frame +1) CDYDRPPGGRGVCDVDVKNWFPCTSENNFNHQSPPCVFLKLNKIIGWQPEYNETEGFPDNMPGDLKRHIAQQKSI NKLFMQTWITCEGEGPLDKENAGEIQIPRQGFPGFYFPTN A SEQ ID NO: 1090 (amino terminus end) (frame +2) SSRLEATRLVVPVGCLYQPLKERPDLPVQYDPLVCLTRNTCRAILNPLCQVDYRAKLWVCNFCQRPFPQYAAISEQ HQAELIPSFSTIEYITRAQTMPPMFVLVDTCLDDEELGALKDSLQMSLSLLPPNALIGLITFGKMVQVHELGCDCGCSK SYVFRGVKDLTAKQIQDMLGIGKMAAAPQPMQQRIPGAAPSVNRFQPVGKCDMSLTDLGELQRDPWNVAQGKR PLR STGVALSIAVGLLECT SEQ ID NO: 1116 (carboxy terminus end) (frame +3) LNVKGCVSDDTIGLGGTSQWKMCFTPHTTCAFFFEVWNQHAAPIPQGGRGCIQFITQYQHSSGQRRIRVTTIARNWA DASTNLAHISAGFDQEGAVLMARMVWVHRAETDDGPDVMRWADRMRLRLCQRFGEYSKDDPNFSRLPENFTLYPQFM YHLRRSQFLQVFNNSPDETSYYRHLMRDLTQSLIMIQILYSYSFNGPPEPVLLDTSSIQPDRILLMDTFFQILIFHGETI A
NL010	1089	
	1115	
NL011	1091	SEQ ID NO: 1092 (frame +2) DGGTGKTTFVKRHLTGFEKKYVATLGEVHPLVFHTNRGVIRFNWVDTAGQKFGGLRDGYIQQGCAIMFEDVTSRV TYKNVPNWHRDLVRVCENIPIVLCGNKVDIKRKKAKSIVFHRKKNLQYYDISAKSNYNFEKPFLLWAKKLIGDPNLEFV AMPALLPEVTMDPQX SEQ ID NO: 1094 (frame +2) QQTQAAQVDEVVDIMKTNVEKVLERDQKLSLDDRADALQQGASQFEQQAGLKRKF
NL012	1093	
NL013	1095	SEQ ID NO: 1096 (frame +2) AEQVYISSLLALLKMLKHGRAGVPMEVMGLMLGEFVDDYTVRVIDVFAMPQSGTGVSVAEVDPVFAQKMLDMLKQTGR PEMVVGWYHSHPGFGCWLSGVDINTQESFEQLSKRAVAVVV SEQ ID NO: 1098 (frame +2) FIEQEANEKAEIEDAKAEFEFNIEKGRLVQHQRKIMEYYDRKEKQVELQKKIQSSNMLNQARLKALKVREDHVRSLVEE SRKRLGEVTRNPAKYKEVLQYLIVQGLQLLESNVVLRVR EADVSLIEGIVGSCAEQYAKMTGKEVVVKLDADNFLAAETCGGVELFARNGRKIPNTLESRLDISQQLVPEIRVALF SEQ ID NO: 1100 (frame +1) IVLSDETCPFEKIRMNRVVRKNLVRSLDIVSIQPCPDVKYGRKRIHVLPIDDTVEGLTGNLFEVYLKPYFLEAYRPIHKDDA FIVRGGMRAVEFKWETDPSYICVAPDVIHCEGDPKREDEEDAANAVGYDDIGGCRKQLAQIKEMVVELPLRHPSLFK AIGVKPPRGILLYGPPGTGKTLIARAVANETGAFFLINGPEIMSKLAGESNLKAFEEADKNAPAIIFIDELDAIAPKRE KTHGEVERRIVSQLLTLMMDGLKQSSHVIVMAATNRPNSIDAALRRFGRFDREIDIGIPDATGRLEVLRIHTKNMKMLADDVD
NL014	1097	
NL015	1099	

NL016	1101	LEX SEQ ID NO: 1102 (frame +2) TPVSEDMGRVFNKGKPIDKGPILAEDYLDIQGPINPWSRIYPEEMIQTGISAIDVMNSIARGQKIPFSAAGLPHNEIA AQICRQAGLVKLPKGSVLDSDSEDFNFAIVFAAMGVNMETARFFKQDFEENGSMENVCFLNLANOPTIERIITPRALTAEE FLAYQCEKHVLVILTDMSSYAEALREVSAAREEVPGRRRGFGPYMTDLATYERAGRVEGRNGSIT
NL018	1103	SEQ ID NO: 1104 (frame +2) MQMPVPRPQIESTQQFIRSEKTTYNSNGFTTIEEDFKVDTFEYRLLREVSRFRESLRNLYHEADMQMSTVVDRLGPPSAP HIQKPRNSKIQEGGDAVFSIKLSANPKPRLVWFKNGQRIGQTQKHQASYSNQATLKVNVSAQDSGHYTLTLLAENPQ GCTVSSAYLAVESAGTQDTGYSEQYSRQEVETTEAVDSSKMLAPNFVRPADRDASEGKMTFRDCRVTRGRYPDVA WFINGQQVADDAATHKILVNESGNHSLMITGVTRLDHGVGVCIA RNKAGETSFQCCLNVIEKELVWAPKVERFAQVNVK EGEPWLSARAVGTPVPRITWQKDGAPIQSGPSVSLFVDGGATSLDIPYAKAS
NL019	1105	SEQ ID NO: 1106 (frame +2) DDTYTESYSTIGVDFKIRTIIDLDGKTIKLIQWDTAGQERFRTITSSYYRGAGHGIIVYDCTDQESFNLLKQWLEEDRYAC DNVNKLLVGNKCDQTNKKVVDYTAKEYADQLGIPFLETSAKNATNVEQAF
NL021	1107	SEQ ID NO: 1108 (frame +2) VLSNSVTDISTTFILKPQENVKITLEGAQACFISHERLVISLKGGEYVLTLYSDSMRSVRSFHFLEKAAASVLTTCICVCEE NYLFLGSRNLGNSLLLRFTTEKELNLIETRAIESSQSNPAKKKLDLTLDGWMASDVTEIRDLDELEVYGSSETQTSQMIA SY F
NL022	1109	SEQ ID NO: 1110 (frame +2) TLHREFLSEPDLSQSVMIIDEAHERTLHTDILFGLVKDVARFRPDLKLLISSATLDAQKSEFFDDAPIFRIPGRFRFPVDIY YTKAPEADYVDACVVSILQIHATQPLGLVFLTGQEEIETCQELLQDVRRLGPRIKELLIPVYNLPSDMQAKIFLPTPP NARKVVLATNIAETSLTDNIIVIDPGFCCKQNNFNSRTGMESLVVVPVSKASANQRAGRVAAGKCFRLYT
NL023	1111	SEQ ID NO: 1112 (frame +2) RSFSQERQHEEMKESGRMHSDPLIVETHSGHVRGISKTVLGREVHVFTGIPFAKPPIGPLRFRKPVVPDPWHGVLD TALPNSCYQERYEYFPGFEGEEMWNPNTNLSEDCLYNIWVPHRLRHRANSEENKPRAKVPVLIWIYGGYMSGTA TLDVYDADMVAATSDVIVASMQYRVGAFGLYLAQDLPRGSEEAAPGNMGLWDQALAIRWLKDNI AAFGGDPELMTLFG ESAGGGSVSIHLVSPITRGLARRGIMQSGTMNAPWSFMTAERATEIAKTLDCCGNSLLTDAPSRVMSCMRSVEAKII SVQQWNSYSGILGLPSAPTDIDGIFLPKHPLDLKKEGDFQDTEILIGSNQDEGTIFILYDFIDFFQKDGPSFLQRDKFLDIINT IFKNMTKIEREAIQYTDWEHVMMDGYLNQKMIGDVGDYFFICPTNHFAQAFAEHKKVYFFFTQRTSTSLWGEWGMG VMHGDEIEYVFGHPLNMSLQFNARERDLRLIMQAYSRRFALTGKVPDPDVNWPYISKDQPPQYIFNAETSGTGRGPRA TACAF
NL027	1113	SEQ ID NO: 1114 (frame +2) PIVLTGSEDTVRWHSHTYRLESSLNYGLERWWTICCMRGSNVVALGYDEGSIMVKVGREEP AISMDVNGEKIWWARH SEIQQVNLKAMPEGVEIKDGERLPVAVKDMGSCIEYPQTIAHNPNGRFLVCGDGEYIHTSMVLRNKAFAFGSAQEFIWG

		QDSSEYAIREGTSTVKVFNKFKKSKPEFGAESIFGGYLLGVCSLGLALYDWETLELVRRIEIQPKHHVYWSSEGELV ALATDDSYFVRLRYDAQAVLAARDAGDDAVTPDGVEDAFEVLGEVHETVKTGLWVGDCFIYT
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Table 3-CS

Target ID	cDNA SEQ ID NO	Corresponding amino acid sequence of cDNA clone
CS001	1682	SEQ ID NO: 1683 (frame +1) KAWMLDKLGGVYAPRPSTGPHKLRECLPLVIFLRNRLKYALTGNEVLKIVKQRLIKVDGKVRTDPTYPAGFMDWV SIEKTNELFRLIYDVKGRTIHRITPEEAKYKCKVRRVATGPKNVPLYVTHDGRVRYPDPLIKVNDISQLDIATSK IMDFIKFESGNLCMITGGRNLGRVGTIVSRERHPGSGFDIVHIRSTGHTFATRLNNVFIIGKGTAKAYISLPRGKGVR LT
CS002	1684	SEQ ID NO: 1685 (frame +1) SFFSKVFGGKKEEGPSTHEAIQKLRETEELLQKKQEFLEKIDTELQTARKHGTKNKRAAIAALKRKKRYEKQLT QIDGTLTQIEAQREALEGANTNTQVLNTRDAATAMRLAHKIDIDVDKVHDLMDI
CS003	1686	SEQ ID NO: 1687 (frame +1) GLRNKREVWRVKYTLARIRKAAARELLTLEEKDPKRLFEGNALLRRLVRIGVLDEKQMKLDYVLGLKIEDFLERRLQ TQVFKAGLAKSIHHARILIRQRHVRKQVNIPIFVRLDSGKHIDFSLKSPFGGGRP
CS006	1688	SEQ ID NO: 1689 (frame +1) TCQGMARNALYDKLDDGGIAPGIRVSGDDVIGKTITLPENDDLEGTSSRRYSKRDASTFLRNSETGIVDQVMTL NSEGYKFCIKIRVRSVRIPQIGDKFASRHGQKGTGCIQYRQEDMPFTCEGLTPDIINPHAIPIPSRMTIGHLIECIGK VSSNKGEIGDATPFENDAVNVQKI
CS007	1690	SEQ ID NO: 1691 (frame +3) SEISCNQRFWGLSSIAVSSTLQKFNMNVPKLFWEWIFFVKAKSGMGKTAVFVLATLQQLEPSENHVYVLMC HTRELAFQISKEYERFSKYMAGVRVSVFFGGMPIQKDEEVLKTACPHIVVGTGPRILALVNNKKLNLKHLKHFLD ECDKMLESDMRRDVQEIFRNTPHGKQVMMFSATLSKEIRPVCKKFMQDPMEVYVDDAKLTLHGLQQHYVKL KENEKNKKLFFELLDVLEFNQVVFVKSQVRCIALAQLLTDQNFPAIGIHRNMTQDERLSRYQQQKDFQKRILVATN LFGRGMDIERVNI/FNYDMP
CS009	1692	SEQ ID NO: 1693 (frame +1) LVAICIWTFQLRQDSREPMWQLDESIIGNPGLGFRPTPEVASSVIWYKGNDPNSQQQVWQETSNFLTAYKRD GKKAGAGQNIHNCDFKLPPPAGKVCVDVISAWSPCVEDKHFGYHKSTPCIFLKLNFKIFGWRPHFYNSSDSLPTD MPDDLKEHIRNMTAYDKNYLNMVWVSCGENP

CS011	1694	SEQ ID NO: 1695 (frame +1) GSGKTTFVKRHLTGEFEKRYVATLGVVEHPLVFHTNRGPIRFNVWDTAGQEKFGGLRDGYIQQGQCAIMFDVT SRVTYKNVPNWHRDLVRVCEGPIVLCGNKVDIKDRKVAKAKTIVFHRKKNLQYYDISAKSNYNFEKPFELWLARKLI GDGNLEFVAMQPCFH
CS013	1696	SEQ ID NO: 1697 (frame +2) DAPVVDTAEQYVYSSLLALLKMLKHGRAGVPMEVMGLMGEFVDDYTVRVIDVFAMPQTGTGVSEAVDPVFQA KMLDMLKQTGRPEMVGVYHSHPGFGCWLSGVDINTQQSFEALSERAVAVVDPISVKKG
CS014	1698	SEQ ID NO: 1699 (frame +2) QKQIKHMMAFIEQEAANEKAEIDAKAEFEENIEKGRVQQQRKIMEYYEKKQVELQKKIQSSNMLNQARLKV LKVREDHVRNVLDARKRLAEVPKDVKLYTDLLVTLVWQALFQLMEPTVTVRVRQADVSLVQSSILGKAQQDYKA KIKDVQLKIDTENSPLADTCGGVELIAARGRIKISNTLESRLIEIAQQLPEIRTALF
CS015	1700	SEQ ID NO: 1701 (frame +1) IVLSDNCPDEKIRMNRVVRNLRVRLSDIVSIAPCPSVKYGKRVHILPIDDSVEGLTGNLFEVYLKPYFMEAYRPI HRDDTFMVRGGMRAVEFKWETDPPYCVAPDTVIHCEGDPKREEEEAALNAVGYDDIGGCRKQLAQIKEMV ELPLRHPSLFAIGVKPPRGILMYGPPGTGKTLARAVANETGAFFLINGPEIMSKLAGESSENLRKAFEEADKN SPAIFIDELDAIAPKREKTHGEVERRIVSQLLTMDGMKSSHVIVMAATNRPNSIDPAL
CS016	1702	SEQ ID NO: 1703 (frame -3) TPVSEDMGRVFNCGSKPIDKGPPIAEDFLDIQGGPINPWSRIYPEEMIQTGISAIDVMNSIARGQKPIFSAAGLP HNEIAAQICRQAGLVKIPGKSVLDDHEDNFAIVFAAMGVNMETARFFKQDFEENGSMENVCFLFLNLANDPTIERII TPRLALTAAEFLAYQCEKHVLVILDMSSYAEALREVSAAAREEVPGRGPGMYTDLATYERAGRVEGRNGSI TQIPILTMPNDDITHIPDLTGYTEGQIVVDRQLHNRQIYPPVNVLPSSLRLMKSAIGEGMTRKDHSDVSNQLYAC YAIGKDVQAMKAVVGEEALTPDDLLYLEFLTKEKNFITQGNENRTVFESLDJGWQLLRIFPKEMLKRI PASI
CS018	1704	SEQ ID NO: 1705 (frame +2) SVYIQEGVPVPAQQSQQQSYRHSVESVEHKS YGTQGYTTSEQTQTKQKVAYTNGSDYSSTDDFKVDTFEY RLLRVSVFRESITKRYIGETDIQISTEVDKSLGWVTPPKIAQKPRNSKLQEGADAQFVQLSGNPRPRVSWFKNG QRIVNSNKHIEIVTTHNQTLRVRNTQKSDTGNVYLLAENPNCVWTSAYLAVESPQETYGGDHKSQYIMDNQQT AVEERVEVNEKALAPQFVRVCQDRDVTGKMTFRDQVTPGRPYEVTWFINDRQIRDDYXHKILVNESCNHAL MITNVDLSDSGVVSCIARNKTGETSFQCRNLNIEKEQVAPKPFVERFSTLNVREGEVQLHARAVGTPTRITWQ KDGVCQVIPNPELINTEGGASTLDIPRAKASDAGWYRC

Table 3-PX

Target ID	cDNA SEQ ID NO	Corresponding amino acid sequence of cDNA clone
PX001	2100	SEQ ID NO: 2101 (frame +1) GPKHLRLNAPRAWMLDKLGGVYAPRPSTGPHKLRECLPLVFLQPPVRAQRQGAEDREAAPHQGGRRQGP RPHLPGWIHGCCVD*KDQ*AVPSDLRCEGLHPPHHSRGGQVAVQGEARGDGPQERAVHRDAQRPHAALPRP AHQGRRLHPARHRHLQDHGHHQVRLR*PVHDHGRA*LGASGHHRVPREAPRELHRPHQGHHRTHLRHQVEQRV HHRQGHE
PX009	2102	SEQ ID NO: 2103 (frame +3) TLIWKGTGYDSYKYWENQLIDFLSVYKKKGQTAGAGQNFCDFRNPPPHGKVCVDVIRGWEPCEIDENHFSFHS SPCIFLKLNKYGRPEFYNDTANLPEAMPVDLQTHIRNITAFNRDYANMVWVVSCHGETPADKENIGPVRYLPYPGFP GYFYPYENAEGLSPLVAVHLERPRTGIVINIECKAWA
PX010	2104	SEQ ID NO: 2105 (frame +3) GCIQFITQYQHSSGQRRVRVTTARNWGDAAANLHHISAGFDQEAADVVMARLVYRAEQEDGPDVLRWLDRMLIR LCQKFGEYAKDDPNSEFSLYPQFMYHLRRSQFLQVFNNSPDETTFYRHMLMREDLTQSLMIQPILYSYSFG GAPEPVLLDTSSIQPDRIILLMDTFFQILYHGETMAQWRALRYQDMAEYENFKQLLRAPVDDAQEILQTRFPVRYIDT EHGGSQARELLSKVNPSQTHNNMYAYGGAMPIPSADGGAPVLTDDVSLQVFMQEP
PX015	2106	SEQ ID NO: 2107 (frame +3) RKETVCIVLSDDNCPDEKIRMNRVVRNNLRVRLSDIVSIAPCPSVKYGKRVHILPIDDSVEGLTGNLFEVYLKPYFMEA YRPIHRDDTFMVRGGMRAVEFKWETDPSYCIVAPDTVIHCEGEPIKREEEEEEALNAVGYDDIGGCRKQLAQIKEMV ELPLRHPSLFAIGVKPPRGILMYGPPGTGKTLIARAVANETGAFFFLINGPEIMSKLAGESESNLRKAFEEADKNSPA ILIDELDAI
PX016	2108	SEQ ID NO: 2109 (frame +2) FTGDILRTPVSEDMGLGRIFNGSGKPIDKGPPIAAEEYLDIQGQPINPWSRIYPEEMIQTGISAIDVMNSIARGQKIPFSA AGLPHNEIAAQICRQAGLVKVPKSVLDDHEDNFAIVFAAMGVNMETARFFKQDFEENGSMENVCFLNLANDPTIE RIITPRALTAAEFAYQCEKHVLVILTDMSSYAEALREVSAAREEVPGRRGPGMYTDLATYERAGRVEGRNGSIT QIPILTMPNDDITHPIPDLTGYITEGQIYVDRQLHNRQIYPPVNVLPSSLRLMKSAIGEGMTRKDHSDVSNQLYACYAIG KDVQAMKAVVGEEALTPDDLLYLEFLTKEKNFITQGSYENRTVFESLDIGWQPLRIFPKEM

Table 3-AD

Target ID	cDNA SEQ ID NO	Corresponding amino acid sequence of cDNA clone
AD001	2364	SEQ ID NO: 2365 (frame +1) GPKKHLRLNAPKAWMLDKLGGVFAPRPSTGPHKLRECLPLVFLRNRLKYALTNCEVTKIVMQRLIKVDGKVRTDPN YPAGFMDVWTIEKTGEFFRLVYDVKGRTIHRISAEAEAKYKLCVRRVQTGPKGIPFLVTHDGRITIRYPDPVVKVNDISI QLDIATCKIMDHIRFESGNLCMITGGRNLGRVGTVSRERHPGSFDIVHIKDTQGHTEATRLNNVFIIGKATKPYISLPK GKGVKLSIAEERDK
AD002	2366	SEQ ID NO: 2367 (frame +2) SFFSKVFGGKKDGKAPTGTGEAIQKLRETEEMLIKQKEFLEKKIEQINVAKKNGTKNKRRAAIQALKRKKRYEKQLQQID GTLSTIEMQREALEGANTNTAVLQTMKSAADALKAHQHMDVDKVHDLMDDI
AD009	2368	SEQ ID NO: 2369 (frame +3) VLAALVAVCLWVFFQTLDPRIPTWQLDSSIIGTSPGLGFRMPEDSNVESTLIWYRGTDRRDDFRQWTDTLDEFLAVY KTPGLTPGRGQNIHNCDDYDKPPKKGQVCNVVDIKNWHPCIQENHYNHYKSSPCIFIKLNKIYNWPIEYNESTNLPEQM PEDLKQYIHNLESNNSREMNNTVWVSCEGENP
AD015	2370	SEQ ID NO: 2371 (frame +2) DELQFRGDTVLLKGKRRKETVCIVLSDDTCPDGKIRMNRVVRNLRVRLSDWSVQPCPDVKYGKRIHVLPIDDTVE GLTGNLFEVYLKPYFLEAYRPIHKDDAFIVRGGMRAVEFKVWETDPSYCVIAPDTVIHCEGDPKREEEEEEALNAVGY DDIGGCRKQLAQIKEMVELPLRHPSLFKAIGVKPPRGILLYGPPTGKTLIARAVANETGAFFFLINGPEIMSKLAGESE SNLRKAFFEEADKNAPAIIFIDELDAIAPKREKTHGEVERRIVSQLLTMDGLKQSSHVIVMAATNRPNSIDGALRRFGRF DREIDIGIPDATGRLEILRIHTKNMKLADDVDLEQIAAESHG
AD016	2372	SEQ ID NO: 2373 (frame +2) FTGDILRVVPVSEDMLGRFTNGSGIPIDGGPPPIVAETVLDVQGMPIPNQTRIYPEEMIQTGISTIDVMTSIARGQKPIFSG AGLPHNEIAAQICRQAGLVQHKENKDDFAIVFAAMGVNMETARFFKREFAQTGACNVVFLNLANDPTIERIITPRAL TVAEFLAYQCCKNHVLMVIMTDMTSAEALREVSAAREEVPGRRGFPGYMYTDLSTIYERAGRVQGRPGSITQIPILTMP NDDITHPI

Table 4-LD

Target ID	SEQ ID NO	Sequences*	Example Gi-number and species
LD001	49	GGCCCCAAGAAGCATTTGAAGCGTTT	3101175 (<i>Drosophila melanogaster</i>), 92477283 (<i>Drosophila erecta</i>)
LD001	50	AATGCCCCAAAAGCATGGATGTTGGATAAA TTGGGAGGTGT	70909480 (<i>Carabus granulatus</i>), 77325294 (<i>Chironomus tentans</i>), 900945 (<i>Ctenocephalides felis</i>), 60297219 (<i>Diaprepes abbreviatus</i>), 37951951 (<i>Ips pini</i>), 75735533 (<i>Tribolium castaneum</i>), 22039624 (<i>Ctenocephalides felis</i>)
LD001	51	GAAGTTACTAAGATTGTTATGCA	33368080 (<i>Glossina morsitans</i>)
LD001	52	ATTGAAAAAACTGGTGAATTTTCCG	60297219 (<i>Diaprepes abbreviatus</i>)
LD001	53	ACACACGACGGCCGCCACCATCCGCT	27555937 (<i>Anopheles gambiae</i>), 33355008 (<i>Drosophila yakuba</i>), 22474232 (<i>Helicoverpa armigera</i>), 3738704 (<i>Manduca sexta</i>)
LD001	54	ACACACGACGGCCGCCACCATCCGCTA	92477283 (<i>Drosophila erecta</i>)
LD001	55	CCCAAGAAGCATTTGAAGCGTTTG	92954810 (<i>Drosophila ananassae</i>), 92231605 (<i>Drosophila willistoni</i>)
LD002	56	GCAATGTCATCCATCATGTCGTG	17861597 (<i>Drosophila melanogaster</i>), 92223378 (<i>Drosophila willistoni</i>), 92471309 (<i>Drosophila erecta</i>)
LD003	57	CAGGTTCTTCCTCTTGACGCGTCCAGG	24975810 (<i>Anopheles gambiae</i>), 3478578 (<i>Antheraea yamamai</i>), 42764756 (<i>Armigeres subalbatus</i>), 24661714 (<i>Drosophila melanogaster</i>), 68267151 (<i>Drosophila simulans</i>), 33355000 (<i>Drosophila yakuba</i>), 49532931 (<i>Plutella xylostella</i>), 76552910 (<i>Spodoptera frugiperda</i>), 92959651 (<i>Drosophila ananassae</i>), 92467993 (<i>Drosophila erecta</i>)
LD003	58	TTGAGCGAGAAGTCAATATGCTTCT	49558930 (<i>Boophilus microplus</i>)
LD003	59	TTCCAAGAAATCTTCAATCTTCAAACCCAA	62238687 (<i>Diabrotica virgifera</i>), 76169907 (<i>Diptoptera punctata</i>), 67872253 (<i>Drosophila pseudoobscura</i>), 55877642 (<i>Locusta migratoria</i>), 66548956 (<i>Apis mellifera</i>)

LD003	60	TTCATCCAACACTCCAATACG	22040140 (Ctenocephalides felis)
LD003	61	AAGAGCATTCGCCCTCAACAACCT	2459311 (Antheraea yamamai)
LD003	62	AGTTCTCTGGCAGCTTTACGGATTTT	76169907 (Diploptera punctata)
LD003	63	CCACACTTCACGTTTGTTCTCT	57963694 (Heliconius melpomene)
LD003	64	CCGTATGAAGCTTGATTACGT	108742527 (Gryllus rubens), 108742525 (Gryllus pennsylvanicus), 108742523 (Gryllus veletis), 108742521 (Gryllus bimaculatus), 108742519 (Gryllus firmus), 109194897 (Myzus persicae)
LD003	65	AGGAACAAACGTGAAGTGTGGCG	109194897 (Myzus persicae)
LD006	66	AGCGCTATGGGTAAGCAAGCTATGGG	27819970 (Drosophila melanogaster)
LD006	67	TGTTATACTGGTTATAATCAAGAAGAT	55801622 (Acyrthosiphon pisum), 66535130 (Apis mellifera)
LD007	68	GAAGTTCAGCACGAAATGTATTCC	50563603 (Homalodisca coagulata)
LD007	69	CAAGCAAGTGATGATGTTCAAGTGCCAC	50563603 (Homalodisca coagulata)
LD007	70	TGCAAGAAATTCATGCAAGATCC	21068658 (Chironomus tentans)
LD007	71	AAATGAAAAGAATAAAAAAATT	49201437 (Drosophila melanogaster)
LD007	72	CAGAAATTTCCCAGCCCATAGGAAT	67895225 (Drosophila pseudoobscura)
LD007	73	AGCAGTTCAAAGATTTCCAGAAAG	77848709 (Aedes aegypti)
LD007	74	TTCCAAATCAGCAAAGAGTACGAG	91083250 (Tribolium castaneum)
LD010	75	TACCCGCGAGTTTCATGTACCAT	29558345 (Bombyx mori)
LD010	76	CAGTCGCTGATCATGATCCAGCC	49559866 (Boophilus microplus)
LD010	77	CTCATGGACACGTTCTTCCAGAT	60293559 (Homalodisca coagulata)
LD010	78	GGGGCTGCATACAGTTTCATCAC	92971011 (Drosophila mojavensis)
LD010	79	CCCGCAGTTTCATGTACCATTTG	92952825 (Drosophila ananassae)
LD010	80	GACAATGCCAAATACATGAAGAA	92921253 (Drosophila virilis)

LD010	81	TTCGATCAGGAGGCCGCGAGTG	92921253 (<i>Drosophila virilis</i>)
LD011	82	AGCAGGGCTGGCATGGCGACAAA	28317118 (<i>Drosophila melanogaster</i>)
LD011	83	TTCTCAAAAGTTGTAGTTAGATTGGC	37951963 (<i>Ips pini</i>)
LD011	84	TACTGCAAAATTCCTTCTCCTATG	55883846 (<i>Locusta migratoria</i>)
LD011	85	GGTACATTCTTGATGTAACCTC	67885713 (<i>Drosophila pseudoobscura</i>)
LD011	86	TCAAACATGATAATAGCACACTG	68771114 (<i>Acanthoscurria gomesiana</i>)
LD011	87	TCTCCTGACCGGCAGTGTCACATA	17944197 (<i>Drosophila melanogaster</i>), 77843537 (<i>Aedes aegypti</i>), 94469127 (<i>Aedes aegypti</i>), 24664595 (<i>Drosophila melanogaster</i>)
LD011	88	GCTACTTTGGGAGTTGAAGTCCATCC	101410627 (<i>Plodia interpunctella</i>)
LD011	89	TAACTACAACCTTTGAGAAAGCCCTTCCT	90813103 (<i>Nasonia vitripennis</i>)
LD011	90	AAGTTTGGTGTCTCCGIGATGG	84267747 (<i>Aedes aegypti</i>)
LD014	91	GCAGATCAAGCATATGATGGC	9732 (<i>Manduca sexta</i>), 90814338 (<i>Nasonia vitripennis</i>), 87266590 (<i>Choristoneura fumiferana</i>)
LD014	92	ATCAAGCATATGATGGCTTTTCATTGA	75470953 (<i>Tribolium castaneum</i>), 76169390 (<i>Diploptera punctata</i>)
LD014	93	AATATTGAAAAGGGGCGCCTTGT	78055682 (<i>Heliconius erato</i>)
LD014	94	CAACGTCTCAAGATTATGGAATA	37659584 (<i>Bombyx mori</i>)
LD014	95	ATTATGGAATATTATGAGAAAGA	66556286 (<i>Apis mellifera</i>)
LD014	96	AACAAAATCAAGATCAGCAATACT	25958976 (<i>Curculio glandium</i>)
LD016	97	ATGTCGTCGTTGGGCATAGTCA	27372076 (<i>Spodoptera littoralis</i>)
LD016	98	GTAGCTAAATCGGTGTACATGTAACTGGG AAACCACGACG	27372076 (<i>Spodoptera littoralis</i>), 55797015 (<i>Acyrtosiphon pisum</i>), 73615307 (<i>Aphis gossypii</i>), 4680479 (<i>Aedes aegypti</i>), 9713 (<i>Manduca sexta</i>), 76555122 (<i>Spodoptera frugiperda</i>), 237458 (<i>Heliothis virescens</i>), 53883819 (<i>Plutella xylostella</i>), 22038926 (<i>Ctenocephalides felis</i>), 101403557 (<i>Plodia interpunctella</i>), 92969578 (<i>Drosophila grimshawi</i>), 91829127

			(Bombyx mori)	
LD016	99	GCAGATACCTCACGCAAAGCTTC	62239897 (<i>Diabrotica virgifera</i>)	
LD016	100	GGATCGTTGGCCAAATTCAAGAACAGGCA	67882712 (<i>Drosophila pseudoobscura</i>), 92985459 (<i>Drosophila grimshawi</i>)	
LD016	101	TTCTCCATAGAACCGTTCTCTTCGAAATCCT G	4680479 (<i>Aedes aegypti</i>), 27372076 (<i>Spodoptera littoralis</i>)	
LD016	102	GCTGTTTCCATGTTAACACCCCAT	49558344 (<i>Boophilus microplus</i>)	
LD016	103	TCCATGTTAACACCCCATAGCAGCGA	62238871 (<i>Diabrotica virgifera</i>)	
LD016	104	CTACAGATCTGGCAGCAATTTTCATTGTG	22038926 (<i>Ctenocephalides felis</i>), 16898595 (<i>Ctenocephalides felis</i>)	
LD016	105	GGCAGACCAGCTGCAGAGAAAAT	22038926 (<i>Ctenocephalides felis</i>), 16898595 (<i>Ctenocephalides felis</i>)	
LD016	106	GAGAAATGGGGATCTTCTGACCACGAGCA ATGGAGTTCATCACGTC	4680479 (<i>Aedes aegypti</i>), 9713 (<i>Manduca sexta</i>), 22038926 (<i>Ctenocephalides felis</i>), 16898595 (<i>Ctenocephalides felis</i>), 67877903 (<i>Drosophila pseudoobscura</i>), 10763875 (<i>Manduca sexta</i>), 76554661 (<i>Spodoptera frugiperda</i>), 77905105 (<i>Aedes aegypti</i>), 50562965 (<i>Homalodisca coagulata</i>), 27372076 (<i>Spodoptera littoralis</i>)	
LD016	107	ATGGAGTTCATCACGTCAATAGC	9713 (<i>Manduca sexta</i>), 237458 (<i>Heliothis virescens</i>), 76554661 (<i>Spodoptera frugiperda</i>), 22474331 (<i>Helicoverpa armigera</i>)	
LD016	108	GTCTGGATCATTTCTCCTCAGGATAGATACGG GACCACGGATTGATTGTTGACCCCTGGATG TCCAAAGAGTCTTCAGCCCAAATTTGGGGGA CCTTTGTC	16898595 (<i>Ctenocephalides felis</i>), 22038926 (<i>Ctenocephalides felis</i>), 50562965 (<i>Homalodisca coagulata</i>), 49395165 (<i>Drosophila melanogaster</i>), 6901845 (<i>Bombyx mori</i>), 92931000 (<i>Drosophila virilis</i>)	
LD016	109	ATTGGGGGACCTTTGTGCGATGGG	10763875 (<i>Manduca sexta</i>)	

LD016	110	ATGGGTTTTCTGATCCATTGAAAAACACGTC CCAACATATCTTCAGAAAACAGGAGTCCTCA AAATATCTCCTGTGTAATTCACAAGCGGTGTT TTTGGCGTCGATTCTCTGATGTGCCCTCGAA CACTTGAACACACAGCTTT	49395165 (<i>Drosophila melanogaster</i>), 55905051 (<i>Locusta migratoria</i>)
LD016	111	ACAGCTTTTGACCCCACTGACTTCCAG	21642266 (<i>Amblyomma variegatum</i>)
LD016	112	GACCCACTGACTTCCAGAACTTGTCCTCGAA CGTATAGTGCCATCAGCCAGTTTGAGT	49395165 (<i>Drosophila melanogaster</i>)
LD016	113	GGACCGTTCCACACCAGACACAGT	24646342 (<i>Drosophila melanogaster</i>)
LD016	114	GACTGTGTCTGGTGTGAACGGTCTCTCT	103769163 (<i>Drosophila melanogaster</i>), 92048971 (<i>Drosophila willistoni</i>)
LD016	115	TTCCTCTCGAAATCCTGTTTGAA	84116133 (<i>Dermatophagoides farinae</i>)
LD016	116	GACTGTGTGTTGGTGTGAACGGTCC	24646342 (<i>Drosophila melanogaster</i>)
LD016	117	GGTCGTGCTGGTTTCCCGAGGTTACATGTAC ACCGATTT	92231646 (<i>Drosophila willistoni</i>), 91755555 (<i>Bombyx mori</i>), 84228226 (<i>Aedes aegypti</i>)
LD016	118	TGACAGCTGCCGAATTCCTTGGC	92231646 (<i>Drosophila willistoni</i>)
LD018	119	CAAGTCACCGACGACCAACCAACACAA	91080016 (<i>Tribolium castaneum</i>)
LD018	120	ATCGCGATTGACGGTGGAGCC	91080016 (<i>Tribolium castaneum</i>)
LD027	121	AGACGATCGGTTGGTTAAAATC	66501387 (<i>Apis mellifera</i>)
LD027	122	GATATGGGAGCATGTGAAATATA	77326476 (<i>Chironomus tentans</i>)
LD027	123	TTAGAGAAATTGTTTGAATTAT	90129719 (<i>Bicyclus anynana</i>)

Table 4-PC

Target ID	SEQ ID NO	Sequence *	Example GI-number and species
PC001	275	AAAATTGTCATGCAAAAGGTTGAT	37952206 (<i>Ips pini</i>)

PC001	276	AAAGCATGGATGTTGGACAAA	98994282 (Antheraea mylitta) 109978109 (Gryllus pennsylvanicus) 55904580 (Locusta migratoria)
PC001	277	AAAGCATGGATGTTGGACAAAATT	31366663 (Toxoptera citricida)
PC001	278	AAAGCATGGATGTTGGACAAAATTGGG	60311985 (Papilio dardanus)
PC001	279	AAAGCATGGATGTTGGACAAAATTGGGGGTGT	37951951 (Ips pini)
PC001	280	AAATACAAAGTTGTGTAAGTAA	84647793 (Myzus persicae)
PC001	281	AAGCATGGATGTTGGACAAAATTGGGGGTGT	70909486 (Mycetophagus quadripustulatus)
PC001	282	ATGGATGTCATTACTATTGAGAA	25957367 (Carabus granulatus)
PC001	283	CATCAAAATTTGAATCTGGCAACCT	37952206 (Ips pini)
PC001	284	CATGATGGCAGAACCATTCGTTA	60303405 (Julodis onopordi)
PC001	285	CCAAAGCATGGATGTTGGACAAA	90138164 (Spodoptera frugiperda)
PC001	286	CCATTTTGTGTAACACATGATGG	111011915 (Apis mellifera)
PC001	287	CCCAAAGCATGGATGTTGGACAAA	50565112 (Homalodisca coagulata)
PC001	288	CCCAAAGCATGGATGTTGGACAAA	103790417 (Heliconius erato) 101419954 (Plodia interpunctella)
PC001	289	CCCAAAGCATGGATGTTGGACAAAATT	73612809 (Aphis gossypii)
PC001	290	CCCAAAGCATGGATGTTGGACAAAATTGGG	77329254 (Chironomus tentans)
PC001	291	CCCAAAGCATGGATGTTGGACAAAATTGGGGGTGT	60305420 (Mycetophagus quadripustulatus)
PC001	292	CCCAAAGCATGGATGTTGGACAAAATTGGGGGTGTCTTCGC	84647995 (Myzus persicae)
PC001	293	CGTTACCCCTGACCCCAACATCAA	73613065 (Aphis gossypii)
PC001	294	GCAAAATACAAGTTGTGTAAAGTAA	83662334 (Myzus persicae)
PC001	295	GCATGGATGTTGGACAAAATTGGG	92969396 (Drosophila grimshawi)
PC001	296	GCATGGATGTTGGACAAAATTGGGGG	67885868 (Drosophila pseudoobscura)
PC001	297	GCATGGATGTTGGACAAAATTGGGGGTGT	25956479 (Biphylus lunatus)
PC001	298	GCATGGATGTTGGACAAAATTGGGGGTGTCT	90814901 (Nasonia vitripennis)
PC001	299	GCTCCCAAAGCATGGATGTTGGA	110260785 (Spodoptera frugiperda)
PC001	300	GCTCCCAAAGCATGGATGTTGGACAAA	76551269 (Spodoptera frugiperda)
PC001	301	GCTCCCAAAGCATGGATGTTGGACAAA	56085210 (Bombyx mori)
PC001	302	GCTCCCAAAGCATGGATGTTGGACAAAATTGGG	22474232 (Helicoverpa armigera)
PC001	303	GGTCCCAAAGGAATCCCATTTTGGT	50565112 (Homalodisca coagulata)
PC001	304	GGTGCTTCGCCCTCGTCCA	82575022 (Acyrthosiphon pisum)
PC001	305	GTGAAGTCACTAAAAATGTCATGCAAG	25956820 (Biphylus lunatus)

PC001	306	TCCACCGGGCCCTCACAAGTTGCG	58371410 (<i>Lonomia obliqua</i>)
PC001	307	TCCCAAAGCATGGATGTTGGA	110263957 (<i>Spodoptera frugiperda</i>)
PC001	308	TGCTCCCAAAGCATGGATGTTGACAA	48927129 (<i>Hydropsyche</i> sp.)
PC001	309	TGGATGTTGGACAAATTGGGGGGTGTCT	90814560 (<i>Nasonia vitripennis</i>)
PC003	310	AAAATTGAAGATTTCTTGGAA	108742519 (<i>Gryllus firmus</i>) 109978291 (<i>Gryllus pennsylvanicus</i>) 62083482 (<i>Lysiphlebus testaceipes</i>) 56150446 (<i>Rhynchosciara americana</i>)
PC003	311	AACAAACGTGAAGTGTGGAGAGT	57963755 (<i>Heliconius melpomene</i>)
PC003	312	AAGTCGCCCTTCGGGGGTGGCCG	77884026 (<i>Aedes aegypti</i>)
PC003	313	ACTTCTCCCTGAAGTCGCCCTTCGG	92992453 (<i>Drosophila mojavensis</i>)
PC003	314	AGATTGTTTGAAGGTAATGCACCTTCT	60298816 (<i>Diaphorina citri</i>)
PC003	315	ATCCGTAAAGCTGCTCGTGAA	33373689 (<i>Glossina morsitans</i>)
PC003	316	ATCGACTTCTCCCTGAAGTCGCC	92987113 (<i>Drosophila grimshawi</i>)
PC003	317	ATCGACTTCTCCCTGAAGTCGCCCT	1899548 (<i>Drosophila melanogaster</i>)
PC003	318	ATGAAGCTTGATTATGTTTGGTCTGAAATTGAAGATTTCT TGGAAAGA	71539459 (<i>Diaphorina citri</i>)
PC003	319	ATTGAAGATTTCTTGGAAAGA	62240069 (<i>Diabrotica virgifera</i>)
PC003	320	CACATCGACTTCTCCCTGAAGTC	71550961 (<i>Oncometopia nigricans</i>)
PC003	321	CAGAAGCACATCGACTTCTCCCTGAAGTCGCCCTTCGG	68267151 (<i>Drosophila simulans</i>) 33355000 (<i>Drosophila yakuba</i>)
PC003	322	CAGAAGCACATCGACTTCTCCCTGAAGTCGCCCTTCGGGGG	2152719 (<i>Drosophila melanogaster</i>)
PC003	323	CGACTTCTCCCTGAAGTCGCC	107324644 (<i>Drosophila melanogaster</i>)
PC003	324	CTCCCTGAAGTCGCCCTTCGG	15461311 (<i>Drosophila melanogaster</i>)
PC003	325	CTGGACTCGCAGAAAGCACATCGACTTCTCCCTGAA	38624772 (<i>Drosophila melanogaster</i>)
PC003	326	GACTTCTCCCTGAAGTCGCCCTTCGG	92959651 (<i>Drosophila ananassae</i>) 92981958 (<i>Drosophila mojavensis</i>) 76552467 (<i>Spodoptera frugiperda</i>)
PC003	327	GCTAAATCCGTAAAGTGCTCGTGA	60296953 (<i>Diaprepes abbreviatus</i>)
PC003	328	GCTAAATCCGTAAAGTGCTCGTGAAC	77329341 (<i>Chironomus tentans</i>)
PC003	329	GTGCGCAAGCAGGTGGTGAACATCCC	60312414 (<i>Papilio dardanus</i>)
PC003	330	TACACTTTGGCTAAATCCGTAAAGCTGC	22040140 (<i>Ctenocephalides felis</i>)
PC003	331	TCGAGAAGCACATCGACTTCTC	18883211 (<i>Anopheles gambiae</i>)

PC003	332	TCGCAGAAAGCACATCGACTTCTCCCTGAAGTCGCCCTTCGG	92963738 (<i>Drosophila grimshawi</i>)
PC003	333	TCTCCCTGAAGTCGCCCTTCGG	38047836 (<i>Drosophila yakuba</i>) 27260897 (<i>Spodoptera frugiperda</i>)
PC003	334	TGAAAAATTGAAGATTTCTTGGA	61646980 (<i>Acyrtosiphon pisum</i>) 73615225 (<i>Aphis gossypii</i>) 83661890 (<i>Myzus persicae</i>) 37804775 (<i>Rhopalosiphum padi</i>) 30049209 (<i>Toxoptera citricida</i>)
PC003	335	TGAAAAATTGAAGATTTCTTGGAAGA	90813959 (<i>Nasonia vitripennis</i>)
PC003	336	TGGAATCGCAGAAAGCACATCGACTTCTCCCT	25959408 (<i>Meladema coriacea</i>)
PC003	337	TGGCTAAAATCCGTAAAGCTGC	76169907 (<i>Diploptera punctata</i>)
PC003	338	TGGGTCTGAAAAATTGAAGATTTCTTGGA	34788046 (<i>Callosobruchus maculatus</i>)
PC003	339	TTCTCCCTGAAGTCGCCCTTCGG	107331362 (<i>Drosophila melanogaster</i>) 110240861 (<i>Spodoptera frugiperda</i>)
PC003	340	TTGGGTCTGAAAAATTGAAGATTTCTTGGAAG	37952462 (<i>Ips pini</i>)
PC003	341	GGGTGCGCAAGCAGGTGTGAAC	11088729 (<i>Argas monolakensis</i>)
PC005	342	CTCCTCAAAAAGTACAGGAGGCCAAGAA	63512537 (<i>Ixodes scapularis</i>)
PC005	343	AAAAAGAAGGTGTGTTGGATCC	33491424 (<i>Trichoplusia ni</i>)
PC005	344	AAAAAGAAGGTGTGTTGGATCCAAATGAAATCAA	91759273 (<i>Bombyx mori</i>) 55908261 (<i>Locusta migratoria</i>)
PC005	345	AAAGAAGGTGTGTTGGATCCAAATGAAATCAA	101414616 (<i>Plodia interpunctella</i>)
PC005	346	AACACCAACTCAAGACAAAAACAT	25957531 (<i>Cicindela campestris</i>)
PC005	347	AACACCAACTCAAGACAAAAACATCCGTAA	25958948 (<i>Curculio glandium</i>)
PC005	348	AACTCAAGACAAAAACATCCGTAA	60314333 (<i>Panorpa cf. vulgaris</i> APV-2005)
PC005	349	AAGAACACTGAAGCCAGAGGAAGGGAAGGCATTGTGG	25958948 (<i>Curculio glandium</i>)
PC005	350	AATGAAATCAACGAAATCGCCAACAC	92979160 (<i>Drosophila grimshawi</i>) 92232072 (<i>Drosophila willistoni</i>)
PC005	351	ATGGAGTACATCCACAAGAAGAAGGC	15454802 (<i>Drosophila melanogaster</i>)
PC005	352	CAAGATGCTGTCTGACCAGGC	67872905 (<i>Drosophila pseudoobscura</i>)
PC005	353	CGCCTCCTCAAAAAGTACAGGGAGGC	75471260 (<i>Tribolium castaneum</i>)
PC005	354	CGTATCGCCACCAAGAAGCAG	68267374 (<i>Drosophila simulans</i>)
PC005	355	CTGTACATGAAAGCGAAGGGTAA	25957246 (<i>Carabus granulatus</i>)
PC005	356	GAACAAGAGGGTCTCTTATGGAG	90977107 (<i>Aedes aegypti</i>)

PC005	357	GAACAAGAGGGTCCTTATGGAGTACATCCA	40544432 (<i>Tribolium castaneum</i>)
PC005	358	GAGCGTATCGCCACCAAGCA	92480972 (<i>Drosophila erecta</i>) 33354497 (<i>Drosophila yakuba</i>)
PC005	359	GAGTACATCCACAAGAAGGCG	15516174 (<i>Drosophila melanogaster</i>)
PC005	360	GATCCAAATGAAATCAACGAAAT	56149737 (<i>Rhynchosciara americana</i>)
PC005	361	GCCAACACCAACTCAAGACAAAACATCCG	103019061 (<i>Tribolium castaneum</i>)
PC005	362	GCCAACACCAACTCAAGACAAAACATCCGTAAGCTCAT	56149737 (<i>Rhynchosciara americana</i>)
PC005	363	GGCAAAAAGAGGTGTGGTTGGATCCAAATGAAATCA	101417042 (<i>Plodia interpunctella</i>)
PC005	364	GGTCCTTATGGAGTACATCCACAAGAA	67885759 (<i>Drosophila pseudoobscura</i>)
PC005	365	TGCGATCGGGCAAAAAGAGGT	56149531 (<i>Rhynchosciara americana</i>)
PC005	366	TGGTTGGATCCAAATGAAATCAACGAAAT	15355452 (<i>Apis mellifera</i>) 83662749 (<i>Myzus persicae</i>)
PC005	367	TTGGATCCAAATGAAATCAACGAAAT	110985444 (<i>Apis mellifera</i>) 111158439 (<i>Myzus persicae</i>)
PC010	368	CCGCAGTTCATGTACCATTTG	92952825 (<i>Drosophila ananassae</i>)
PC010	369	CTGATGGAGATGAAGCAGTGCTGCAATTC	58395529 (<i>Anopheles gambiae</i> str. PEST)
PC010	370	GACGTGCTCAGATGGGTGGACAG	56152422 (<i>Rhynchosciara americana</i>)
PC010	371	GCCCGAGCCTGTGTGTGGGA	92939820 (<i>Drosophila virilis</i>)
PC010	372	GGCACATGCTGATGCGTGAGGAT	83937570 (<i>Lutzomyia longipalpis</i>)
PC010	373	GGGCACATGGTCATGGGCGATTTC	3337934 (<i>Drosophila melanogaster</i>)
PC014	374	AAGATCATGGAGTACTACGAGAA	85577611 (<i>Aedes aegypti</i>)
PC014	375	ACGAGAAAAAGGAGAAAGCAAG	67838315 (<i>Drosophila pseudoobscura</i>)
PC014	376	ATGGAGTACTACGAGAAAAAGGAGAAGCAAGT	92928915 (<i>Drosophila virilis</i>)
PC014	377	CAAAAAACAAATCAAAACACATGATGGC	82574001 (<i>Acyrtosiphon pisum</i>) 111160670 (<i>Myzus persicae</i>)
PC014	378	CTCAAGATCATGGAGTACTACGA	55692554 (<i>Drosophila yakuba</i>)
PC014	379	CTCAAGATCATGGAGTACTACGAGAA	92942301 (<i>Drosophila ananassae</i>) 92476196 (<i>Drosophila erecta</i>) 53884266 (<i>Plutella xylostella</i>)
PC014	380	GAACAAGAAGCCCAATGAGAAAGC	111160670 (<i>Myzus persicae</i>)
PC014	381	GACTCAAGATCATGGAGTACT	112432414 (<i>Myzus persicae</i>)
PC014	382	GATGTTCAAAAAACAAATCAAAACACATGATGGC	73618688 (<i>Aphis gossypii</i>)
PC014	383	TACTACGAGAAAAAGGAGAAGC	62239529 (<i>Diabrotica virgifera</i>)

PC014	384	TTCAATTGAACAAGAAGCCAATGA	15357365 (<i>Apis mellifera</i>)
PC016	385	ACACGACCGGCGCGCTCGTAAAT	75710699 (<i>Tribolium castaneum</i>)
PC016	386	ACCAGCACGTGCTTCTCGCACTGGTAGGCCAAGAATTCGGC	92048971 (<i>Drosophila willistoni</i>)
PC016	387	AGCACGTGCTTCTCGCACTGGTAGGC	92985459 (<i>Drosophila grimshawi</i>)
PC016	388	ATACGCGACCAACGGGTTGATCGG	18886609 (<i>Anopheles gambiae</i>)
			31206154 (<i>Anopheles gambiae</i> str. PEST)
PC016	389	ATCGGTGTACATGTAAACCGGGGAAACC	2921501 (<i>Culex pipiens</i>) 62239897 (<i>Diabrotica virgifera</i>) 92957249 (<i>Drosophila ananassae</i>) 92477818 (<i>Drosophila erecta</i>) 92965644 (<i>Drosophila grimshawi</i>) 24646342 (<i>Drosophila melanogaster</i>) 67896654 (<i>Drosophila pseudoobscura</i>) 75710699 (<i>Tribolium castaneum</i>)
PC016	390	ATCGTTGGCCCAAGTTCAGAACAG	92950254 (<i>Drosophila ananassae</i>)
PC016	391	CACGTGCTTCTCGCACTGGTAGGCCAAGAA	4680479 (<i>Aedes aegypti</i>)
PC016	392	CCAGTCTGGATCATATTCCTCGGG	67884189 (<i>Drosophila pseudoobscura</i>)
PC016	393	CCAGTCTGGATCATATTCCTCGGGATA	92940287 (<i>Drosophila virilis</i>)
PC016	394	CGCTCGATGGTCCGATCGTTGGCCCAAGTTCAGAACA	2921501 (<i>Culex pipiens</i>)
PC016	395	CGCTCGATGGTCCGATCGTTGGCCCAAGTTCAGAACAAGACA CACGTTCTCCAT	92477818 (<i>Drosophila erecta</i>) 15061308 (<i>Drosophila melanogaster</i>)
PC016	396	CGTGCTTCTCGCACTGGTAGGCCAAGAA	13752998 (<i>Drosophila melanogaster</i>)
PC016	397	CTGGCAGTTTCCATGTTGACACCCATAGC	16898595 (<i>Ctenocephalides felis</i>)
PC016	398	CTTAGCATCAATACCTGATGT	61646107 (<i>Acyrtosiphon pisum</i>)
PC016	399	GACATGTCGGTCAAGATGACCAAGCACGTG	9713 (<i>Manduca sexta</i>)
PC016	400	GACATGTCGGTCAAGATGACCAAGCACGTGCTTCTCGCACTG	92933153 (<i>Drosophila virilis</i>)
PC016	401	GACATGTCGGTCAAGATGACCAAGCACGTGCTTCTCGCACTG GTA	2921501 (<i>Culex pipiens</i>)
PC016	402	GAGCCGTTCTCTCGAAGTCCTG	237458 (<i>Heliothis virescens</i>)
PC016	403	GATGACCAGCACGTGCTTCTC	18883474 (<i>Anopheles gambiae</i>)
PC016	404	GATGACCAGCACGTGCTTCTCGCACTG	92477818 (<i>Drosophila erecta</i>)
PC016	405	GATGACCAGCACGTGCTTCTCGCACTGGTAGGCCAAGAA	15061308 (<i>Drosophila melanogaster</i>) 67883622 (<i>Drosophila pseudoobscura</i>)

PC016	406	GATGACCAGCACGTGCTTCTCGCACTGGTAGGCCAAGAAATTC GGC	31206154 (Anopheles gambiae str. PEST)
PC016	407	GATGGGATCTGCGTGATGA	101403557 (Plodia interpunctella)
PC016	408	GATGGGATCTGCGTGATGGAGCCGTTGGGCCCTCCAC	53883819 (Plutella xylostella)
PC016	409	GGAATAGGATGGGTGATGTCGTCGTTGGGCATAGT	110240379 (Spodoptera frugiperda)
PC016	410	GGAATAGGATGGGTGATGTCGTCGTTGGGCATAGTCA	27372076 (Spodoptera littoralis)
PC016	411	GGATCGTTGGCCAAGTTCAAGAA	91757299 (Bombyx mori)
PC016	412	GGATCGTTGGCCAAGTTCAAGAA	103020368 (Tribolium castaneum)
PC016	413	GGATCGTTGGCCAAGTTCAAGAA	237458 (Heliothis virescens)
PC016	414	GGATGGGTGATGTCGTCGTTGGGCAT	101403557 (Plodia interpunctella)
PC016	415	GGCAGTTCCATGTTGACACCCATAGC	4680479 (Aedes aegypti)
PC016	416	GGCATAGTCAAGATGGGATCTG	92924977 (Drosophila virilis)
PC016	417	GTCTGGATCATTTCTCGGGATA	92966144 (Drosophila grimshawi)
PC016	418	GTGATGATGCGCTCGATGGTGGGATCGTTGGCCAAAGTTCAA GAACAGACACACGTTCTCCAT	15514750 (Drosophila melanogaster)
PC016	419	GTGTACATGTAACCGGGGAAACC	92924977 (Drosophila virilis)
PC016	420	GTTTCCATGTTGACACCCATAGC	91826756 (Bombyx mori)
PC016	421	TCAATGGGTTTTCTGATCCATTGAA	49395165 (Drosophila melanogaster)
PC016	422	TCAATCCAGCACAGACTTGCCAG	99009492 (Leptinotarsa decemlineata)
PC016	423	TCAATCCAGCACAGACTTGCCAGG	10763875 (Manduca sexta)
PC016	424	TCCATGTTGACACCCATAGCAGC	9713 (Manduca sexta)
PC016	425	TCCATGTTGACACCCATAGCAGCAACAC	92962756 (Drosophila ananassae)
PC016	426	TCGAAGTCCTGCTTGAAGAACCTGGC	60295607 (Homalodisca coagulata)
PC016	427	TCGATGGTCGGATCGTTGGCCAAAGTTCAAGAACAGACACAC GTTCTCCAT	101403557 (Plodia interpunctella)
PC016	428	TCGGATCGTTGGCCAAGTTCAAGAACAGACACACGTTCTCCA T	4680479 (Aedes aegypti)
PC016	429	TCGTTGGCCAAGTTCAAGAACAG	2793275 (Drosophila melanogaster)
PC016	430	TGGGTGATGTCGTCGTTGGGCAT	90137502 (Spodoptera frugiperda)
PC016	431	TTCTCGCACTGGTAGGCCAAGAA	53883819 (Plutella xylostella)
PC016	432	TTCTCTTCAAGTCCTGCTTGAAGAACCTGGC	110240379 (Spodoptera frugiperda)
PC016	433	TTGGCCAAGTTCAAGAACAGACACACGTT	27372076 (Spodoptera littoralis)
			9713 (Manduca sexta)
			55905051 (Locusta migratoria)

PC016	434	GTTTCCATGTTGACACCCCATAGCAGCAAA	84116133 (Dermatophagoides farinae)
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Table 4-EV

Target ID	SEQ ID NO	Sequence *	Example Gi-number and species
EV005	533	AAGCGACGTGAAGAGCGTATCGC	76553206 (Spodoptera frugiperda)
EV005	534	ATTAAAGATGGTCTTATTATTA	15355452 (Apis mellifera)
EV005	535	CGTAAGCGACGTGAAGAGCGTATCGC	33491424 (Trichoplusia ni)
EV005	536	GGTCGTCATTGTGGATTGGTAAAG	60314333 (Panorpa cf. vulgaris APV-2005)
EV005	537	TGCGATCGCGCAAGAAGAAGT	15048930 (Drosophila melanogaster)
EV005		TGCGGCAAGAAGAAGGTTTGG	93002524 (Drosophila mojavensis)
	538		92930455 (Drosophila virilis)
			92044532 (Drosophila willistoni)
EV005	539	TTGTGGATTGGTAAAGGAA	60306723 (Sphaerius sp.)
EV010	540	CAAGTGTTCAATAATTCACCA	83937567 (Lutzomyia longipalpis)
EV010	541	CATTCTATAGGCACATGTTGATG	29558345 (Bombyx mori)
EV010		CTGGCGGCCACATGGTCATGGG	92476940 (Drosophila erecta)
	542		92977931 (Drosophila grimshawi)
			2871327 (Drosophila melanogaster)
EV015	543	AACAGGCCCAATTCCATCGACCC	92947821 (Drosophila ananassae)
EV015	544	AGAGAAAAATGGACCTCATCGAC	62239128 (Diabrotica virgifera)
EV015	545	CGCCATCCGTCGCTGTTCAAGCGGATCGG	18866954 (Anopheles gambiae)
EV015	546	CTGGCAGTTACCATGGAGAACTTCCGTACGCCATG	62239128 (Diabrotica virgifera)
EV015	547	GTGATCGTGATGGCGGCCACGAA	18887285 (Anopheles gambiae)
EV015	548	GTGATCGTGATGGCGGCCACGAA	83423460 (Bombyx mori)
EV015	549	TGATGGACGGCATGAAGAAAAG	91086234 (Tribolium castaneum)
EV016	550	AATATGGAAACAGCCAGATTCTT	109193559 (Myzus persicae)
EV016	551	ATGATCCAGACTGGTATTCTGC	92938857 (Drosophila virilis)
EV016	552	ATTGATGTGATGAATCCATTGCC	55905051 (Locusta migratoria)
EV016	553	GAATGATCCAGACTGGTATTCTGC	50562965 (Homalodisca coagulata)
EV016	554	GAAGAAATGATCCAGACTGGTAT	92969748 (Drosophila mojavensis)
EV016		GACTGTGCTGTTGTGAACGG	2286639 (Drosophila melanogaster)
	555		92042621 (Drosophila willistoni)

EV016	556	GATATGTTGGTGGTGGTGGTAA	92969748 (<i>Drosophila mojavensis</i>)
EV016	557	GATCCTACCATTTGAAAGAATTAT	99011193 (<i>Leptinotarsa decemlineata</i>)
EV016	558	GTGTCGAAGATATGTTGGTGGTGT	76554661 (<i>Spodoptera frugiperda</i>)
EV016	559	GTGTCGGTGTGAACGGACCG	22474331 (<i>Helicoverpa armigera</i>)
EV016	560	TCTGAAGATATGTTGGTGGTGT	27372076 (<i>Spodoptera littoralis</i>)
EV016	561	TGGCATATCAATGTGAGAAAGCA	60336595 (<i>Homalodisca coagulata</i>)
EV016	562	TTGAACCTGGCCCAATGATCCTACCAT	91827863 (<i>Bombyx mori</i>)

Table 4-AG

Target ID	SEQ ID NO	Sequence *	Example Gi-number and species
AG001	621	AAAACTGGTGAATCTTCCGTTTGAT	37953169 (<i>Ips pini</i>)
AG001	622	AAAGCATGGATGTTGGACAAA	98994282 (<i>Antheraea mylitta</i>) 109978109 (<i>Gryllus pennsylvanicus</i>) 55904580 (<i>Locusta migratoria</i>)
AG001	623	AAAGCATGGATGTTGGACAAATT	31366663 (<i>Toxoptera citricida</i>)
AG001	624	AAAGCATGGATGTTGGACAAATTGGG	60311985 (<i>Papilio dardanus</i>)
AG001	625	AAAGCATGGATGTTGGACAAATTGGGGGTGT	37951951 (<i>Ips pini</i>) 109195107 (<i>Myzus persicae</i>)
AG001	626	AAATACAAATTGTGCAAGTCCG	25958703 (<i>Curculio glandium</i>)
AG001	627	AACTTGTCATGATCACC GGAG	22039624 (<i>Ctenocephalides felis</i>)
AG001	628	AAGCATGGATGTTGGACAAATTGGGGG	112433559 (<i>Myzus persicae</i>)
AG001	629	AAGCATGGATGTTGGACAAATTGGGGGGTGT	70909486 (<i>Mycelophagus quadripustulatus</i>)
AG001	630	ACTGGTGAAATCTCCGTTTGAT	77327303 (<i>Chironomus tentans</i>)
AG001	631	ATTGAAAAAACTGGTGAATCTTCCGTTTGATCTATGATGTTA A	22039624 (<i>Ctenocephalides felis</i>)
AG001	632	CCAAAGCATGGATGTTGGACAA	90138164 (<i>Spodoptera frugiperda</i>)
AG001	633	CCCAAAGCATGGATGTTGGACAA	48927129 (<i>Hydropsyche</i> sp.) 76551269 (<i>Spodoptera frugiperda</i>)
AG001	634	CCCAAAGCATGGATGTTGGACAAA	91835558 (<i>Bombyx mori</i>) 103783745 (<i>Heliconius erato</i>) 101419954 (<i>Plodia interpunctella</i>)
AG001	635	CCCAAAGCATGGATGTTGGACAAATT	73619372 (<i>Aphis gossypii</i>)

AG001	636	CCCAAAGCATGGATGTTGGACAAATTGGG	77329254 (Chironomus tentans) 22474232 (Helicoverpa armigera)
AG001	637	CCCAAAGCATGGATGTTGGACAAATTGGGGG	84647382 (Myzus persicae)
AG001	638	CCCAAAGCATGGATGTTGGACAAATTGGGGGTGT	84647995 (Myzus persicae)
AG001	639	CCCAAAGCATGGATGTTGGACAAATTGGGGGTGTGT	60305420 (Mycetophagus quadripustulatus)
AG001	640	CTGGATTCATGGATGTGATCA	27617172 (Anopheles gambiae)
AG001	641	GAATTCCTCCGTTTGATCTATGATGT	50565112 (Homalodisca coagulata) 71049326 (Oncometopia nigricans)
AG001	642	GCATGGATGTTGGACAAATTGGG	92969396 (Drosophila grimshawi) 93001617 (Drosophila mojavensis) 92929731 (Drosophila virilis)
AG001	643	GCATGGATGTTGGACAAATTGGGGG	67885868 (Drosophila pseudoobscura)
AG001	644	GCATGGATGTTGGACAAATTGGGGGTGT	90814901 (Nasonia vitripennis)
AG001	645	GCATGGATGTTGGACAAATTGGGGGTGTTCGCCCC	25956479 (Biphylus lunatus)
AG001	646	GCCCCAAAGCATGGATGTTGGACAA	50565112 (Homalodisca coagulata)
AG001	647	GCTGGATTCATGGATGTGATC	103775903 (Heliconius erato)
AG001	648	GGATCATTCGATATTGTCCACAT	113017118 (Bemisia tabaci)
AG001	649	GGCAACTTGTGCATGATCACC GGAGG	25958703 (Curculio glandium)
AG001	650	TACAAATTGTGCAAAAGTCCGCAA	56161193 (Rhynchosciara americana)
AG001	651	TATCCTGCTGGATTTCATGGATGT	40934103 (Bombyx mori)
AG001	652	TCACCATTGAAAAAACTGGTGAATTCCTC	62083410 (Lysiphlebus testaceipes)
AG001	653	TGCATGATCACCGGAGGCAGGAA	3478550 (Antheraea yamamai)
AG001	654	TGCATGATCACCGGAGGCAGGAATTTGGG	14627585 (Drosophila melanogaster) 33355008 (Drosophila yakuba)
AG001	655	TGGATGTTGGACAAATTGGGGGTGT	90814560 (Nasonia vitripennis)
AG001	656	TGTGCATGATCACCGGAGGCAG	92949859 (Drosophila ananassae) 92999306 (Drosophila grimshawi)
AG001	657	TGTGCATGATCACCGGAGGCAGGAATTTGGG	67842487 (Drosophila pseudoobscura)
AG005	658	AAGATCGACAGGCATCTGTACCACG	83935651 (Lutzomyia longipalpis)
AG005	659	AAGATCGACAGGCATCTGTACCACGCCCTGTACATGAAGGC	7652995 (Spodoptera frugiperda)
AG005	660	AAGGGTAACGTGTTCAGAAGACAA	18932248 (Anopheles gambiae) 60306606 (Sphaerius sp.)

AG005	661	AAGGGTAACGTGTTCAAGAACAAG	18953735 (Anopheles gambiae) 25957811 (Cicindela campestris) 60311920 (Euclidia glyphica)
AG005	662	AAGGGTAACGTGTTCAAGAACAAGAGAGT	25958948 (Curculio glandium) 90812513 (Nasonia giraulti)
AG005	663	ACAAGAAGAAGGCTGAGAAGGC	60311700 (Euclidia glyphica)
AG005	664	ATCAAGGATGTTTGATCATTA	25957811 (Cicindela campestris)
AG005	665	ATGGAATACATCCACAAGAAGAAG	56149737 (Rhynchosciara americana)
AG005	666	CAAAACATCCGTAATGATCAAGGATGGT	60314333 (Panorpa cf. vulgaris APV-2005)
AG005	667	CAAAACATCCGTAATGATCAAGGATGGTTTGATCAT	25958948 (Curculio glandium)
AG005	668	CAAGGGTAACGTGTTCAAGAA	476608 (Drosophila melanogaster) 38048300 (Drosophila yakuba)
AG005	669	CAAGGGTAACGTGTTCAAGAACAAG	92946023 (Drosophila ananassae) 2871633 (Drosophila melanogaster) 68267374 (Drosophila simulans) 33354497 (Drosophila yakuba) 83937096 (Lutzomyia longipalpis)
AG005	670	CATCTGTACCACGCCCTGTACATGAAGGC	101417042 (Plodia interpunctella)
AG005	671	GAAGAAGGCTGAGAAGGCCCG	40874303 (Bombyx mori)
AG005	672	GACAGGCATCTGTACCACGCCCTGTACATGAAGGC	90135865 (Bicyclus anynana)
AG005	673	GAGAAGGCCCGTGCCCAAGATGTTG	82572137 (Acyrtosiphon pisum)
AG005	674	GATCCAAATGAAATCAATGAGATTGC	60312128 (Papilio dardanus)
AG005	675	GCTCGTATGCCTCAAAAAGGAACTATGG	25957246 (Carabus granulatus)
AG005	676	GGGTAACGTGTTCAAGAACAAG	4447348 (Drosophila melanogaster)
AG005	677	GGTAACGTGTTCAAGAACAAG	18948649 (Anopheles gambiae)
AG005	678	TACATCCACAAGAAGAAGGCTGAGAAG	2871633 (Drosophila melanogaster)
AG005	679	TACCACGCCCTGTACATGAAGGC	10764114 (Manduca sexta)
AG005	680	TCAATGAGATTGCCAACACCAACTC	83935651 (Lutzomyia longipalpis)
AG005	681	TGATCAAGGATGGTTTGATCAT	77642775 (Aedes aegypti) 27615052 (Anopheles gambiae) 92982271 (Drosophila grimshawi) 67896961 (Drosophila pseudoobscura)
AG005	682	TGATCAAGGATGGTTTGATCATTAAGAA	92042883 (Drosophila willistoni)

AG005	683	TGGTTGGATCCAAATGAAATCA	40867709 (Bombyx mori) 101417042 (Plodia interpunctella)
AG005	684	TGGTTGGATCCAAATGAAATCAA	15355452 (Apis mellifera) 83662749 (Myzus persicae)
AG005	685	TGGTTGGATCCAAATGAAATCAATGAGAT	63013469 (Bombyx mori) 55908261 (Locusta migratoria)
AG005	686	TGTACCACGCCCTGTACATGAAGGC	23573622 (Spodoptera frugiperda)
AG005	687	TTGATCAAGGATGGTTTGATCA	113019292 (Bemisia tabaci)
AG005	688	TTGATCAAGGATGGTTTGATCAT	61674956 (Aedes aegypti) 41576849 (Culicoides sonorensis)
AG005	689	TTGATGGAATACATCCACAAGAAAGGC	92225847 (Drosophila willistoni)
AG005	690	AGGATGCGTGTCTTGAGGCGTCT	110887217 (Argas monolakensis)
AG005	691	AAGGCCAAGGTAACGTGTTCAGAAACAAG	110887217 (Argas monolakensis)
AG010	692	CGTTTGTGTCAAAAGTTTGAGAATA	78539702 (Glossina morsitans)
AG010	693	GATGTTTTAAGATGGGTCGATCG	110759793 (Apis mellifera)
AG010	694	TTTTACAGGCATATGCTTATGAGGGAAGATTT	55902158 (Locusta migratoria)
AG010	695	TTTTTCGAGGTGGTCAATCAGCATTCGGC	92925934 (Drosophila virilis)
AG014	696	AACATGCTGAACCAAGCCCGT	75466802 (Tribolium castaneum)
AG014	697	AACATGCTGAACCAAGCCCGTCT	87266590 (Choristoneura fumiferana) 103779114 (Heliconius erato)
AG014	698	AAGATCATGGAATACTATGAGAAGAA	101403826 (Plodia interpunctella)
AG014	699	AAGATCATGGAATACTATGAGAAGAAAGGAGAA	81520950 (Lutzomyia longipalpis)
AG014	700	AATGAAAAGGCCCGAGGAAATTGATGC	62239529 (Diabrotica virgifera)
AG014	701	ATGGAATACTATGAGAAGAAAGGA	16901350 (Ctenocephalides felis)
AG014	702	CAATCCTCCAACATGCTGAACCA	53148472 (Plutella xylostella)
AG014	703	CAGATCAAGCATATGATGGCCTTCAT	53148472 (Plutella xylostella)
AG014	704	GCAGATCAAGCATATGATGGCCTTCAT	87266590 (Choristoneura fumiferana) 9732 (Manduca sexta) 90814338 (Nasonia vitripennis)
AG014	705	GCGGAAGAAGAATTTAACATTGAAAAGGG	50558386 (Homalodisca coagulata) 71552170 (Oncometopia nigricans)
AG016	706	AACGACGACATCACCCATCCTATTC	110248186 (Spodoptera frugiperda) 27372076 (Spodoptera littoralis)

AG016	707	AACGGTCCATGGAGAACGTGTG	2921501 (Culex pipiens) 92950254 (Drosophila ananassae) 110240379 (Spodoptera frugiperda)
AG016	708	AACGGTCCATGGAGAACGTGTGTCT	24646342 (Drosophila melanogaster)
AG016	709	AACGGTCCATGGAGAACGTGTCTCTCTTTGAA	91829127 (Bombyx mori)
AG016	710	ATGATCCAGACCCGGTATCTCCGC	22474040 (Helicoverpa armigera)
AG016	711	ATGCCGAACGACGACATCACCCATCC	31206154 (Anopheles gambiae str. PEST)
AG016	712	CAATGCGAGAAACACGTGCTGGT	9713 (Manduca sexta)
AG016	713	CCGCACAACGAAATCGCCGCCCAAAT	75469507 (Tribolium castaneum)
AG016	714	CGTTCTTCAAGCAGGACTTCGA	83937868 (Lutzomyia longipalpis)
AG016	715	CTTGGACATCCAAGGTCAACCCATCAACCCATGGTC	104530890 (Belgica antarctica)
AG016	716	GAAATGATCCAGACCCGGTATCTC	2921501 (Culex pipiens) 92966144 (Drosophila grimshawi)
AG016	717	GAAATGATCCAGACCCGGTATCTCCGCCATCGACGTGATGAAC TC	31206154 (Anopheles gambiae str. PEST)
AG016	718	GAAGAAATGATCCAGACCCGGTAT	75469507 (Tribolium castaneum)
AG016	719	GAAGAAGTACCCGGACGTCGTGG	22038926 (Ctenocephalides felis)
AG016	720	GACATCCAAGGTCAACCCCATCAA	16898595 (Ctenocephalides felis)
AG016	721	GCCCCCTTCTTCAAGCAGGACTTCGA	31206154 (Anopheles gambiae str. PEST)
AG016	722	GCCGCCCAATCTGTAGACAGGC	60295607 (Homalodisca coagulata)
AG016	723	GGATCAGGAAAAACCCCATTGACAAAGGTCC	49395165 (Drosophila melanogaster) 99009492 (Leptinotarsa decemlineata)
AG016	724	GGTTACATGTACACCCGATTGGC	91829127 (Bombyx mori)
AG016	725	GGTTACATGTACACCCGATTGGCCACCATTTACGAA	77750765 (Aedes aegypti) 9713 (Manduca sexta) 110248186 (Spodoptera frugiperda) 27372076 (Spodoptera littoralis)
AG016	726	GGTTACATGTACACCCGATTGGCCACCATTTACGAA	92231646 (Drosophila willistoni)
AG016	727	GTGTCCGAGGATATGTTGGGCCG	92460250 (Drosophila erecta) 24646342 (Drosophila melanogaster) 55694673 (Drosophila yakuba)
AG016	728	TACATGTACACCCGATTGGCCACCAT	31206154 (Anopheles gambiae str. PEST)
AG016	729	TTCAACGGATCAGGAAAAACCCATTGACAAAGGTCC	99010653 (Leptinotarsa decemlineata)

AG016	730	TTCCCCGGTTACATGTACACCGGATTTGGCCAC	2921501 (<i>Culex pipiens</i>) 75710699 (<i>Tribolium castaneum</i>)
AG016	731	TTCCCCGGTTACATGTACACCGGATTTGGCCACCAT	62239897 (<i>Diabrotica virgifera</i>) 92957249 (<i>Drosophila ananassae</i>) 92477149 (<i>Drosophila erecta</i>) 67896654 (<i>Drosophila pseudoobscura</i>)
AG016	732	TTCCCCGGTTACATGTACACCGGATTTGGCCACCATTTA	92969578 (<i>Drosophila grimshawi</i>)
AG016	733	TTCCCCGGTTACATGTACACCGGATTTGGCCACCATTTACGA	103744758 (<i>Drosophila melanogaster</i>)
AG016	734	TTGGCCATCGTGTTCGCCGCCCATGGGTGT	31206154 (<i>Anopheles gambiae</i> str. PEST)
AG016	735	TTCTCAAGCAGGACTTCGAAGA	9713 (<i>Manduca sexta</i>)
AG016	736	TTCTTGAATTTGGCCCAACGATCC	92972277 (<i>Drosophila grimshawi</i>) 99011193 (<i>Leptinotarsa decemlineata</i>)
AG016	737	TTCTTGAATTTGGCCCAACGATCCCAACCATCGAG	67839381 (<i>Drosophila pseudoobscura</i>)
AG016	738	GCCGAAATTTTGGCTTATCAATG	84116133 (<i>Dermatophagoides farinae</i>)

Table 4-TC

Target ID	SEQ ID NO	Sequence *	Example GI-number and species
TC001	813	AAAGCATGGATGTTGGATAAA	70909480 (<i>Carabus granulatus</i>) 16898765 (<i>Ctenocephalides felis</i>) 60298000 (<i>Diaprepes abbreviatus</i>)
TC001	814	AATTTGTGTATGATTACTGGAGG	55904576 (<i>Locusta migratoria</i>)
TC001	815	ACTGGAGGTCGTAACCTTGGGCGGTGT	60298000 (<i>Diaprepes abbreviatus</i>)
TC001	816	ATGATTACTGGAGGTCGTAACCTTGGGCGGTGT	73619372 (<i>Aphis gossypii</i>) 37804548 (<i>Rhopalosiphum padi</i>)
TC001	817	ATGCAAAGATTGATTAAAGTTGACGG	70909478 (<i>Biphylus lunatus</i>)
TC001	818	ATTAAAGTTGACGGAAAAGTT	110763874 (<i>Apis mellifera</i>)
TC001	819	ATTGAGAAAACCTGGGAATCTCTCCG	37952206 (<i>Ips pini</i>)
TC001	820	ATTGTTATGCAAGATTGATTAAAGTTGACGGAAAAGT	70909486 (<i>Mycetophagus quadripustulatus</i>)
TC001	821	CCAAGAAGCATTTGAAGCGTCT	55904580 (<i>Locusta migratoria</i>)
TC001	822	CCAAGAAGCATTTGAAGCGTCTC	83935971 (<i>Lutzomyia longipalpis</i>)
TC001	823	GCGCCCAAAGCATGGATGTTGGA	103790417 (<i>Heliconius erato</i>) 101419954 (<i>Plodia interpunctella</i>)

TC001	824	GGCCCCAAGAAGCATTTGAAGCGT	14700642 (<i>Drosophila melanogaster</i>)
TC001	825	TGATTACTGGAGGTCGTAACITGGGCGTGT	73612212 (<i>Aphis gossypii</i>)
TC001	826	TGTATGATTACTGGAGGTCGTAACITGGGCGTGT	70909478 (<i>Biphylus lunatus</i>)
TC001	827	TTGATTTATGATGTTAAGGGA	77325485 (<i>Chironomus tentans</i>)
TC001	828	TTGTGTATGATTACTGGAGGTCGTAA	60305816 (<i>Mycetophagus quadripustulatus</i>)
TC002	829	AAAAACAAACGAGCGGCCATCCAGGC	18920284 (<i>Anopheles gambiae</i>)
TC002	830	ATCGACCAAGAGATCCTCACAGCGAAGAAAAACGGGTGCGAAA AACAAACGAGCGGCCATCCAGGCC	75717966 (<i>Tribolium castaneum</i>)
TC002	831	CTCCAGCAGATCGATGGCACCCCT	92475657 (<i>Drosophila erecta</i>) 13763220 (<i>Drosophila melanogaster</i>)
TC002	832	TCAAGAGGAAGAAACGCTACGAAAAAGCAGCTCCAGCAGATC GATGGCACCCCTCAGCACCATCGAGATGCGAGCGGGAGGCCCT CGAGGGGGCCCAACACCAACACAGCCGTACTCTCAAAACGATGA AAAAACGAGCGGCCCTCAAAAATGCCCCACCTCAACATG GATGTTGATGAGGT	75717966 (<i>Tribolium castaneum</i>)
TC010	833	AACCTCAAGTACCAGGACATGCCCGA	90973566 (<i>Aedes aegypti</i>)
TC010	834	AGCCGATTTGTACAGTTATA	92944620 (<i>Drosophila ananassae</i>)
TC010	835	ATGGACACATTTTCCAAAT	33427937 (<i>Glossina morsitans</i>)
TC010	836	ATGGACACATTTTCCAAATTTTGATTTTCCACGG	56151768 (<i>Rhynchosciara americana</i>)
TC010	837	CAAGTACCAGGACATGCCCGA	18911059 (<i>Anopheles gambiae</i>)
TC010	838	CACATGCTGATGCGGGAGGACCTC	67893321 (<i>Drosophila pseudoobscura</i>)
TC010	839	CCTCAAGTACCAGGACATGCCCGA	67893324 (<i>Drosophila pseudoobscura</i>)
TC010	840	TCAAGTACCAGGACATGCCCGA	67893321 (<i>Drosophila pseudoobscura</i>)
TC010	841	TTCAATGTACCATTTGCGCCGCTC	92952825 (<i>Drosophila ananassae</i>)
TC014	842	AAAATTCAGTCGTCAAAACATGCTGAA	76169390 (<i>Diptera punctata</i>)
TC014	843	AACATGCTGAACCAAGCCCGT	87266590 (<i>Choristoneura fumiferana</i>) 103779114 (<i>Heliconius erato</i>)
TC014	844	CACAGCAACTTGTGCCAGAAAT	92923718 (<i>Drosophila virilis</i>)
TC014	845	GAGAAAGCCGAAGAAATCGATGC	77325830 (<i>Chironomus tentans</i>)
TC014	846	GCCCGCAACGCTGGCGGAA	92232132 (<i>Drosophila willistoni</i>)
TC014	847	TAAAAGTGCGTGAAGACCACGT	58371699 (<i>Lonomia obliqua</i>)
TC015	848	ACACTGATGGACGGCATGAAGAA	78531609 (<i>Glossina morsitans</i>)
TC015	849	ATCGGCGGTTGTCGCAACAACACT	6904417 (<i>Bombyx mori</i>)
TC015	850	CCCGATGAGAAGATCCGGATGAA	83922984 (<i>Lutzomyia longipalpis</i>)

TC015	851	CTGCCCCGATGAGAAGATCCG	92948836 (<i>Drosophila ananassae</i>)
TC015	852	AACGAAACCGGTGCTTCTTCTT	84116975 (<i>Dermatophagoides farinae</i>)

Table 4-MP

Target ID	SEQ ID NO	Sequence *	Example Gi-number and species
MP001	908	AAAGCATGGATGTTGGACAAA	98994282 (<i>Antheraea mylitta</i>)
			108789768 (<i>Bombyx mori</i>)
			109978109 (<i>Gryllus pennsylvanicus</i>)
			55904580 (<i>Locusta migratoria</i>)
MP001	909	AAAGCATGGATGTTGGACAAAT	77325485 (<i>Chironomus tentans</i>)
			37951951 (<i>Ips pini</i>)
			60311985 (<i>Papilio dardanus</i>)
			30031258 (<i>Toxoptera citricida</i>)
MP001	910	AAGAAGCATTTGAAGCGTTTAAACGCACC	3658572 (<i>Manduca sexta</i>)
MP001	911	AAGCATTTGAAGCGTTTAAACGC	103790417 (<i>Heliconius erato</i>)
			22474232 (<i>Helicoverpa armigera</i>)
MP001	912	AAGCATTTGAAGCGTTTAAACGCACC	25957217 (<i>Carabus granulatus</i>)
MP001	913	AAGTCCGTACCGACCCCTAATTATCCAGC	46994131 (<i>Acyrtosiphon pisum</i>)
MP001	914	ACGCACCCAAAGCATGGATGTT	46999037 (<i>Acyrtosiphon pisum</i>)
MP001	915	ACTATTAGATACGATATTGCA	46998791 (<i>Acyrtosiphon pisum</i>)
MP001	916	ACTGGACCCAAAGGTGTGCCATTTTAACTACTCATGATGGC CGTACTAT	46997137 (<i>Acyrtosiphon pisum</i>)
MP001	917	AGAAGCATTTGAAGCGTTTAA	27620566 (<i>Anopheles gambiae</i>)
MP001	918	AGAAGCATTTGAAGCGTTTAAACGCACC	98994282 (<i>Antheraea mylitta</i>)
MP001	919	AGAAGCATTTGAAGCGTTTAAACGCACCCAAAGCATGGATGT TGGACAAAT	73619191 (<i>Aphis gossypii</i>)
MP001	920	AGTAAGGGAGTTAAATTGACTA	46998791 (<i>Acyrtosiphon pisum</i>)
MP001	921	ATACAAAGTTGTAAAGTAAAG	29553519 (<i>Bombyx mori</i>)
MP001	922	ATGGATGTTATATCTATCCAAAAGACCCAGTGAGCACCTTTAGAT TGATCTATGATGTGAAAGGTCGTTTCAC	46998791 (<i>Acyrtosiphon pisum</i>)
MP001	923	ATTGATCTATGATGTGAAAGGTCGTTTCAC	46999037 (<i>Acyrtosiphon pisum</i>)
MP001	924	CAAAAGACCAGTGAGCACCTTTAGATTGAT	30031258 (<i>Toxoptera citricida</i>)
MP001	925	CACAGAATTACTCCTGAAGAAGC	73619191 (<i>Aphis gossypii</i>)

MP001	926	CACAGAATTACTCCTGAAGAAAGCAAAATACAAG	46998791 (Acyrthosiphon pisum) 30031258 (Toxoptera citricida)
MP001	927	CATCCAGGATCTTTTGATATTGTTACATTAA	31364848 (Toxoptera citricida)
MP001	928	CATCCAGGATCTTTTGATATTGTTACATTAAAGGATGCAAATG AACATATTTTGTCTAC	37804548 (Rhopalosiphum padi)
MP001	929	CATCTAAAAATTTTGGATCATATCCGTTTTTGAAAACCTGGAAACTT GTGCATGAT	46998791 (Acyrthosiphon pisum)
MP001	930	CATTTGAAGCGTTTAAACGCACC	30031258 (Toxoptera citricida)
MP001	931	CATTTGAAGCGTTTAAACGCACCACCAAGCATGGATGTT	46998791 (Acyrthosiphon pisum)
MP001	932	CCAAAGCATGGATGTTGGACAA	90138164 (Spodoptera frugiperda)
MP001	933	CCAAAGGAGTAAGGGAGTTAAATTGACTA	73615238 (Aphis gossypii) 31364848 (Toxoptera citricida)
MP001	934	CCCAAAGCATGGATGTTGGAC	108789768 (Bombyx mori)
MP001	935	CCCAAAGCATGGATGTTGGACAA	50565112 (Homalodisca coagulata) 48927129 (Hydropsyche sp.) 76551269 (Spodoptera frugiperda)
MP001	936	CCCAAAGCATGGATGTTGGACAAA	56085210 (Bombyx mori) 103792451 (Heliconius erato) 101419954 (Plodia interpunctella)
MP001	937	CCCAAAGCATGGATGTTGGACAAAT	22474095 (Helicoverpa armigera)
MP001	938	CGTCCAAGCACCCGGTCCACACAAACT	47537863 (Acyrthosiphon pisum)
MP001	939	CTGGAAACTTGTGCATGATAAAGTGGAGG	78524585 (Glossina morsitans)
MP001	940	GAAAGACATCCAGGATCTTTTGATATTGTTTCACATTAAAGGATG CAAATGAACATATTTTGTCTACCCGGATGAACAATGTTTTTAT TATTGGAAAAGGTCAAAGAAGTACATTCTCTACCAAG	46997137 (Acyrthosiphon pisum)
MP001	941	GATCATATCCGTTTTTGAAACTGGAACTTGTGCATGAT	73614725 (Aphis gossypii)
MP001	942	GATGCAAAATGAACATATTTTGTCTAC	31364848 (Toxoptera citricida)
MP001	943	GCACCCAAAGCATGGATGTTGGA	70909486 (Mycetophagus quadripustulatus)
MP001	944	GCACCCAAAGCATGGATGTTGGACAAAT	77329254 (Chironomus tentans) 60305420 (Mycetophagus quadripustulatus)
MP001	945	GGATCTTTTGATATTGTTTCACAT	60303405 (Julodis onopordi)
MP001	946	GGATCTTTTGATATTGTTTCACATTAAGGATGCAAATGAACATA TTTTTGTCTAC	73619191 (Aphis gossypii)
MP001	947	GGCCCCAAGAAGCATTTGAAGCGTTTAA	14693528 (Drosophila melanogaster)

MP001	948	GGGCGTGTGGTATTGTTACCAACAG	31365398 (Toxoptera citricida)
MP001	949	GGGCGTGTGGTATTGTTACCAACAGGGAAG	73612212 (Aphis gossypii)
MP001	950	GGTACAAACTGGACCCCAAGG	37804548 (Rhopalosiphum padi)
MP001	951	GTTTTATTATTGGAAAAGGTCAAAGAACTACATTTCTCT	60297572 (Diaprepes abbreviatus)
MP001	952	TGAAGTATGCACCTTACTGGTGC	73619191 (Aphis gossypii)
MP001	953	TGTAAAGTAAAGAGGGGTACAAACTGGACCCCAAGGTGT	73619191 (Aphis gossypii)
MP001	954	TGTGTAAAGTAAAGAGGGGTACAAACTGGACCCCAAGGTGT	30031258 (Toxoptera citricida)
MP001	955	TTCTTGCCTAATCGTTTGAAGTATGCACCTTACTGGTGCCGAA GTCACCAAGATTGTCTATGCAAGATTAAATCAAGGTTGATGGC AAAGTCCGTACCGACCCCTAATTATCCAGC	46998791 (Acyrthosiphon pisum)
MP001	956	TTGGAAAAGGTCAAAGAACTACATTTCTCT	73615060 (Aphis gossypii)
MP001	957	TTGGATCATATCCGTTTGGAACTGGAACCTTGTCATGAT	37804548 (Rhopalosiphum padi)
MP002	958	AAAAAAAATGGTACAACTAATAAACGAGCTGCATTGCAAGC	47537017 (Acyrthosiphon pisum)
MP002	959	AAGAAACGGTACGAACAACAA	15363283 (Apis mellifera)
MP002	960	ACAAGAATTTTGTAGAAAAAATAATTGAACAAGAGTAGCGATA GC	47537017 (Acyrthosiphon pisum)
MP002	961	CAAAATGATGGTACCATGTTAACTATTGAACAACACGCG	47537017 (Acyrthosiphon pisum)
MP002	962	GAAGATGCGATACAAAAGCTTCGATCCAC	47537017 (Acyrthosiphon pisum)
MP002	963	GAGTTCTTTAGTAAAGTATTCGGTGG	110762684 (Apis mellifera)
MP010	964	AAAAGATGATCCAAATAGTTT	110759793 (Apis mellifera)
MP010	965	AAATATTATTGATGGACACATTTTCCATATTTTGATATTCCA	47520567 (Acyrthosiphon pisum)
MP010	966	AATAGTCTGATGAAACATCATATTATAG	47520567 (Acyrthosiphon pisum)
MP010	967	CAAAAAGATGATCCAAATAGTTTCCGATTGCCAGAAAACCTTCA GTTTATATCCACAGTTTCATGTATCATTTAAGAAGGTCTCAATTT CTACAAAGTTTTTAA	47520567 (Acyrthosiphon pisum)
MP010	968	CAACATTCAGTGGCTATAAACGAAT	47520567 (Acyrthosiphon pisum)
MP010	969	CACATGTTGATGCGTGAAGATGTTAC	47520567 (Acyrthosiphon pisum)
MP010	970	CCAAATTCGTATAGCTATAGTTTTAATGGTAGGCCAGAACCTG TACTTTTGGATACCG	47520567 (Acyrthosiphon pisum)
MP010	971	CCATCTCAAAACACATAATAATATGTATGCTTATGGAGG	55814942 (Acyrthosiphon pisum)
MP010	972	CTCAAACTCGATTCCTCAATGCCCTGGTATATTGACACAGAA CAAGGTGGTAGTCAGGCAAGATTTTACTATGCAAGT	55814942 (Acyrthosiphon pisum)

MP010	973	GGTGATGGTGGAGCACCAGTTTTGACAGATGATGTAAGCTTG CA	55814942 (Acyrtosiphon pisum)
MP010	974	GTGGCTGCATACAGTTCATTACGCAGTA	28571527 (Drosophila melanogaster)
MP010	975	TAATGGCTCGTATGTAAGTGAACCGTGCTGAAACTGA	47520567 (Acyrtosiphon pisum)
MP010	976	TATAGGCACATGTTGATGCGTGAAGAT	40924332 (Bombyx mori)
MP010	977	TGGCTGATCGTACGCTTATACGCTTGTTGTCA	47520567 (Acyrtosiphon pisum)
MP010	978	TTAGCTAGGAATGGGCAGACCCCTGT	47520567 (Acyrtosiphon pisum)
MP016	979	AAACAAGATTTTGGAGGAAAATGG	35508791 (Acyrtosiphon pisum)
MP016	980	AACCTGGTAAATCAGTTCCTTGA	35508791 (Acyrtosiphon pisum)
MP016	981	AACGACGACATCACCCATCCTATTC	110240379 (Spodoptera frugiperda)
MP016	982	AATTTAGCTAATGATCCTACTATTGA	27372076 (Spodoptera littoralis)
MP016	983	ACTATGCCCTAACGACGACATCACCCATCC	15366446 (Apis mellifera)
MP016	984	ATAGTATTTGCTGCTATGGTGTAAATATGAAAC	237458 (Heliothis virescens)
MP016	985	CAAAATTTGTAGACAAGCTGGTCT	30124460 (Toxoptera citricida)
MP016	986	CATGAAGACAATTTTGTCTATAGTATTTGCTGCTATGGTGTTA ATATGGAAAC	103020368 (Tribolium castaneum)
MP016	987	CCGATAGATAAAGGACCTCCTATTTGGCTGAAGATTATTTGG ATATTGAAGGCCAACCTATTATCCATA	35508791 (Acyrtosiphon pisum)
MP016	988	CCTATTTTGGCTGAAGATTAT	35508791 (Acyrtosiphon pisum)
MP016	989	CGTATCATTACACCACGCTTGCTTTAACTGCTGCTGAATTTT TAGCTTA	55905051 (Locusta migratoria)
MP016	990	CGCTTGCTTTAACTGCTGCTGAATTTTATGCTTA	30124460 (Toxoptera citricida)
MP016	991	GAAGAAGTACCTGGGCGTGGTTCCTGCTTACATGTAC AC	35508791 (Acyrtosiphon pisum)
MP016	992	GAAGGAAGAAATGGTTCTATCACACAAATACCTATTTTAACTA TGCCTAA	30124460 (Toxoptera citricida)
MP016	993	GAAGGAAGAAATGGTTCTATCACACAAATACCTATTTTAACTA TGCCTAACGA	73615307 (Aphis gossypii)
MP016	994	GATTTAGCTACAATTTATGAACG	30124460 (Toxoptera citricida)
MP016	995	GCCAGATTTCTTAAACAAGATTTTGAGGAAAATGG	30124460 (Toxoptera citricida)
MP016	996	GCTATGGGTGTTAATATGGAAC	75469507 (Tribolium castaneum)
MP016	997	GCTGCAGGTTTACCACATAATGAGATTGCTCAAAATTTG	35508791 (Acyrtosiphon pisum)
MP016	998	GCTGGGCGGTGTAAGGAAGAAATGGTTCTATCACACAAATA	55813096 (Acyrtosiphon pisum)

		CCTATTTTAACTATGCCTAACGA	
MP016	999	GGTTACATGTACACCGATTAGCTACAATTTATGAACG	55813096 (Acyrtosiphon pisum) 73615307 (Aphis gossypii)
MP016	1000	GTGGACAAAAAATCCAAATATTTTC	55813096 (Acyrtosiphon pisum)
MP016	1001	GTGTCGGAGGATATGTTGGGCCG	92460250 (Drosophila erecta) 2286639 (Drosophila melanogaster) 55694673 (Drosophila yakuba)
MP016	1002	GTTCTTGAATTTAGCTAATGATCCTACTATTGA	82563007 (Acyrtosiphon pisum)
MP016	1003	TCAATGGAGAAATGTTTGTCTTGAATTTAGCTAATGATC CTACTATTGA	35508791 (Acyrtosiphon pisum) 30124460 (Toxoptera citricida)
MP016	1004	TCAGCTATTGATATCATGAACCTCTATTGCTCGTGGACAAAAA TTCCAATATTTTC	35508791 (Acyrtosiphon pisum)
MP016	1005	TCATATGCTGAAGCTTTAAGAGAAGTTTCTGCTGCTCG	30124460 (Toxoptera citricida)
MP016	1006	TCCAGAACATATCCTCAAGAAATGATTCAAACTGGTAT	35508791 (Acyrtosiphon pisum)
MP016	1007	TCTATTGCTCGTGGACAAAAAATTC	110764393 (Apis mellifera)
MP016	1008	TGTGAAAAGCATGCTTAGTTATTTTAACTGACATGAGTTTCAT ATGCTGAAGCTTTAAGAGAAGTTTCTGCTGCTCGTGAAGAAG TACCTGGCGCTCGTGGTTTCCC	55813096 (Acyrtosiphon pisum)
MP016	1009	TAACTGACATGAGTTTCATATGCTGAAGCTTTAAGAGAAGTTT CTGCTGCTCGTGAAGAAGTACCTGG	73615307 (Aphis gossypii)
MP027	1010	TTTTTAAAAATTTTAAAGAAAAA	47522167 (Acyrtosiphon pisum)

Table 4-NL

Target ID	SEQ ID NO	Sequence *	Example GI-number and species
NL001	1161	CTGAAGAAGCTAAGTACAAGCT	16566724 (Spodoptera frugiperda)
NL001	1162	TTCTCCGTTTGATCTATGATGTTAA	16900870 (Ctenocephalides felis)
NL001	1163	CAGCTGAAGAAGCTAAGTACAA	16900870 (Ctenocephalides felis), 56199521 (Culicoides sonorensis)
NL001	1164	GAGTTCTTCCGTTTGATCTATGATGTTAA	16900945 (Ctenocephalides felis)
NL001	1165	AAGTACAAGCTGTGCAAGTGAAG	22474232 (Helicoverpa armigera)

NL001	1166	TTCGACATCGTGCACATCAAGGAC	22474232 (<i>Helicoverpa armigera</i>)
NL001	1167	ATCACAGCTGAAGAAGCTAAGTACAAG	25956820 (<i>Biphyllus lunatus</i>)
NL001	1168	TGTGTATGATCACTGGAGGTCGTAA	25957367 (<i>Carabus granulatus</i>)
NL001	1169	AACGTTTTTCATCATCGGCAAG	27613698 (<i>Anopheles gambiae</i>)
NL001	1170	CCAAAATCATGGACTTCATCA	3738704 (<i>Manduca sexta</i>)
NL001	1171	TGATCTATGATGTTAAGGGACG	3738704 (<i>Manduca sexta</i>)
NL001	1172	CATGGATGTTGGACAAAATTGGG	37951951 (<i>Ips pini</i>), 56772312 (<i>Drosophila virilis</i>), 60305420 (<i>Mycetophagus quadripustulatus</i>), 67885868 (<i>Drosophila pseudoobscura</i>), 77321575 (<i>Chironomus tentans</i>), 25956479 (<i>Biphyllus lunatus</i>), 22474232 (<i>Helicoverpa armigera</i>);
NL001	1173	TTTTGCCACTAGGTTGAACAACGT	37953169 (<i>Ips pini</i>)
NL001	1174	GCAGCGTCTCATCAAGTTGACGGCAA	48927129 (<i>Hydropsyche</i> sp.)
NL001	1175	AAGGGACGTTTCACCATCCAC	50818668 (<i>Heliconius melpomene</i>)
NL001	1176	AACCTGTGTATGATCACTGGAGG	60293875 (<i>Homalodisca coagulata</i>)
NL001	1177	ACTAACTGTGAAGTGAAGAAAATTGT	60293875 (<i>Homalodisca coagulata</i>)
NL001	1178	TTCTTCGGTTTGATCTATGATGT	60293875 (<i>Homalodisca coagulata</i>), 71047771 (<i>Oncometopia nigricans</i>)
NL001	1179	TGTATGATCACTGGAGGTCGTAAC TTGGG	60297219 (<i>Diaprepes abbreviatus</i>)
NL001	1180	CATGGATGTTGGACAAAATTGGGTGG	60311985 (<i>Papilio dardanus</i>)
NL001	1181	GCTGAAGAAGCTAAGTACAAG	68758383 (<i>Acanthoscurria gomesiana</i>)
NL001	1182	GGAGGTCGTAAC TTGGGTCGTGT	77327303 (<i>Chironomus tentans</i>)
NL001	1183	TATGATGTTAAGGGACGTTTCACCAT	77327303 (<i>Chironomus tentans</i>)
NL001	1184	CATGGATGTTGGACAAAATTGGG	93002561 (<i>Drosophila grimshawi</i>) 93001617 (<i>Drosophila mojavensis</i>) 92939328 (<i>Drosophila virilis</i>) 112433559 (<i>Myzus persicae</i>)

			90814922 (<i>Nasonia vitripennis</i>)
NL001	1185	CTGAAGAAGCTAAGTACAAGCT	110264122 (<i>Spodoptera frugiperda</i>)
NL001	1186	GAAGAAGCTAAGTACAAGCTGTG	90820001 (<i>Graphocephala atropunctata</i>)
NL001	1187	TTGCACAGCTTGACTTAGCTTCTC	90134075 (<i>Bicyclus anynana</i>)
NL001	1188	AAGTACAAGCTGTGCAAAGTGAAG	112350104 (<i>Helicoverpa armigera</i>)
NL001	1189	ATGATCACTGGAGTCGTAACTTGGGTCG	113017118 (<i>Bemisia tabaci</i>)
NL001	1190	GGTCGTAAC TTGGGTCGTGTGGG	109978109 (<i>Gryllus pennsylvanicus</i>)
NL001	1191	TTCGACATCGTGCCACATCAAGGAC	112350104 (<i>Helicoverpa armigera</i>)
NL001	1192	ACATCGTGCCACATCAAGGACG	90981811 (<i>Aedes aegypti</i>)
NL003	1193	CAGGAGTTGAAGATCATCGGAGATATGG	15457393 (<i>Drosophila melanogaster</i>), 76551770 (<i>Spodoptera frugiperda</i>)
NL003	1194	CGTAAGGCCGCTCGTGAGCTG	1797555 (<i>Drosophila melanogaster</i>)
NL003	1195	AAGGTAACGCCCTGCTGCGTCG	18863433 (<i>Anopheles gambiae</i>)
NL003	1196	CAGGAGTTGAAGATCATCGGAGAGTA	2459311 (<i>Antheraea yamamai</i>), 49532931 (<i>Plutella xylostella</i>)
NL003	1197	GCCAAAGTCCATCCATCACGCCCG	33354488 (<i>Drosophila yakuba</i>), 60312414 (<i>Papilio dardanus</i>)
NL003	1198	AAGTCCATCCATCACGCCCGT	33528372 (<i>Trichoplusia ni</i>)
NL003	1199	TGTTTGAAGGTAACGCCCTGCT	34788046 (<i>Callosobruchus maculatus</i>)
NL003	1200	CAGGAGTTGAAGATCATCGGAGA	35505798 (<i>Acyrtosiphon pisum</i>), 56772256 (<i>Drosophila virilis</i>)
NL003	1201	GTGCGCCTGGACTCGCAGAAGCACAT	38624772 (<i>Drosophila melanogaster</i>)
NL003	1202	GAGTTGAAGATCATCGGAGAGTA	4158332 (<i>Bombyx mori</i>)
NL003	1203	TTGGGTTTAAAAATTGAAGATTTC	56150446 (<i>Rhynchosciara americana</i>)
NL003	1204	TCGCAGAAGCACATTGACTTCTC	56772256 (<i>Drosophila virilis</i>)
NL003	1205	AGAATGAAGCTCGATTACGTC	60306665 (<i>Sphaerius</i> sp.)
NL003	1206	TTTGTGGTGCGCCTGGACTCG	60312414 (<i>Papilio dardanus</i>)
NL003	1207	AGAAGCACATTGACTTCTCGCTGAAGTC	63514675 (<i>Ixodes scapularis</i>)

NL003	1208	TCGCAGAAAGCACATTGACTTCTCGCT	70979521 (<i>Anopheles albimanus</i>)
NL003	1209	CTCATCAGACAAAGACATATCAGAGT	71536734 (<i>Diaphorina citri</i>)
NL003	1210	TTGAAGATCATCGGAGAGTATGG	73612958 (<i>Aphis gossypii</i>)
NL003	1211	AAAATTGAAGATTTCTTGAA	75467497 (<i>Tribolium castaneum</i>)
NL003	1212	CAGAAGCACATTGACTTCTCGCT	77730066 (<i>Aedes aegypti</i>)
NL003	1213	CGTAAGGCCGCTCGTGAGCTG	24661714 (<i>Drosophila melanogaster</i>)
NL003	1214	GCGTGATGGATGGACTTGGCCAA	90813959 (<i>Nasonia vitripennis</i>)
NL003	1215	GCCAAGTCCATCCATCACGCCCG	92467993 (<i>Drosophila erecta</i>)
NL003	1216	GCCAAGTCCATCCATCACGCCCGT	112349903 (<i>Helicoverpa armigera</i>)
NL003	1217	CTCATCAGACAAAGACATATCAGAGT	110671455 (<i>Diaphorina citri</i>)
NL003	1218	CAGGAGTTGAAGATCATCGGAGA	86464397 (<i>Acyrtosiphon pisum</i>)
NL003	1219	CAGGAGTTGAAGATCATCGGAGATGAG	92938865 (<i>Drosophila virilis</i>)
NL003	1220	GAGTTGAAGATCATCGGAGAGTA	101417830 (<i>Plodia interpunctella</i>)
NL003	1221	TCGCAGAAAGCACATTGACTTCTC	110254389 (<i>Spodoptera frugiperda</i>)
NL003	1222	TTGAAGATCATCGGAGAGTATGG	112984021 (<i>Bombyx mori</i>)
NL003	1223	CAGAAGCACATTGACTTCTCGCTGAA	93002641 (<i>Drosophila mojavensis</i>)
NL003	1224	CTCCGTAACAAGCGTGAGGTGTGG	92938865 (<i>Drosophila virilis</i>)
NL003	1225	CGTAACAAGCGTGAGGTGTGG	111158779 (<i>Myzus persicae</i>)
NL003	1226	GTCAAATACGCCCTGGCCAAGAT	92232387 (<i>Drosophila willistoni</i>)
NL004	1227	TACGCCCATTTCCCCCATCAACTGTGT	92232387 (<i>Drosophila willistoni</i>)
NL004	1228	TGCTCTCACATCGAAAACATG	110558371 (<i>Drosophila ananassae</i>)
NL004	1229	AACTTCTCTGGCGGAGAAATACATC	93001117 (<i>Drosophila grimshawi</i>)
NL004	1230	GCCGTGTACGCCCATTTCCCCCATCAACTG	14994663 (<i>Spodoptera frugiperda</i> , 53883415 (<i>Plutella xylostella</i>))
NL004	1231	GTGTACGCCCATTTCCCCCATCAACTGTGTGAC	22039837 (<i>Ctenocephalides felis</i>)
NL004	1232	GTGTACGCCCATTTCCCCCATCAACTGTGT	25959088 (<i>Meladema coriacea</i>)
NL004	1233	ATGCGTGCCGTGTACGCCCATTT	25959088 (<i>Meladema coriacea</i>)
			2761563 (<i>Drosophila melanogaster</i>)
			33354902 (<i>Drosophila yakuba</i>)
			33433477 (<i>Glossina morsitans</i>)

NL004	1234	TCAGCTGCCCTCATCCAACAGTC	33491496 (<i>Trichoplusia ni</i>)
NL004	1235	AAGGATATTCTGTAATTCCTTGA	37952094 (<i>Ips pini</i>), 56199511 (<i>Culicoides sonorensis</i>)
NL004	1236	GCCCATTTCCCCATCAACTGTGT	42766318 (<i>Armigeres subalbatus</i>)
NL004	1237	AACCTCTGGGCGAGAGTACAT	49547659 (<i>Rhipicephalus appendiculatus</i>)
NL004	1238	AAGAACAAGGATATTCGTAAATCTTGA	56152793 (<i>Rhynchosciara americana</i>)
NL004	1239	AACTTCCTGGGCGAGAGTACATCCG	58079798 (<i>Amblyomma americanum</i>), 49554219 (<i>Boophilus microplus</i>)
NL004	1240	CATTTCCCATCAACTGTGTGAC	60312171 (<i>Papilio dardanus</i>)
NL004	1241	CGTAACCTCCTGGGCGAGAGTACATCCG	63516417 (<i>Ixodes scapularis</i>)
NL004	1242	AGATCAGCTGCCCTCATCCAACA	71539722 (<i>Diaphorina citri</i>)
NL004	1243	GTGTACGCCCATTTCCCATCAACTGTGT	24583601 (<i>Drosophila melanogaster</i>)
NL004	1244	TACGCCCATTTCCCATCAACTGT	113017826 (<i>Bemisia tabaci</i>)
NL004	1245	TACGCCCATTTCCCATCAACTGTGT	110263092 (<i>Spodoptera frugiperda</i>)
NL004	1246	GCCCATTTCCCATCAACTGTGT	94468811 (<i>Aedes aegypti</i>)
NL004	1247	ACACAGTTGATGGGGAATGGGC	90136736 (<i>Bicyclus anynana</i>)
NL004	1248	GCCCATTTCCCATCAACTGTGT	110671493 (<i>Diaphorina citri</i>)
NL004	1249	GTCACACAGTTGATGGGGAATGGGC	110249018 (<i>Spodoptera frugiperda</i>)
NL004	1250	CCATTTCCCATCAACTGTGT	87266195 (<i>Choristoneura fumiferana</i>)
NL005	1251	AAGGGTAACGTATTCAAGAACAAAGCG	90981351 (<i>Aedes aegypti</i>)
NL005	1252	AAGGGTAACGTATTCAAGAACAAAG	1900283 (<i>Drosophila melanogaster</i>)
NL005	1253	CGTGTATTGATGGAGTTTCATTCA	25956594 (<i>Biphyllus lunatus</i>)
NL005	1254	AAAGGTAAGGAGGCCAAGAAG	30124405 (<i>Toxoptera citricida</i>), 60294294 (<i>Homalodisca coagulata</i>), 71046487 (<i>Oncometopia nigricans</i>), 73612243 (<i>Aphis gossypii</i>)
NL005	1255	AAGATGTTGAACGACCAAGGCTGAAGC	67875089 (<i>Drosophila pseudoobscura</i>)
NL005	1256	ACGTTACCTTAGCCTTCATGTA	77324118 (<i>Chironomus tentans</i>)
NL005	1257	AAGGGTAACGTATTCAAGAACAAAGCG	90812513 (<i>Nasonia giraulti</i>)
NL005	1258	CGTGTATTGATGGAGTTTCATTCA	45552830 (<i>Drosophila melanogaster</i>)
NL005	1258	CGTGTATTGATGGAGTTTCATTCA	112433619 (<i>Myzus persicae</i>)

NL005	1259	AGGTCAAGGAGGCCAAGAAGC	92941126 (<i>Drosophila virilis</i>)
NL005	1260	ACGTTACCCCTTAGCCCTTCATGTA	90812513 (<i>Nasonia giraulti</i>)
NL005	1261	AAGGGTAACGTATTCAAGACAAGCG	45552830 (<i>Drosophila melanogaster</i>)
NL006	1262	AGTCCCAGGAACACCTATCAG	21464337 (<i>Drosophila melanogaster</i>)
NL006	1263	ATTATTCCTTCCCCGATCACAA	24646762 (<i>Drosophila melanogaster</i>)
NL006	1264	CACGCTATCCCATCTCGTATGACAATTGG	24646762 (<i>Drosophila melanogaster</i>)
NL006	1265	TACAAGTTCTGCAAAATTGGAGT	49573116 (<i>Boophilus microplus</i>)
NL006	1266	ATGACAATTGGCCATTTAATTGAATG	50564037 (<i>Homalodisca coagulata</i>)
NL006	1267	ACCTACACGCACTGCGAGATCCA	58384759 (<i>Anopheles gambiae</i> str. PEST)
NL006	1268	GGTGTGGTGAGTACATTGACAC	58384759 (<i>Anopheles gambiae</i> str. PEST)
NL006	1269	ATTATTCCTTCCCCGATCACAA	24646762 (<i>Drosophila melanogaster</i>)
NL006	1270	AGTCCCAGGAACACCTATCAG	22026793 (<i>Drosophila melanogaster</i>)
NL006	1271	CACGCTATCCCATCTCGTATGACAATTGG	24646762 (<i>Drosophila melanogaster</i>)
NL006	1272	TCTCGTATGACAATTGGCCATTT	93000469 (<i>Drosophila mojavensis</i>)
NL007	1273	GCAACAAGTCATGATGTTGAG	15354019 (<i>Apis mellifera</i>)
NL007	1274	GGTATGGGAAAAAAGTCTGTATTGTGTT	15354019 (<i>Apis mellifera</i>)
NL007	1275	GAATGCATTCCTCAAGCTGTA	21068658 (<i>Chironomus tentans</i>)
NL007	1276	TGCAAGAAATTCATGCAAGATCC	21068658 (<i>Chironomus tentans</i>)
NL007	1277	TTCCAAATCAGCAAAAGAGTATGA	28904413 (<i>Drosophila melanogaster</i>)
NL007	1278	GATGACGAGGCCAAGCTGACGCT	49536419 (<i>Rhipicephalus appendiculatus</i>)
NL007	1279	TGTGGTTTTGAACATCCATCTGAAGTACAACA	60308907 (<i>Hister</i> sp.)
NL007	1280	GAAAACGAAAAAGAACAAAAAG	77642464 (<i>Aedes aegypti</i>)
NL007	1281	GGTATGGGAAAAAAGTCTGTATTGTGTT	110759359 (<i>Apis mellifera</i>)
NL007	1282	GCAACAAGTCATGATGTTGAG	110759359 (<i>Apis mellifera</i>)
NL007	1283	CTGCAGCAGCACTATGTCAAACTCAA	90137538 (<i>Spodoptera frugiperda</i>)
NL007	1284	GAAAACGAAAAAGAACAAAAAG	94468805 (<i>Aedes aegypti</i>)
NL008	1285	TGCCAAGCCTAAAGATTTGGG	60315277 (<i>Dysdera erythrina</i>)
NL008	1286	ATGTTCAAGAAAGTTAATGCTAGAGA	60336214 (<i>Homalodisca coagulata</i>)

NL008	1287	GAGTTGTTGGTGTCTCTTTGGGATG	66522334 (<i>Apis mellifera</i>)
NL008	1288	TTTCAAACAGTTTTGCAGTTCC	75735289 (<i>Tribolium castaneum</i>)
NL008	1289	GAGTTGTTGGTGTCTCTTTGGGATG	110762109 (<i>Apis mellifera</i>)
NL010_1	1290	AAGGACCTGACTGCCAAGCAG	2761430 (<i>Drosophila melanogaster</i>)
NL010_1	1291	GCCAAAGCAGATCCAGGACATG	49559867 (<i>Boophilus microplus</i>)
NL010_1	1292	TGCTCGAAGAGCTACGTGTTCGG	49559867 (<i>Boophilus microplus</i>)
NL010_1	1293	AAGAGCTACGTGTTCGGTGGC	92043082 (<i>Drosophila willistoni</i>)
NL010_1	1294	AAGGACCTGACTGCCAAGCAG	92481328 (<i>Drosophila erecta</i>) 28571527 (<i>Drosophila melanogaster</i>)
NL010_2	1295	ATGGACACATTTTTCCAAATTCAT	33427937 (<i>Glossina morsitans</i>)
NL010_2	1296	ACCAGCAGTATTCACACCCGACA	47520567 (<i>Acyrtosiphon pisum</i>)
NL010_2	1297	TATTGATGGACACATTTTTCCA	47520567 (<i>Acyrtosiphon pisum</i>)
NL010_2	1298	TTCAACAACAGTCCTGATGAAAC	55891325 (<i>Locusta migratoria</i>)
NL010_2	1299	ATGGACACATTTTTCCAAATT	56151768 (<i>Rhynchosciara americana</i>), 75736992 (<i>Tribolium castaneum</i>)
NL010_2	1300	CCGCAGTTTCATGTACCATCTGCG	6932015 (<i>Anopheles gambiae</i>), 295558345 (<i>Bombyx mori</i>)
NL010_2	1301	ATGGACACATTTTTCCAAATT	91086194 (<i>Tribolium castaneum</i>)
NL011	1302	AAGAAGTATGTTGCCACCCCTTGG	21640529 (<i>Amblyomma variegatum</i>)
NL011	1303	GACATCAAGGACAGGAAAGTCAAGGCCAAGAGC ATAGT	25959135 (<i>Meladema coriacea</i>)
NL011	1304	CAACTACAACCTTCGAGAAGCCGTTCCCTGTGG	25959135 (<i>Meladema coriacea</i>), 77646995 (<i>Aedes aegypti</i>)
NL011	1305	TACAAGAACGTTCCCAACTGGCA	3114090 (<i>Drosophila melanogaster</i>)
NL011	1306	TGCGAAAACATTCCCATTTGTACT	37951963 (<i>Ips pini</i>)
NL011	1307	AGGAAGAAGAACCTTCAGTACTACGA	40544671 (<i>Tribolium castaneum</i>)
NL011	1308	AGCAACTACAACCTTCGAGAAGCC	49565237 (<i>Boophilus microplus</i>), 49538692 (<i>Rhipicephalus appendiculatus</i>)
NL011	1309	AACAAAGTAGACATCAAGGACAGGAAAGTCAA	76552920 (<i>Spodoptera frugiperda</i>)

NL011	1310	CCCAACTGGCACAGAGATTAGTG	78230577 (Heliconius erato/himera mixed EST library)
NL011	1311	GATGGTGGTACCGGCAAACTAC	78538667 (Glossina morsitans)
NL011	1312	TACAAGAACGTTCCCACTGGCAC	84267747 (Aedes aegypti)
NL011	1313	AACAAAGTAGACATCAAGGACAGGAAAGTCAA	110263840 (Spodoptera frugiperda)
NL011	1314	TTGACTTTCCTGCTCCTTGATGTC	90136305 (Bicyclus anynana)
NL011	1315	GACATCAAGGACAGGAAAGTCAAGGC	90813103 (Nasonia vitripennis)
NL011	1316	AGGAAGAAGAACCTTCAGTACTACGA	91091115 (Tribolium castaneum)
NL011	1317	GATGTCGTAGTACTGAAGGTTCTT	90136305 (Bicyclus anynana)
NL011	1318	CAACTACAACCTCGAGAAGCCGTTCTGTGG	90977910 (Aedes aegypti)
NL011	1319	CCAACCTGGAGTTCGTCGCCATGCC	92465523 (Drosophila erecta)
NL011	1320	GAATTGAAAAGAAAGTATGTTGC	113015058 (Bemisia tabaci)
NL011	1321	CTTCAGTACTACGACATCAGTGCGAA	110086408 (Amblyomma cajennense)
NL011	1322	AGCAACTACAACTTCGAGAAGCC	110086408 (Amblyomma cajennense)
NL011	1323	AAGCTGATCGGTGACCCCAACCTGGAGTT	110086408 (Amblyomma cajennense)
NL012	1324	CACAGTTTGAACAGCAAGCTGG	29552409 (Bombyx mori)
NL012	1325	GCAGCAGACGCGACGACAGGTAGA	77823921 (Aedes aegypti)
NL012	1326	CACAGTTTGAACAGCAAGCTGG	94435913 (Bombyx mori)
NL013	1327	CAAGCGAAGATGTTGGACATGCT	15536506 (Drosophila melanogaster)
NL013	1328	ATGGTGTGGGCTGGTACCACCTCGCACCC	49547019 (Rhhipicephalus appendiculatus)
NL013	1329	GTGGTGGGCTGGTACCACCTCGCACCC	58079586 (Amblyomma americanum)
NL013	1330	GTGGGCTGGTACCACCTCGCACCC	82848521 (Boophilus microplus)
NL013	1331	AAGATGTTGGACATGCTAAAGCAGACAGG	92229701 (Drosophila willistoni)
NL013	1332	TGTCGGGTGTCGACATCAACAC	92962655 (Drosophila ananassae)
NL013	1333	GTTCCCATGGAAGTTATGGGC	112433067 (Myzus persicae)
NL013	1334	GTGGGCTGGTACCACCTCGCACCC	110085175 (Amblyomma cajennense)
NL014	1335	GAGATCGATGCCAAGGCCGAGGA	1033187 (Drosophila melanogaster)
NL014	1336	GAATTCACATTGAAAAAGGGA	16900951 (Ctenocephalides felis)
NL014	1337	GAAGAAATTCACATTGAAAAAGGG	47518467 (Acyrtosiphon pisum)
NL014	1338	GAAGCCCAATGAGAAAGCCGAAGA	47518467 (Acyrtosiphon pisum)
NL014	1339	TCGTCAAAACATGCTGAACCAAGC	61954844 (Tribolium castaneum)

NL014	1340	TTTCATTGAGCAAGAAAGCCCAATGA	62239529 (<i>Diabrotica virgifera</i>), 76169390 (<i>Diploptera punctata</i>), 61954844 (<i>Tribolium castaneum</i>), 16900951 (<i>Ctenocephalides felis</i>)
NL014	1341	CAAGAAGCCCAATGAGAAAGCCGA	111160670 (<i>Myzus persicae</i>)
NL014	1342	TTTCATTGAGCAAGAAAGCCCAATGA	91092061 (<i>Tribolium castaneum</i>)
NL014	1343	AGAAGCCCAATGAGAAAGCCGA	112432414 (<i>Myzus persicae</i>)
NL014	1344	TCGTCAACATGCTGAACCAAGC	91092061 (<i>Tribolium castaneum</i>)
NL014	1345	GCCAATGAGAAAGCCGAAGAGATCGATGCCAA	93001435 (<i>Drosophila grimshawi</i>)
NL014	1346	AAAGCCGAAGAGATCGATGCCAA	92936169 (<i>Drosophila virilis</i>)
NL014	1347	GAGATCGATGCCAAGGCCGAGGA	24644299 (<i>Drosophila melanogaster</i>)
NL014	1348	GAAGAAATCAACATTGAAAAGGG	86463006 (<i>Acyrtosiphon pisum</i>)
NL014	1349	GAAGAAATCAACATTGAAAAGGGAGGCT	111160670 (<i>Myzus persicae</i>)
NL014	1350	AAGAATCAACATTGAAAAGGG	90819999 (<i>Graphocephala atropunctata</i>)
NL015	1351	GAGGTGCTGCGCATCCACACCAA	111158385 (<i>Myzus persicae</i>)
NL015	1352	ATCCATGTGCTGCCCATTTGATGA	18887285 (<i>Anopheles gambiae</i>)
NL015	1353	CATGTGCTGCCCATTTGATGAT	21641659 (<i>Amblyomma variegatum</i>)
NL015	1354	CTGCGCATCCACACCAAGAACATGAAGTTGG	22039735 (<i>Ctenocephalides felis</i>)
NL015	1355	TTCTTCTTCCTCATCAACGGACC	22474136 (<i>Helicoverpa armigera</i>)
NL015	1356	GAGATGGTGGAGTTGCCGCTG	49552586 (<i>Rhipicephalus appendiculatus</i>)
NL015	1357	CAGATCAAGAGATGGTGGAG	58371722 (<i>Lonomia obliqua</i>)
NL015	1358	ATCAACGGACCCGAGATTATG	92947821 (<i>Drosophila ananassae</i>)
NL015	1359	ATGAAGATGATGCCCGGTCCGTT	92947821 (<i>Drosophila ananassae</i>)
NL015	1360	CCGGCCATCATCTTCATCGATGAG	92470977 (<i>Drosophila erecta</i>)
NL015	1361	ATCATCTTCATCGATGAGCTGGACGC	92480997 (<i>Drosophila erecta</i>)
NL015	1362	CAGCTGCTGACGCTGATGACGG	99007898 (<i>Leptinotarsa decemlineata</i>)
NL015	1363	ATCGACATTGGCATCCCGATGCCACCCGG	92941440 (<i>Drosophila virilis</i>)
NL016	1364	TCTATGGAGAACGCTGTCCTGTTCTTGAAC	92947821 (<i>Drosophila ananassae</i>)
NL016	1365	TACCAGTGCGAGAACGACGTGCT	27372076 (<i>Spodoptera littoralis</i>)
NL016	1366	ATGGAGAACGTGTGCCTGTTCCTTGAACCTGGC	2921501 (<i>Culex pipiens</i>)
NL016	1367	CGTGGCCAGAAAAATCCCCATCTT	31206154 (<i>Anopheles gambiae</i> str. PEST)
			3945243 (<i>Drosophila melanogaster</i>)

NL016	1368	TGGCCTACCAGTGCAGAAACACCGTG	4680479 (<i>Aedes aegypti</i>)
NL016	1369	TGGCCACCATCTACGAGCGCGCCGG	53883819 (<i>Plutella xylostella</i>)
NL016	1370	ATGGAGAACGTGTGCCTGTTCTTGAA	67883622 (<i>Drosophila pseudoobscura</i>)
NL016	1371	CCCGAGGAAATGATCCAGACTGG	67883622 (<i>Drosophila pseudoobscura</i>)
NL016	1372	TGGCCTACCAGTGCAGAAACACCGTGCT	67883622 (<i>Drosophila pseudoobscura</i>), 31206154 (<i>Anopheles gambiae</i> str. PEST)
NL016	1373	GAGGAGGTGCCCGCGCGTGTGTTTCCCGG TTACATGTACACCGAT	67896654 (<i>Drosophila pseudoobscura</i>)
NL016	1374	GAGGTGCGCAACGGCTCCATCAC	67896654 (<i>Drosophila pseudoobscura</i>)
NL016	1375	GAGGTGCCCCGCGCGTGTGTTCCCGGTTAC ATGTACACCGAT	75710699 (<i>Tribolium castaneum</i>)
NL016	1376	ATGGAGAACGTGTGCCTGTTCTTGAAC	76554661 (<i>Spodoptera frugiperda</i>)
NL016	1377	TGGCCTACCAGTGCAGAAACACGTGCTCGTCA TCCT	9992660 (<i>Drosophila melanogaster</i>)
NL016	1378	CGTCGTGGTTTCCCGGTTACATGTACACCGAT	9992660 (<i>Drosophila melanogaster</i>), 2921501 (<i>Culex pipiens</i>), 62239897 (<i>Diabrotica virgifera</i>)
NL016	1379	TGGTCGCGTATCTATCCCGAGGAAATGATCCAG AC	92999374 (<i>Drosophila grimshawi</i>)
NL016	1380	TGGTCGCGTATCTATCCCGAGGAAATGATCCAG ACTGG	92940538 (<i>Drosophila virilis</i>)
NL016	1381	TCTATGGAGAACGTGTGCCTGTTCTTGAAC	92938622 (<i>Drosophila virilis</i>)
NL016	1382	ATGGAGAACGTGTGCCTGTTCTTGAAC	92950254 (<i>Drosophila ananassae</i>) 90137502 (<i>Spodoptera frugiperda</i>)
NL016	1383	AACGTGTGCCTGTTCTTGAAC	92946927 (<i>Drosophila ananassae</i>)
NL016	1384	TGGCCTACCAGTGCAGAAACACCGTGCT	24646342 (<i>Drosophila melanogaster</i>) 92231646 (<i>Drosophila willistoni</i>)
NL016	1385	TGGCCTACCAGTGCAGAAACACGTGCTCGTCA TCCT	107256717 (<i>Drosophila melanogaster</i>)
NL016	1386	GCCTACCAGTGCAGAAACACGTGCT	92985459 (<i>Drosophila grimshawi</i>)
NL016	1387	GAGGAGGTGCCCGCGCGTGTGTTTCCCGG TTACATGTACAC	92938622 (<i>Drosophila virilis</i>)

NL016	1388	GAGGAGGTCCCGCGCGTCGTGTTTCCCGG	92477818 (<i>Drosophila erecta</i>)
NL016	1389	TTACATGTACACCGAT	91090030 (<i>Tribolium castaneum</i>)
NL016	1390	GAGGTGCCCGCGCGTCGTGTTTCCCGGTTAC	104530890 (<i>Belgica antarctica</i>)
NL016	1391	ATGTACACCGAT	92981037 (<i>Drosophila grimshawi</i>)
NL016	1392	CGTCGTGTTTCCCGCGTTACAT	24646342 (<i>Drosophila melanogaster</i>)
NL016	1393	CGTCGTGTTTCCCGCGTTACATGTACACCGAT	92957249 (<i>Drosophila ananassae</i>)
NL016	1394	CGTCGTGTTTCCCGCGTTACATGTACACCGAT	103744758 (<i>Drosophila melanogaster</i>)
NL016	1395	ATCGGTGTACATGTAAACCGGGAACCA	91829127 (<i>Bombyx mori</i>)
NL016	1396	CGTCCGGCGCGCTCGTAGATGGT	92957249 (<i>Drosophila ananassae</i>)
NL018	1397	GAGGTCGCAACGGCTCCATCAC	92479742 (<i>Drosophila erecta</i>)
NL019	1398	CGACGTGGCCTGTTTCATCA	84343006 (<i>Aedes aegypti</i>)
NL019	1399	GTGGTGACGACTGCACCGACCCAGGAGTCGTTT	113018639 (<i>Bemisia tabaci</i>)
NL019	1400	AAACAAC	85857059 (<i>Aedes aegypti</i>)
NL019	1401	GAAAGTTACATCAGTACCATTTGGTGT	91087112 (<i>Tribolium castaneum</i>)
NL019	1402	CACCGACCGAGGATCGTTCAACAAC	78542465 (<i>Glossina morsitans</i>)
NL019	1403	AGTACCATTTGGTGTAGATTTTAAAT	92232411 (<i>Drosophila willistoni</i>)
NL019	1404	ATTGGTGTAGATTTTAAATTTAGAAC	90986845 (<i>Aedes aegypti</i>)
NL019	1405	GGTGTAGATTTTAAATTTAGAACAAAT	92043152 (<i>Drosophila willistoni</i>)
NL019	1406	GTTCTAATTTTAAATCTACAC	91091115 (<i>Tribolium castaneum</i>)
NL019	1407	TGGACACGGCCGGCCAGGAG	90982219 (<i>Aedes aegypti</i>)
NL019	1408	TGGACACGGCCGGCCAGGAGCGG	94433465 (<i>Bombyx mori</i>)
NL019	1409	TGGACACGGCCGGCCAGGAGCGGT	10708384 (<i>Amblyomma americanum</i>)
NL019	1410	GACCACTGGGCATTCCGTTCT	18864897 (<i>Anopheles gambiae</i>)
NL019	1411	ATTGGTGTAGATTTTAAAT	18888926 (<i>Anopheles gambiae</i>)
NL019	1412	TGGACACGGCCGGCCAGGAGCGGTT	21640713 (<i>Amblyomma variegatum</i>)
NL019	1413	CAGGAGCGGTTCCGCACGATCAC	22039832 (<i>Ctenocephalides felis</i>)
NL019	1414	ATTGGTGTAGATTTTAAATTTAGAAC	33378174 (<i>Glossina morsitans</i>)
NL019	1415	ATTGGTGTAGATTTTAAATTTAGAAC	3738872 (<i>Manduca sexta</i>), 25959135 (<i>Meladema coriacea</i>), 40542849 (<i>Tribolium castaneum</i>), 67840088 (<i>Drosophila pseudoobscura</i>)

NL019	1415	TGGACACGGCCGGCCAGGAGCGGT	4161805 (<i>Bombyx mori</i>)
NL019	1416	GATGACACATACACAGAAAGTTACATCAGTAC	50562545 (<i>Homalodisca coagulata</i>), 71047909 (<i>Oncometopia nigricans</i>)
NL019	1417	ACGGCCGGCCAGGAGCGGTTCCG	58378591 (<i>Anopheles gambiae</i> str. PEST)
NL019	1418	AGTACCATTTGGTAGATTTTAAAAAT	61954135 (<i>Tribolium castaneum</i>)
NL019	1419	TAAAGCTTCAGATTTGGGACAC	68758530 (<i>Acanthoscurria gomesiana</i>)
NL019	1420	ATTTGGGACACGGCCGGCCAGGA	77667315 (<i>Aedes aegypti</i>)
NL019	1421	GTGGTGTAAGACTGCACCGACCGAGGAGTCGTTTCAACAAC	77705629 (<i>Aedes aegypti</i>)
NL019	1422	GGTGTAGATTTTAAAAATTAGAACAAAT	77890715 (<i>Aedes aegypti</i>)
NL019	1423	TGGGACACGGCCGGCCAGGAGCG	82851662 (<i>Boophilus microplus</i>), 49536894 (<i>Rhipicephalus appendiculatus</i>)
NL022	1424	TCTTCCTCACCGGTCAGGAGGAGAT	6928515 (<i>Anopheles gambiae</i>)
NL022	1425	AAATTCCTCCGAGTTTTTCGACGATGC	91082872 (<i>Tribolium castaneum</i>)
NL022	1426	TTCCTCACCGGTCAGGAGGAGAT	90976120 (<i>Aedes aegypti</i>)
NL022	1427	TAGTATTGGCCACAAATATTGCAGA	92042565 (<i>Drosophila willistoni</i>)
NL023	1428	TATTTGAACATATGGGTGCCGCA	20384699 (<i>Plutella xylostella</i>)
NL023	1429	GAGGGAGAGGAAATGTGGAATCC	22085301 (<i>Helicoverpa armigera</i>)
NL023	1430	CCGAAGATTGTCTGTATTGAA	27531022 (<i>Apis mellifera</i>)
NL023	1431	GATTCGGTTTGGGAAACCTCC	57929927 (<i>Anopheles gambiae</i> str. PEST)
NL023	1432	GGTGGTTCCGGCTTCTCTACCT	58380563 (<i>Anopheles gambiae</i> str. PEST)
NL023	1433	CAATTCATGCTAGGAAAGG	110759012 (<i>Apis mellifera</i>)
NL023	1434	GAGGGAGAGGAAATGTGGAATCC	55793188 (<i>Helicoverpa assulta</i>)
NL023	1435	CCGAAGATTGTCTGTATTGAA	58585075 (<i>Apis mellifera</i>)
NL023	1436	GACGTCATCGTCGCCCTCCATGCA	91077117 (<i>Tribolium castaneum</i>)
NL027	1437	GGAGACCCTGGAGCTGGTGCG	49543279 (<i>Rhipicephalus appendiculatus</i>)

Table 4-CS

Target ID	SEQ ID NO	Sequence *	Example GI-number and species
CS001	1730	AAAGCATGGATGTTGGACAAA	73619372 (Aphis gossypii); 77325485 (Chironomus tentans); 22474232 (Helicoverpa armigera); 37951951 (Ips pini); 60305420 (Mycetophagus quadripustulatus); 84647995 (Myzus persicae)
CS001	1731	AAAGCATGGATGTTGGACAAACT	40877657 (Bombyx mori); 103783745 (Heliconius erato); 55904580 (Locusta migratoria); 101413238 (Plodia interpunctella)
CS001	1732	AACCGGCTCAAGTACGGCGCTCAC	22474232 (Helicoverpa armigera)
CS001	1733	AACCGGCTCAAGTACGGCGCTCACGGG	90134075 (Bicyclus anynana)
CS001	1734	AAGATCATGGACTTCATCAAGTT	90134075 (Bicyclus anynana)
CS001	1735	ACCAGATTGAACAACGTGTTTCAT	71536878 (Diaphorina citri) 3658573 (Manduca sexta)
CS001	1736	ATCATGGACTTCATCAAGTTTGAATC	103783745 (Heliconius erato)
CS001	1737	CAAGATCATGGACTTCATCAAGTT	3478550 (Antheraea yamamai)
CS001	1738	CCCCACAAGTTGCCGAGTGC	63011732 (Bombyx mori)
CS001	1739	CCCGCTGGATTTATGGATGTTGT	101403940 (Plodia interpunctella)
CS001	1740	CCTCCAAGATCATGGACTTCATCAAGTT	22474232 (Helicoverpa armigera)
CS001	1741	CCTGCCGCTGGTGATCTTCCT	27597800 (Anopheles gambiae)
CS001	1742	CGACGGGCCCCCAAGAACGTGCC	22474232 (Helicoverpa armigera)
CS001	1743	CTCATCAAGGTCAACGACTCC	103783745 (Heliconius erato) 112350001 (Helicoverpa armigera) 101418268 (Plodia interpunctella)
CS001	1744	CTCATCAAGGTCAACGACTCCAGCTCGAC AT	3738704 (Manduca sexta)
CS001	1745	CTCATCAAGGTCAACGACTCCATCCAGCTCGAC ATCGCCACCT	53884106 (Plutella xylostella)
CS001	1746	CTGCCGCTGGTGATCTTCCTC	27603050 (Anopheles gambiae)

CS001	1747	GACCCACATATCCCGCTGGATT	103783745 (Heliconius erato)
CS001	1748	GCAGCGACTTATCAAGTTGA	109978109 (Gryllus pennsylvanicus)
CS001	1749	GCATGGATGTTGGACAAACTGGG	67899746 (Drosophila pseudoobscura)
CS001	1750	GCACCTCCAAGATCATGGACTTCAT	110259010 (Spodoptera frugiperda)
CS001	1751	CGCGTGGCGACGGGCCCAAGAAGTGCC	53884106 (Plutella xylostella)
CS001	1752	GCTGGATTATGGATGTTGTTT	29553519 (Bombyx mori)
CS001	1753	GGCTCAAGTACGGCTCACCGG	5498893 (Antheraea yamamai)
CS001	1754	GTGGGCACCATCGTGTCGCCGCGAG	3953837 (Bombyx mandarina)
CS001	1755	GTGGGCACCATCGTGTCGCCGCGAGCG	53884106 (Plutella xylostella)
CS001	1756	GTGGGCACCATCGTGTCGCCGCGAGCATCCCG	3478550 (Antheraea yamamai)
CS001	1757	TAAAGCATGGATGTTGGACAA	22474232 (Helicoverpa armigera)
CS001	1758	TAAAGCATGGATGTTGGACAAA	58371410 (Lonomia obliqua)
CS001	1759	TAAAGCATGGATGTTGGACAAACT	60311985 (Papilio dardanus)
CS001	1760	TAAAGCATGGATGTTGGACAAACTGGG	31366663 (Toxoptera citricida)
CS001	1761	TACAAAGCTGTGCAAGGTGCGGCGCGTGGCGACGGCCC	109978109 (Gryllus pennsylvanicus)
CS001	1762	TACAAAGCTGTGCAAGGTGCGGCGCGTGGCGGACGGCCCCAA	98994282 (Antheraea mylitta)
CS001	1763	TACCCCGACCCACTCATCAAGGT	98993531 (Antheraea mylitta)
CS001	1764	TGAACAACGTGTTTCATAATCGG	22474232 (Helicoverpa armigera)
CS001	1765	TGCGCGAGTGCCTGCCGCTGGT	60311445 (Euclidia glyphica)
CS001	1766	TGTATGATCACGGGAGGCCGTAACTTGGG	3953837 (Bombyx mandarina)
CS001	1767	TGTATGATCACGGGAGGCCGTAACTTGGGGCG	91826697 (Bombyx mori)
CS001	1768	TGTATGATCACGGGAGGCCGTAACTTGGGGCGCGTGGGCACCATCGTGTCGCCGAG	3478550 (Antheraea yamamai)
CS001	1769	TGTGCAAGGTGCGGCGCGTGGCGACGGGGCCCAAG	3953837 (Bombyx mandarina)
CS001	1770	TTGAACAACGTGTTTCATAATCGGCAAGGGCAGGAA	40915191 (Bombyx mori)
CS002	1771	ATTGAGGCCCAAGGGAAGCGCTAGAAGG	91849872 (Bombyx mori)
CS002	1772	CACGATCTGATGGATGACATTG	33498783 (Anopheles gambiae)

CS002	1773	GAGTTCCTTTAGTAAAGTATTCGGTGG	110762684 (<i>Apis mellifera</i>)
CS002	1774	TATGAAAAGCAGCTTACCCAGAT	49552807 (<i>Rhipicephalus appendiculatus</i>)
CS003	1775	AGGCACATCCGTGTCCGCAAGCA	10707186 (<i>Amblyomma americanum</i>)
CS003	1776	AAGATTGAGGACTTCTTGGA	60295192 (<i>Homalodisca coagulata</i>)
CS003	1777	AAGCACATTGACTTCTCGCTGAA	92219983 (<i>Drosophila willistoni</i>)
CS003	1778	ATCAGACAGAGGCACATCCGTGT	27260897 (<i>Spodoptera frugiperda</i>)
CS003	1779	ATCCGTAAGCTGCCCGTGAG	101413529 (<i>Plodia interpunctella</i>)
CS003	1780	ATCCGTAAGCTGCCCGTGAGCTG	92042852 (<i>Drosophila willistoni</i>)
CS003	1781	ATCCGTAAGCTGCCCGTGAGCTGCT	92959651 (<i>Drosophila ananassae</i>) 112349903 (<i>Helicoverpa armigera</i>)
CS003	1782	ATCCGTAAGCTGCCCGTGAGCTGCTCAC	90138123 (<i>Spodoptera frugiperda</i>)
CS003	1783	CACATCCGTGTCCGCAAGCAAG	60306665 (<i>Sphaerius</i> sp.)
CS003	1784	CACATCCGTGTCCGCAAGCAAGT	77329341 (<i>Chironomus tentans</i>)
CS003	1785	CACATCCGTGTCCGCAAGCAAGTTG	60306676 (<i>Sphaerius</i> sp.)
CS003	1786	CGCAACAAGCGTGAGGTGTGG	92473214 (<i>Drosophila erecta</i>) 67888665 (<i>Drosophila pseudoobscura</i>)
CS003	1787	CGTGTCGCAAGCAAGTTGTGAACATCCC	90134575 (<i>Bicyclus anynana</i>) 29553137 (<i>Bombyx mori</i>)
CS003	1788	CTCGCTGAAGTCTCCGTTCCGCGCGGCGG	3986375 (<i>Antheraea yamamai</i>)
CS003	1789	CTCGGTCTGAAGATTGAGGACTT	112349903 (<i>Helicoverpa armigera</i>) 49532931 (<i>Plutella xylostella</i>)
CS003	1790	CTGGACTCTGGCAAGCACATTGACTTCTC	29553137 (<i>Bombyx mori</i>) 58371398 (<i>Lonomia obliqua</i>)
CS003	1791	GACTTCTCGCTGAAGTCTCCGTTCCGCGGCGG	60312414 (<i>Papilio dardanus</i>)
CS003	1792	GACTTCTCGCTGAAGTCTCCGTTCCGCGGCGG CCG	49532931 (<i>Plutella xylostella</i>)
CS003	1793	GAGGAGAAAGACCCTAAGAGGTTATTGGAAGG TAA	37952462 (<i>Ips pini</i>)
CS003	1794	GATCCGTAAGGCTGCCCGTGA	67568544 (<i>Anoplophora glabripennis</i>)
CS003	1795	GATCCGTAAGGCTGCCCGTGAGCTGCT	67843629 (<i>Drosophila pseudoobscura</i>) 56772258 (<i>Drosophila virilis</i>)
CS003	1796	GATTATGTACTCGGTCTGAAGATTGAGGACTT	101413529 (<i>Plodia interpunctella</i>)
CS003	1797	GGTCTGAAGATTGAGGACTTCTTGGA	2699490 (<i>Drosophila melanogaster</i>)

CS003	1798	GTGTGGAGGGTGAAGTACACGCT	60312414 (Papilio dardanus)
CS003	1799	GTGTTCAAGGCTGGTCTAGCTAAGTC	78230982 (Heliconius erato/himera mixed EST library)
CS003	1800	GTGTTGGATGAGAAAGCAGATGAAGCTCGATTAT GT	112349903 (Helicoverpa armigera)
CS003	1801	TGAAGATTGAGGACTTCTTGGA	3986375 (Antheraea yamamai)
CS003	1802	TGGACTCTGGCAAGCACATTGACTTCTC	78230982 (Heliconius erato/himera mixed EST library)
CS003	1803	TGGATGAGAAGCAGATGAAGCT	60312414 (Papilio dardanus)
CS003	1804	TGGTCTCCGCAACAAGCGTGAGGT	76552467 (Spodoptera frugiperda)
CS003	1805	TGGTCTCCGCAACAAGCGTGAGGTGG	33528372 (Trichoplusia ni)
CS006	1806	CGTATGACAAATTGGTCACCTTGATTGA	91831926 (Bombyx mori)
CS006	1807	GAAGATATGCCCTTTCACCTTGTAAGG	55801622 (Acyrthosiphon pisum)
CS006	1808	GGAAAAACTATAACTTTGCCAGAAAA	40926289 (Bombyx mori)
CS006	1809	GGTGATGCTACACCAATTTAACGATGCTGT	31366154 (Toxoptera citricida)
CS006	1810	TCTCGTATGACAATTGGTCACTTGAT	49201759 (Drosophila melanogaster)
CS006	1811	CTGTCAACGTCAGAAAGATCTC	49573116 (Boophilus microplus)
CS007	1812	TGGATGAATGTGACAAAATGCTTGAA	84114516 (Blomia tropicalis)
CS007	1813	TTTATGCAAGATCCTATGGAAGT	84114516 (Blomia tropicalis)
CS007	1814	AAATTTATGCAAGATCCTATGGAAGTTTATGT	78525380 (Glossina morsitans)
CS007	1815	AATATGACTCAAGATGAGCGTCT	90137538 (Spodoptera frugiperda)
CS007	1816	ATGACTCAAGATGAGCGTCTCTCCCG	103792212 (Heliconius erato)
CS007	1817	ATGCAAGATCCTATGGAAGTTTA	77336752 (Chironomus tentans)
CS007	1818	ATGCAAGATCCTATGGAAGTTTATGT	77873166 (Aedes aegypti)
CS007	1819	CGCTATCAGCAGTTCAAAGATTTCCAGAAG	77873166 (Aedes aegypti)
CS007	1820	GAAAAATGAAAAAGAAATAAGAAG	110759359 (Apis mellifera)
CS007	1821	GAAGTTCAACATGAATGTATTCC	78525380 (Glossina morsitans)
CS007	1822	GATGAGCGTCTCTCCGCTATCA	110759359 (Apis mellifera)
CS007	1823	TGCCAATTCAGAAAGATGAAGAAGT	40932719 (Bombyx mori)
CS007	1824	TGTAAGAAATTTATGCAAGATC	110759359 (Apis mellifera)
CS009	1825	AGGTGTGCGACGTGGACATCA	45244844 (Bombyx mori)
CS009	1826	GACTTGAAGGAGCACATCAGGAA	92460383 (Drosophila erecta)
CS009	1827	GGCCAGAACATCCCAACTGTGA	29534871 (Bombyx mori)
CS009	1828	TCTTGCGAGGGAGAGAATCCA	29534871 (Bombyx mori)
CS009			111005781 (Apis mellifera)

CS011	1829	AAAACTATTGTTTCCACAGAAAAAGAA	86465126 (Bombyx mori)
CS011	1830	ATCAAGGACAGAAAAAGTCAAAGC	78230577 (Heliconius erato/himera mixed EST library)
CS011	1831	ATCTCTGCCAAGTCAAACACAA	101406907 (Plodia interpunctella)
CS011	1832	CAATGTGCCATCATCATGTTTGA	110242457 (Spodoptera frugiperda)
CS011	1833	CCCAACTGGCACAGAGATTAGTGCG	78230577 (Heliconius erato/himera mixed EST library)
CS011	1834	GACACTTGACTGGAGAGTTTCGAGAAAAGATA	101410627 (Plodia interpunctella)
CS011	1835	GATATCAAGGACAGAAAAAGTCAA	60312108 (Papilio dardanus)
CS011	1836	GCCAAGTCAAACACAAATTTTGA	67873076 (Drosophila pseudoobscura)
CS011	1837	GCTGGCCAAAGAAAAAGTTTGGTGGT	111031693 (Apis mellifera)
CS011	1838	GGCCAAAGAAAAAGTTTGGTGGTCTCCG	84267747 (Aedes aegypti)
CS011	1839	TACAAAAATGTACCCAACTGGCA	92963426 (Drosophila grimshawi)
CS011	1840	TACAAAAATGTACCCAACTGGCACAGAGA	37951963 (Ips pini)
CS011	1841	TATGGGATACTGCTGGCCAAAGAA	60312108 (Papilio dardanus)
CS011	1842	TATGGGATACTGCTGGCCAAAGAA	40929360 (Bombyx mori)
CS011	1843	TGGGATACTGCTGGCCAAAGAA	110749704 (Apis mellifera)
CS011	1844	TGTGCCATCATCATGTTCGATGT	73618835 (Aphis gossypii)
CS011	1845	TTGACTGGAGAGTTTCGAGAAA	112432160 (Myzus persicae)
CS011	1846	TTGACTGGAGAGTTTCGAGAAA	84346664 (Aedes aegypti)
CS011	1847	TGGGATACTGCTGGCCAAAGAA	90136305 (Bicyclus anynana)
CS013	1848	GATCCCATTCAGTCTGTCAAAGG	78230577 (Heliconius erato/himera mixed EST library)
CS013	1849	TTCCAAAGCAAAGATGTTGGATATGTTGAA	60312108 (Papilio dardanus)
CS014	1850	AAAAAGATCCAATCTTCGAACATGCTGAA	86465126 (Bombyx mori)
CS014	1851	AAACAAAGTGAACCTCCAGAAAAA	110262261 (Spodoptera frugiperda)
CS014	1852	AAAGTGGGTGAGGACCACGCTACG	21639295 (Sarcophaga scabiei)
CS014	1853	AAGATCAGCAACACTCTGGAGTC	3626535 (Drosophila melanogaster)
CS014	1854	AAGATCAGCAACACTCTGGAGTCTCG	112433067 (Myzus persicae)
CS014	1855	AAGATCCAATCTTCGAACATG	103775905 (Heliconius erato)
			101403826 (Plodia interpunctella)
			87266590 (Choristoneura fumiferana)
			3738660 (Manduca sexta)
			58371699 (Lonomia obliqua)
			91848497 (Bombyx mori)
			77790417 (Aedes aegypti)

CS014	1856	AAGATCCAATCTTCGAACATGCTGAA	91756466 (<i>Bombyx mori</i>)
CS014	1857	AAGCAGATCAAGCATATGATGGCCTTCATCGAA CA	90814338 (<i>Nasonia vitripennis</i>)
CS014	1858	AAGCAGATCAAGCATATGATGGCCTTCATCGAA CAAGAGGC	87266590 (<i>Choristoneura fumiferana</i>)
CS014	1859	ATGATGGCCTTCATCGAAACAAGA	111158385 (<i>Myzus persicae</i>)
CS014	1860	ATGATGGCCTTCATCGAAACAAGAGGC	98993392 (<i>Antheraea mylitta</i>) 91756466 (<i>Bombyx mori</i>) 103775905 (<i>Heliconius erato</i>)
CS014	1861	CAGATCAAGCATATGATGGCCTTCATCGA	53884266 (<i>Plutella xylostella</i>)
CS014	1862	CAGCAGCGGCTCAAGATCATGGAATACTA	101403826 (<i>Plodia interpunctella</i>)
CS014	1863	CATATGATGGCCTTCATCGAAACAAGAGGC	101403826 (<i>Plodia interpunctella</i>)
CS014	1864	CTCAAAGTGCGTGAGGACCAACGT	103775905 (<i>Heliconius erato</i>)
CS014	1865	CTCAAAGATCATGGAATACTACGA	15068660 (<i>Drosophila melanogaster</i>)
CS014	1866	GAAATCGATGCAAAAGGCCGAAGAGGAGTTCAA	103775905 (<i>Heliconius erato</i>)
CS014	1867	GAACTCCAGAAAAAGATCCAATC	76551032 (<i>Spodoptera frugiperda</i>)
CS014	1868	GAACTCCAGAAAAAGATCCAATCTTCGAACATG CTGAA	87266590 (<i>Choristoneura fumiferana</i>)
CS014	1869	GAGGAAATCGATGC AAAAGGCCGA	76551032 (<i>Spodoptera frugiperda</i>)
CS014	1870	GCCGAAGAGGAGTTCAACATTGAAAAAGG	33374540 (<i>Glossina morsitans</i>)
CS014	1871	GCGCCTGGCTGAGGTGCCCAA	101403826 (<i>Plodia interpunctella</i>)
CS014	1872	GCGCGCTGGTGACGACGACGCG	24975647 (<i>Anopheles gambiae</i>)
CS014	1873	GGCTCAAGATCATGGAATACTA	37593557 (<i>Pedicularis humanus</i>)
CS014	1874	GGCTCAAGATCATGGAATACTACGA	58371699 (<i>Lonomia obliqua</i>)
CS014	1875	TACGAAAAAGAAAGAGAAAAACAAGT	33374540 (<i>Glossina morsitans</i>)
CS014	1876	TGAAGGTGCTCAAAGTGCGTGAGGA	92976185 (<i>Drosophila grimshawi</i>) 92994742 (<i>Drosophila mojavensis</i>)
CS014	1877	TTCAAAAGCAGATCAAGCATATGATGGCCTTCA TCGAAACAAGGC	3738660 (<i>Manduca sexta</i>)
CS015	1878	AACGGCCGGAGATCATGTCCAA	92480997 (<i>Drosophila erecta</i>)
CS015	1879	AAC TGCCCCGATGAGAAAGATCCG	91086234 (<i>Tribolium castaneum</i>)
CS015	1880	ATCTTCATCGATGAAC TGGATGC	56152379 (<i>Rhynchosciara americana</i>)
CS015	1881	CATATATTGCCCATTTGATGATTC	58371642 (<i>Lonomia obliqua</i>)
CS015	1882	CTCATGTATGGCCCGCCTGGTACCGG	83423460 (<i>Bombyx mori</i>)

CS015	1883	CTGCCCCGATGAGAAAGATCCGCATGAACCG	92948836 (<i>Drosophila ananassae</i>)
CS015	1884	GAGAAATCCGCATGAACCCGGT	4691131 (<i>Aedes aegypti</i>) 92466521 (<i>Drosophila erecta</i>) 15070638 (<i>Drosophila melanogaster</i>)
CS015	1885	GTACATATATTGCCCATTTGAT	90133859 (<i>Bicyclus anynana</i>)
CS015	1886	TCATCGCACGTGATCGTAATGGC	22474136 (<i>Helicoverpa armigera</i>)
CS015	1887	TTCATGGTTCCGGGGGCATG	29551125 (<i>Bombyx mori</i>)
CS016	1888	AAATCGGTGTACATGTAACTGGGAAACCCACG	55797015 (<i>Acyrtosiphon pisum</i>) 73615307 (<i>Aphis gossypii</i>)
CS016	1889	AAGTTGTCCTCGTGGTCGTCCA	91826756 (<i>Bombyx mori</i>)
CS016	1890	ACAGATCTGGCGCGCAATTTTC	18950388 (<i>Anopheles gambiae</i>) 31206154 (<i>Anopheles gambiae</i> str. PEST)
CS016	1891	ACAGCCTTCATGGCCTGCACGTCCTT	76169888 (<i>Diptoptera punctata</i>) 92953069 (<i>Drosophila ananassae</i>) 92477149 (<i>Drosophila erecta</i>) 8809 (<i>Drosophila melanogaster</i>) 55694467 (<i>Drosophila yakuba</i>)
CS016	1892	ACATCAGAGTGGTCCTTGCGGGTCAT	55694467 (<i>Drosophila yakuba</i>) 110248186 (<i>Spodoptera frugiperda</i>)
CS016	1893	ACCAGCACGTGTTTCTCACACTGGTA	91829127 (<i>Bombyx mori</i>)
CS016	1894	ACCTCCTCACGGCGCGGGACAC	237458 (<i>Heliothis virescens</i>) 27372076 (<i>Spodoptera littoralis</i>)
CS016	1895	ACGACAGCCTTCATGGCCTGCACGTCCTT	67896654 (<i>Drosophila pseudoobscura</i>)
CS016	1896	ACGTAGATCTGTCCCTCAGTGATGA	53883819 (<i>Plutella xylostella</i>)
CS016	1897	AGAGCCTCCGCGTACGAAGACATGTC	53883819 (<i>Plutella xylostella</i>)
CS016	1898	AGCAATGGAGTTTCATCACGTC	60295607 (<i>Homalodisca coagulata</i>)
CS016	1899	AGCAGCTGCCAGCCGATGTCCAG	92953069 (<i>Drosophila ananassae</i>) 92477149 (<i>Drosophila erecta</i>) 55694467 (<i>Drosophila yakuba</i>) 112349870 (<i>Helicoverpa armigera</i>) 237458 (<i>Heliothis virescens</i>) 9713 (<i>Manduca sexta</i>) 110242332 (<i>Spodoptera frugiperda</i>)

CS016	1900	AGCATCTCCTTGGGGAAGATACG	63005818 (<i>Bombyx mori</i>) 92967975 (<i>Drosophila mojavensis</i>) 92938364 (<i>Drosophila virilis</i>) 92231646 (<i>Drosophila willistoni</i>) 237458 (<i>Heliothis virescens</i>)
CS016	1901	AGGGCTTCCTCACCGACGACAGCCTTCATGGC CTG	4680479 (<i>Aedes aegypti</i>)
CS016	1902	ATACCAAGTCTGGATCATTTCTCAGG	60295607 (<i>Homalodisca coagulata</i>)
CS016	1903	ATACGGGACCAAGGGTTGATGGGCTG	92953552 (<i>Drosophila ananassae</i>)
CS016	1904	ATAGCGGAGATACCAAGTCTGGATCAT	237458 (<i>Heliothis virescens</i>) 76554661 (<i>Spodoptera frugiperda</i>)
CS016	1905	ATCTGGCGGCAATTCGTTGTG	83937869 (<i>Lutzomyia longipalpis</i>)
CS016	1906	ATGGCAGACTTCATGAGACGA	55894053 (<i>Locusta migratoria</i>)
CS016	1907	ATGGTGGCCAAATCGGTGTACATGTAACC	92965644 (<i>Drosophila grimshawi</i>)
CS016	1908	ATGGTGGCCAAATCGGTGTACATGTAACCT	92969578 (<i>Drosophila grimshawi</i>)
CS016	1909	ATGGTGGCCAAATCGGTGTACATGTAACCTGG GAAACCAAG	92231646 (<i>Drosophila willistoni</i>)
CS016	1910	ATTCAAGAACAGGCACACGTTCTCCATGGAGCC GTTCTCCTCGAAGTCTGCTTGAAGAA	67841091 (<i>Drosophila pseudoobscura</i>)
CS016	1911	ATTGGGGGACCTTTGTCAATGGGTTTTCC	49395165 (<i>Drosophila melanogaster</i>) 99009492 (<i>Leptinotarsa decemlineata</i>)
CS016	1912	CACACGTTCTCCATGGAGCCGTTCTCCTCGAAG TCCTGCTTGAAGAA	92477818 (<i>Drosophila erecta</i>)
CS016	1913	CACTGGTAGGCCAAGAACTCAGC	4680479 (<i>Aedes aegypti</i>)
CS016	1914	CATCTCCTTGGGGAAGATACG	16899457 (<i>Ctenocephalides felis</i>) 9713 (<i>Manduca sexta</i>)
CS016	1915	CCCTCACCGATGGCAGACTTCAT	4680479 (<i>Aedes aegypti</i>) 92924977 (<i>Drosophila virilis</i>) 110248186 (<i>Spodoptera frugiperda</i>)
CS016	1916	CCGATGGCAGACTTCATGAGACG	71049259 (<i>Oncometopia nigricans</i>)
CS016	1917	CCGTCCTCATGTTACACCCCATGGCGGCGAAG ACGATGGC	33547658 (<i>Anopheles gambiae</i>)
CS016	1918	CCGTTCTCCTCGAAGTCTGCTTGAAGAA	31206154 (<i>Anopheles gambiae</i> str. PEST) 8809 (<i>Drosophila melanogaster</i>)

CS016	1919	CCGTTCTCCTCGAAGTCCTGCTTGAAGAACC	101403557 (<i>Plodia interpunctella</i>)
CS016	1920	CGAGCAATGGAGTTTCATCAGTCGATAGCGGA GATACCAGTCTGGATCAT	27372076 (<i>Spodoptera littoralis</i>)
CS016	1921	CGGCCCGTCTCCATGTTTCACACCCCATGGCGGC GAACACGATGGC	31206154 (<i>Anopheles gambiae</i> str. PEST)
CS016	1922	CGTCCGGGCACCTCCTCACGGGCGGC	18883474 (<i>Anopheles gambiae</i>) 31206154 (<i>Anopheles gambiae</i> str. PEST)
CS016	1923	CGTCCGGGCACCTCCTCACGGGCGGCGACA C	9713 (<i>Manduca sexta</i>) 110248186 (<i>Spodoptera frugiperda</i>)
CS016	1924	CTACAGATCTGGGCGGCAATTC	91826756 (<i>Bombyx mori</i>) 9713 (<i>Manduca sexta</i>) 27372076 (<i>Spodoptera littoralis</i>)
CS016	1925	CTACAGATCTGGGCGGCAATTCGTTGTG	237458 (<i>Heliothis virescens</i>) 76554661 (<i>Spodoptera frugiperda</i>)
CS016	1926	CTCGTAGATGGTGGCCAAATC	53883819 (<i>Plutella xylostella</i>)
CS016	1927	CTCGTAGATGGTGGCCAAATCGGTGTACATGTA	18883474 (<i>Anopheles gambiae</i>) 31206154 (<i>Anopheles gambiae</i> str. PEST)
CS016	1928	CTCGTAGATGGTGGCCAAATCGGTGTACATGTA ACC	92953069 (<i>Drosophila ananassae</i>) 92477818 (<i>Drosophila erecta</i>) 8809 (<i>Drosophila melanogaster</i>) 67896654 (<i>Drosophila pseudoobscura</i>)
CS016	1929	CTCGTAGATGGTGGCCAAATCGGTGTACATGTA ACCTGGAAACCCACG	9713 (<i>Manduca sexta</i>) 110248186 (<i>Spodoptera frugiperda</i>) 27372076 (<i>Spodoptera littoralis</i>)
CS016	1930	GAACAGGCACACCGTTCTCCATGGA	92962756 (<i>Drosophila ananassae</i>)
CS016	1931	GACTCGAATACTGTGCGGTTCTCGTAGTT	87266757 (<i>Choristoneura fumiferana</i>) 9713 (<i>Manduca sexta</i>)
CS016	1932	GACTTCATGAGACGAGACAGGGAAGGCAGCAC GTT	9713 (<i>Manduca sexta</i>)
CS016	1933	GAGATACCAGTCTGGATCATTTTC	92969748 (<i>Drosophila mojavensis</i>)
CS016	1934	GAGATACCAGTCTGGATCATTTTCCTC	92935139 (<i>Drosophila virilis</i>)
CS016	1935	GATGAAGTCTTCTCGAACTTGG	2921501 (<i>Culex pipiens</i>)

CS016	1936	GATGAAGTTCTTCTCTCGAACTTGTTGGT	4680479 (<i>Aedes aegypti</i>) 31206154 (<i>Anopheles gambiae</i> str. PEST) 92953069 (<i>Drosophila ananassae</i>) 92477149 (<i>Drosophila erecta</i>) 8809 (<i>Drosophila melanogaster</i>) 67896654 (<i>Drosophila pseudoobscura</i>) 55694467 (<i>Drosophila yakuba</i>) 112349870 (<i>Helicoverpa armigera</i>) 237458 (<i>Heliothis virescens</i>)
CS016	1937	GATGAAGTTCTTCTCGAACTTGTTGGTGGAACTC GAGGTAGACA	76555122 (<i>Spodoptera frugiperda</i>)
CS016	1938	GATGGGGATCTGCGTGATGGA	101403557 (<i>Plodia interpunctella</i>) 53883819 (<i>Plutella xylostella</i>)
CS016	1939	GCACACGTTCTCCATGGAGCCGTTCTC	104530890 (<i>Belgica antarctica</i>)
CS016	1940	GCCAAATCGGTGTACATGTAACTGGGAAACCA CGTCGTCGGG	91829127 (<i>Bombyx mori</i>)
CS016	1941	GCCAAGAACTCAGCAGCAGTCA	237458 (<i>Heliothis virescens</i>)
CS016	1942	GCCGTCCTCATGTTACACCCCA	83937868 (<i>Lutzomyia longipalpis</i>)
CS016	1943	GCCGTCCTCATGTTACACCCCAT	92965644 (<i>Drosophila grimshawi</i>)
CS016	1944	GCCTGCACGTCCTTACCGATGGCGTAGCA	112349870 (<i>Helicoverpa armigera</i>) 237458 (<i>Heliothis virescens</i>) 110248186 (<i>Spodoptera frugiperda</i>)
CS016	1945	GCCTTCATGGCCCTGCACGTCCTT	39675733 (<i>Anopheles gambiae</i>) 31206154 (<i>Anopheles gambiae</i> str. PEST)
CS016	1946	GCCTTCATGGCCCTGCACGTCCTTACCGATGGC GTAGCA	2921501 (<i>Culex pipiens</i>)
CS016	1947	GCGGCGAACACGATGGCAAAGTT	2921501 (<i>Culex pipiens</i>) 92965644 (<i>Drosophila grimshawi</i>)
CS016	1948	GCGGCGAACACGATGGCAAAGTTGTCCTCGTG	77905105 (<i>Aedes aegypti</i>)
CS016	1949	GCGTACAGCTGTTGGAAACATC	67896654 (<i>Drosophila pseudoobscura</i>)
CS016	1950	GGAATAGGATGGGTGATGTCGTCGTTGGGCAT AGT	110248186 (<i>Spodoptera frugiperda</i>)
CS016	1951	GGAATAGGATGGGTGATGTCGTCGTTGGGCAT AGTCA	27372076 (<i>Spodoptera littoralis</i>)

CS016	1952	GGATGGGTGATGTCGTCGTTGGGCAT	101403557 (<i>Plodia interpunctella</i>)
CS016	1953	GGCAGACCGGCAGCCGAGAAATGGGATCCTT	67841091 (<i>Drosophila pseudoobscura</i>)
CS016	1954	GGCATAGTCAAGATGGGATCTG	92924977 (<i>Drosophila virilis</i>)
CS016	1955	GGCCGTCTCCATGTTACACCCATGGC	101403557 (<i>Plodia interpunctella</i>)
CS016	1956	GGCGGGTAGATCTGTCTGTTGTG	2921501 (<i>Culex pipiens</i>) 92965644 (<i>Drosophila grimshawi</i>) 92924977 (<i>Drosophila virilis</i>)
CS016	1957	GGCGGGTAGATCTGTCTGTTGTGGAGCTGACG GTCTACGTAGATCTGTCCCTCAGT	237458 (<i>Heliothis virescens</i>) 110248186 (<i>Spodoptera frugiperda</i>)
CS016	1958	GGGAAGATACGGAGCAGCTGCCA	60336551 (<i>Homalodisca coagulata</i>)
CS016	1959	GGGTTGATGGGCTGTCCCTGGATGTCCAA	76554661 (<i>Spodoptera frugiperda</i>) 27372076 (<i>Spodoptera littoralis</i>)
CS016	1960	GGTTTTCCAGAGCCGTTGAATAC	62238871 (<i>Diabrotica virgifera</i>)
CS016	1961	GTGATGAAGTTCTTCTCGAACTTGGT	87266757 (<i>Choristoneura fumiferana</i>)
CS016	1962	GTGCGGTTCTCGTAGTTGCCCTG	31206154 (<i>Anopheles gambiae</i> str. PEST) 92477149 (<i>Drosophila erecta</i>) 8809 (<i>Drosophila melanogaster</i>) 67896654 (<i>Drosophila pseudoobscura</i>) 92938364 (<i>Drosophila virilis</i>) 92231646 (<i>Drosophila willistoni</i>) 55694467 (<i>Drosophila yakuba</i>)
CS016	1963	GTGGCCAAATCGGTGTACATGTAACC	2921501 (<i>Culex pipiens</i>) 75469507 (<i>Tribolium castaneum</i>)
CS016	1964	GTGTACATGTAACCTGGGAAACCACG	101403557 (<i>Plodia interpunctella</i>)
CS016	1965	GTGTACATGTAACCTGGGAAACCACGTCG	237458 (<i>Heliothis virescens</i>)
CS016	1966	GTGTACATGTAACCTGGGAAACCACGTCGTCC GGGCACCTCCTCACGGCGGC	53883819 (<i>Plutella xylostella</i>)
CS016	1967	TCAGAGTGGTCTTTCGCGGTGAT	237458 (<i>Heliothis virescens</i>) 9713 (<i>Manduca sexta</i>)
CS016	1968	TCAGCAAGGATTGGGGACCTTTTGTG	10763875 (<i>Manduca sexta</i>)
CS016	1969	TCCTCACCAGACGACAGCCTTCATGGCCTG	92969578 (<i>Drosophila grimshawi</i>)
CS016	1970	TCCTCAGGGTAGATACGGGACCA	76554661 (<i>Spodoptera frugiperda</i>)

CS016	1971	TCCTCAGGGTAGATACGGGACCAGGGGTTGAT GGGCTG	22474040 (Helicoverpa armigera) 237458 (Heliothis virescens) 9713 (Manduca sexta)
CS016	1972	TCGAAGTCCTGCTTGAAGAACC	9713 (Manduca sexta)
CS016	1973	TCGTAGATGGTGGCCAAATCGGTGTACATGTAA CC	62239897 (Diabrolica virgifera)
CS016	1974	TCGTAGATGGTGGCCAAATCGGTGTACATGTAA CCTGGGAAACACG	4680479 (Aedes aegypti)
CS016	1975	TCTACGTAGATCTGTCCCTCAGTGATGTA	101403557 (Plodia interpunctella)
CS016	1976	TGCACGTCTTACCGATGGCGTAGCA	9713 (Manduca sexta) 75710699 (Tribolium castaneum)
CS016	1977	TGGGTGATGTCGTCGTTGGGCAT	53883819 (Plutella xylostella)
CS016	1978	TGGTAGGCCAAAGAACTCAGCAGC	9713 (Manduca sexta)
CS016	1979	TTCAAGAACAGGCACACGTTCTCCAT	18883474 (Anopheles gambiae) 31206154 (Anopheles gambiae str. PEST) 92933153 (Drosophila virilis) 27372076 (Spodoptera littoralis)
CS016	1980	TTCAAGAACAGGCACACGTTCTCCATGGA	92950254 (Drosophila ananassae) 76554661 (Spodoptera frugiperda)
CS016	1981	TTCTCACACTGGTAGGCCAAGAA	18883474 (Anopheles gambiae)
CS016	1982	TTCTCCTCGAAGTCCTGCTTGAAGAA	83937868 (Lutzomyia longipalpis)
CS016	1983	TTGAGCATCTCCTTGGGGAAGATACG	92477149 (Drosophila erecta) 8809 (Drosophila melanogaster) 67896654 (Drosophila pseudoobscura) 112349870 (Helicoverpa armigera)
CS016	1984	TTGAGCATCTCCTTGGGGAAGATACGGAGCA	83928466 (Lutzomyia longipalpis)
CS016	1985	TTGAGCATCTCCTTGGGGAAGATACGGAGCAG CTGCCA	50559098 (Homalodisca coagulata) 71049259 (Oncometopia nigricans)
CS016	1986	TTGAGCATCTCCTTGGGGAAGATACGGAGCAG CTGCCAGCCGATGC	87266757 (Choristoneura fumiferana)
CS018	1987	TCCGACTACTCTTCCACGGAC	31659029 (Anopheles gambiae)

Table 4-PX

Target ID	SEQ ID NO	Sequence *	Example Gi-number and species
PX001	2120	AACAACGTGTTTCATCATCGGCAAGGCGACGAA	112350001 (Helicoverpa armigera)
PX001	2121	AACGTGTTTCATCATCGGCAAG	27562760 (Anopheles gambiae) 58378595 (Anopheles gambiae str. PEST)
PX001	2122	AACGTGTTTCATCATCGGCAAGG	42764924 (Armigeres subalbatus)
PX001	2123	AACGTGTTTCATCATCGGCAAGGG	71048604 (Oncometopia nigrigans)
PX001	2124	AACGTGTTTCATCATCGGCAAGGCGACGAA	112783858 (Anopheles funestus)
PX001	2125	AAC TTGGGCGAGTGGCAACCATCGTGTC	90132259 (Bicyclus anynana)
PX001	2126	AAC TTGGGCGAGTGGCAACCATCGTGTCGCGGAG	112350001 (Helicoverpa armigera)
PX001	2127	AAGATCGTGAAGCAGCGCCTCATCAAGGTGGACGGCAAGGT	112350001 (Helicoverpa armigera)
PX001	2128	AAGTCCGCACCGACCCCAACCTA	14627585 (Drosophila melanogaster)
PX001	2129	AAGTACAAGCTGTGCAAGGTG	5498893 (Antheraea yamamai) 90132259 (Bicyclus anynana) 92969396 (Drosophila grimshawi) 50818668 (Heliconius melpomene) 58371410 (Lonomia obliqua)
PX001	2130	ACAACGTGTTTCATCATCGGCAAGGCGACGAA	103783745 (Heliconius erato)
PX001	2131	ACGGCAAGGTCCGCACCGACCC	77890923 (Aedes aegypti)
PX001	2132	ACGGCCGCACGCTGCGCTACCCCGACCCGCTCATCAAGGTC AAGCACTCC	101413238 (Plodia interpunctella)
PX001	2133	ACGTGTTTCATCATCGGCAAGGCGCAC	109509107 (Culex pipiens)
PX001	2134	AGGAGGCCAAGTACAAGCTGT	27566312 (Anopheles gambiae) 67889891 (Drosophila pseudoobscura)
PX001	2135	AGGAGGCCAAGTACAAGCTGTGCAAGGT	92944919 (Drosophila ananassae) 67886177 (Drosophila pseudoobscura) 92045792 (Drosophila willistoni)
PX001	2136	AGGAGGCCAAGTACAAGCTGTGCAAGGTG	92929731 (Drosophila virilis)
PX001	2137	CAACGTGTTTCATCATCGGCAA	109509107 (Culex pipiens)
PX001	2138	CAACGTGTTTCATCATCGGCAAGGGCA	55816641 (Drosophila yakuba)
PX001	2139	CACACCTTCGCCACCCAGGTTGAACAACGTGTT	3986403 (Antheraea yamamai)
PX001	2140	CCCCAAGAAGCAATTGAAGCG	2886669 (Drosophila melanogaster)
PX001	2141	CCGAGGAGGCCCAAGTACAAGCT	92944919 (Drosophila ananassae)

PX001	2142	CCGAGGAGGCCAAAGTACAAGCTGTGCAAGGT	15480750 (<i>Drosophila melanogaster</i>)
PX001	2143	CCGCACAAAGCTGCGGAGTGCCCTGCCGCT	22474232 (<i>Helicoverpa armigera</i>)
PX001	2144	CGACGGGCCCCAAGAACGTGCC	112350001 (<i>Helicoverpa armigera</i>)
PX001	2145	CGAGGAGGCCAAGTACAAGCT	58378595 (<i>Anopheles gambiae</i> str. PEST)
PX001	2146	CGAGGAGGCCAAGTACAAGCTG	18914191 (<i>Anopheles gambiae</i>)
PX001	2147	CGAGTGGCACCATCGTGTCCCGCGAG	3986403 (<i>Antheraea yamamai</i>)
PX001	2148	CGTACCCCGACCCGCTCATCAAGTCAACGACTCC	112350001 (<i>Helicoverpa armigera</i>)
PX001	2149	CGCTTACCATCCACCGCATCAC	103783745 (<i>Heliconius erato</i>)
PX001	2150	CGGCAACGAGGTGCTGAAGATCGT	90132259 (<i>Bicyclus anynana</i>)
PX001	2151	CGTAACCTGGGCGAGTGGGCAC	60311985 (<i>Papilio dardanus</i>)
PX001	2152	CTACCCGGCTGGATTTCATGGATGT	42764924 (<i>Armigeres subalbatus</i>)
PX001	2153	CTCATCAAGGTCAACGACTCC	103783745 (<i>Heliconius erato</i>)
PX001	2154	CTCATCAAGGTCAACGACTCCATCCAGCTCGACAT	3738704 (<i>Manduca sexta</i>)
PX001	2155	GACGGCAAGGTCCGCACCGAC	109509107 (<i>Culex pipiens</i>)
PX001	2156	GACGGCAAGGTCCGCACCGACCC	77759638 (<i>Aedes aegypti</i>)
PX001	2157	GAGGAGGCCAAGTACAAGCTGTGCAAGGT	67841491 (<i>Drosophila pseudoobscura</i>)
PX001	2158	GAGGAGGCCAAGTACAAGCTGTGCAAGGTG	56772971 (<i>Drosophila virilis</i>)
PX001	2159	GAGGCCAAGTACAAGCTGTGCAA	112350001 (<i>Helicoverpa armigera</i>)
PX001	2160	GAGGCCAAGTACAAGCTGTGCAAGGTG	98993531 (<i>Antheraea mylitta</i>)
PX001	2161	GCCAAGTACAAGCTGTGCAAGGT	67838306 (<i>Drosophila pseudoobscura</i>)
PX001	2162	GCCCCAAGAAGCATTTGAAGCG	109978109 (<i>Gryllus pennsylvanicus</i>)
PX001	2163	GCGCGTGCGACGGGCCCCCAA	2151718 (<i>Drosophila melanogaster</i>)
PX001	2164	GCGCGTGCGACGGGCCCCCAAAG	5498893 (<i>Antheraea yamamai</i>)
PX001	2165	GGAGGCCAAGTACAAGCTGTGCAAGGT	3986403 (<i>Antheraea yamamai</i>)
PX001	2166	GGCCCCAAGAAGCATTTGAAGCG	92942537 (<i>Drosophila ananassae</i>)
PX001	2167	GGCGCGGTGTACGCGCCCGGCCCC	4459798 (<i>Drosophila melanogaster</i>)
PX001	2168	GTCCGCACCCGACCCCCACCTACCC	98994282 (<i>Antheraea mylitta</i>)
PX001	2169	GTGGGCACCATCGTGTCCCGCGAGAG	92472430 (<i>Drosophila erecta</i>)
PX001	2170	TCAAGGTGGACGGCAAGGTCCGCACCGACCC	55854272 (<i>Drosophila yakuba</i>)
PX001	2171	TGATCTACGATGTGAAGGGACG	3953837 (<i>Bombyx mandarina</i>)
			29554802 (<i>Bombyx mori</i>)
			92944919 (<i>Drosophila ananassae</i>)
			83935965 (<i>Lutzomyia longipalpis</i>)

PX001	2172	TCATGGATGTTGTGTCGATTGAAA	90132259 (<i>Bicyclus anynana</i>)
PX001	2173	GCTGGATTCATGGATGTTGTG	10707240 (<i>Amblyomma americanum</i>)
PX001	2174	AAGCAGCGCCTCATCAAGGTGGACGGCAAGTCCGCACCCGA C	49545866 (<i>Rhipicephalus appendiculatus</i>)
PX009	2175	AACATCTTCAACTGTGACTTC	93001544 (<i>Drosophila mojavensis</i>)
PX009	2176	TGATCAACATCGAGTGCAAAGC	110755556 (<i>Apis mellifera</i>)
PX009	2177	TTCTTGAAGCTGAATAAGATCT	103750396 (<i>Drosophila melanogaster</i>)
PX010	2178	CAGTTCCTGCAGGTCCTCAACAA	71553175 (<i>Oncometopia nigricans</i>)
PX010	2179	CCATCAGCGGACGGTGGCCCCCGTG	90139187 (<i>Spodoptera frugiperda</i>)
PX010	2180	CCGCAGTTTCATGTACCACTGCGCGCTCGCAGTTC	67893194 (<i>Drosophila pseudoobscura</i>)
PX010	2181	CCGAACAGCTTCGGTCTGTGCGAGAACTTCAG	29558345 (<i>Bombyx mori</i>)
PX010	2182	CGCCTGTGCCAGAAAGTTCGGCGAGTACG	58395529 (<i>Anopheles gambiae</i> str. PEST)
PX010	2183	CTGCGCCGCTCGCAGTTCCTGCAGGT	18872210 (<i>Anopheles gambiae</i>)
PX010	2184	CTGTACCCGCGAGTTTCATGTACCA	29558345 (<i>Bombyx mori</i>)
PX010	2185	GACGTGCTGCGCTGGCTCGACCG	29558345 (<i>Bombyx mori</i>)
PX010	2186	GACGTGCTGCTGCAAGTGTTCATGGAGCA	18872210 (<i>Anopheles gambiae</i>)
PX010	2187	GAGTACGAGAACTTCAAGCAGCTGCTGC	77886140 (<i>Aedes aegypti</i>) 18872210 (<i>Anopheles gambiae</i>) 49376735 (<i>Drosophila melanogaster</i>) 67893324 (<i>Drosophila pseudoobscura</i>)
PX010	2188	GGCGGGCGGATGCCGATACCATC	91757875 (<i>Bombyx mori</i>)
PX010	2189	GTGGCTGCATACAGTTTCATTACGCAGTACCAGCAC	28571527 (<i>Drosophila melanogaster</i>)
PX010	2190	TCGCAGTTCCTGCAGGTCCTCAACAA	92932090 (<i>Drosophila virilis</i>)
PX010	2191	TGCGCCGCTCGCAGTTCCTGCAGGTCCTCAACAA	67893324 (<i>Drosophila pseudoobscura</i>)
PX010	2192	TGCGCCGCTCGCAGTTCCTGCAGGTCCTCAACAACTCGCCC GACGAGACCA	92952825 (<i>Drosophila ananassae</i>)
PX010	2193	TTTCATGTACCACTGCGCGCTCGCAGTTCCTGCAGGTCCTC AACAACTGCCCCGACGAGACCA	28571527 (<i>Drosophila melanogaster</i>)
PX010	2194	ATCCTGCTCATGGACACCTTCTTCCA	82842646 (<i>Boophilus microplus</i>)
PX015	2195	CACCGCGACGACAGCTTCATGTGCGCGCGCGG	58371643 (<i>Lonomia obliqua</i>)
PX015	2196	CAGATCAAGGAGATGGTGGAG	92480997 (<i>Drosophila erecta</i>) 58371722 (<i>Lonomia obliqua</i>)
PX015	2197	CCCACGAGAAAGATCCGCATGAA	67873606 (<i>Drosophila pseudoobscura</i>)

PX015	2198	CCCGACGAGAAGATCCGCATGAACCCGCT	15070733 (<i>Drosophila melanogaster</i>)
PX015	2199	CCGACGAGAAGATCCGCATGAACCCGCT	92459970 (<i>Drosophila erecta</i>)
PX015	2200	CGCAAGGAGACCCGTGTGCATTGTGCT	67873506 (<i>Drosophila pseudoobscura</i>)
PX015	2201	GACGAGAAGATCCGCATGAACCCG	18914444 (<i>Anopheles gambiae</i>)
PX015	2202	GACGAGAAGATCCGCATGAACCCGCT	4691131 (<i>Aedes aegypti</i>)
PX015	2203	GCGCAGATCAAGGAGATGGTGGAGCT	99007898 (<i>Leptinotarsa decemlineata</i>)
PX015	2204	GGCATGCGCGCCGTCGAGTTC	6901917 (<i>Bombyx mori</i>)
PX015	2205	GTGCGCGCGGCATGCGCGCC	67891252 (<i>Drosophila pseudoobscura</i>)
PX015	2206	TCAAGGAGATGGTGGAGCTGC	27819993 (<i>Drosophila melanogaster</i>)
PX015	2207	TGAAGCCGTACTTCATGGAGGC	29559940 (<i>Bombyx mori</i>)
PX015	2208	TGCCGCAAGCAGCTGGCGCAGATCAAGGAGATGGT	18914444 (<i>Anopheles gambiae</i>)
PX015	2209	TGGAGGCGTACCGGCCCATCCAC	18914444 (<i>Anopheles gambiae</i>)
PX016	2210	AAGGACCACTCCGACGTGTCCAA	101406307 (<i>Plodia interpunctella</i>)
PX016	2211	AAGGACGTGCAGGCGGATGAAGGC	112349870 (<i>Helicoverpa armigera</i>) 110248186 (<i>Spodoptera frugiperda</i>)
PX016	2212	ACCAAGTTCGAGAAGAACTTCATC	4680479 (<i>Aedes aegypti</i>) 31206154 (<i>Anopheles gambiae</i> str. PEST) 92953069 (<i>Drosophila ananassae</i>) 92477149 (<i>Drosophila erecta</i>) 24646340 (<i>Drosophila melanogaster</i>) 67900295 (<i>Drosophila pseudoobscura</i>) 55694467 (<i>Drosophila yakuba</i>) 112349870 (<i>Helicoverpa armigera</i>) 237458 (<i>Heliothis virescens</i>)
PX016	2213	ACCAAGTTCGAGAAGAACTTCATCAC	87266757 (<i>Choristoneura fumiferana</i>)
PX016	2214	ACCGCCAGGTTCTTCAAGCAGGACTTCGA	9713 (<i>Manduca sexta</i>)
PX016	2215	ACCGCGATATTCTGCGCACGCCGCTCTC	92940287 (<i>Drosophila virilis</i>)
PX016	2216	AGCAGGACTTCGAGGAGAACGG	67880606 (<i>Drosophila pseudoobscura</i>)
PX016	2217	ATCAGCGAGATCCCCATCTGACCATGCC	31206154 (<i>Anopheles gambiae</i> str. PEST)
PX016	2218	ATCTTGACCCGACATGTCTTCATACGC	104530890 (<i>Belgica antarctica</i>) 92231646 (<i>Drosophila willistoni</i>)
PX016	2219	ATGACCAGGAAGGACCACCTCCGACGT	75713096 (<i>Tribolium castaneum</i>)

PX016	2220	ATGCCCAACGACGACATCACCCA	101406307 (Plodia interpunctella) 76555122 (Spodoptera frugiperda) 27372076 (Spodoptera littoralis)
PX016	2221	CAGAAAGATCCCCCATCTTCTCCGCCCGCGGTCTGCCCCACAA CGA	92460896 (Drosophila erecta) 24646340 (Drosophila melanogaster)
PX016	2222	CAGGACTTCGAGGAGAACGGTTCATGGAGAACGT	2921501 (Culex pipiens) 76554661 (Spodoptera frugiperda)
PX016	2223	CCAAGTTCGAGAAGAACTTCATC	2921501 (Culex pipiens)
PX016	2224	CCCATCAACCCGGTGGTCCCGTATCTACCCGGAGGA	2921501 (Culex pipiens)
PX016	2225	CCCGACTTGACCCGGGTACATCACTGAGGGACAGATCTACGT	101406307 (Plodia interpunctella)
PX016	2226	CCCGGACGACGTGGTTTCCAGGTTACATGTACAC	91829127 (Bombyx mori)
PX016	2227	CCTGGACATCCAGGGGCAGCCCATCAACCC	91090030 (Tribolium castaneum)
PX016	2228	CGACGTGGTTTCCAGGTTACATGTACACGGATTGGC	237458 (Heliothis virescens)
PX016	2229	CGTCTCATGAAGTCCGCCATCGG	91829127 (Bombyx mori)
PX016	2230	CGTCTCATGAAGTCCGCCATCGGAGAGGGCATGACC	237458 (Heliothis virescens)
PX016	2231	CGTGGTCAGAAGATCCCCATCTTCTC	27372076 (Spodoptera littoralis)
PX016	2232	CGTGGTCAGAAGATCCCCATCTTCTCCGC	76554661 (Spodoptera frugiperda)
PX016	2233	CGTGTTTCCCAGGTTACATGTACACGGATTGGCCACAATC	55797015 (Acyrtosiphon pisum) 4680479 (Aedes aegypti) 73615307 (Aphis gossypii) 92231646 (Drosophila willistoni) 9713 (Manduca sexta) 76555122 (Spodoptera frugiperda) 27372076 (Spodoptera littoralis)
PX016	2234	CGTGTTTCCCAGGTTACATGTACACGGATTGGCCACAATC TACGAGCGCGCGGGCG	101406307 (Plodia interpunctella)
PX016	2235	CTACGAGAACC GCACAGTGTTCCGATC	112350031 (Helicoverpa armigera) 237458 (Heliothis virescens) 76555122 (Spodoptera frugiperda)

PX016	2236	CTGCGTATCTTCCCCAAGGAGAT	63005818 (Bombyx mori) 92477149 (Drosophila erecta) 24646340 (Drosophila melanogaster) 56773982 (Drosophila pseudoobscura) 92935600 (Drosophila virilis) 92220609 (Drosophila willistoni) 112350031 (Helicoverpa armigera) 237458 (Heliothis virescens) 9713 (Manduca sexta)
PX016	2237	CTGTACGCGTGCTAGGCCATCGG	9713 (Manduca sexta)
PX016	2238	CTGTTCTTGAACITGGCCAAATGA	16898595 (Ctenocephalides felis)
PX016	2239	CTGTTCTTGAACITGGCCAAATGACCC	27372076 (Spodoptera littoralis)
PX016	2240	GACAACTTCGCCCATCGTGTTCGC	92950254 (Drosophila ananassae)
PX016	2241	GACAACTTCGCCCATCGTGTTCGCCGC	92477818 (Drosophila erecta) 24646340 (Drosophila melanogaster) 237458 (Heliothis virescens) 9713 (Manduca sexta) 76554661 (Spodoptera frugiperda)
PX016	2242	GACAACTTCGCCCATCGTGTTCGCCCATGGG	31206154 (Anopheles gambiae str. PEST)
PX016	2243	GACCGTCAGCTGCACAACAGGCA	50564193 (Homalodisca coagulata)
PX016	2244	GACCTGCTCTACCTCGAGTTC	112349870 (Helicoverpa armigera)
PX016	2245	GACGTGATGAACCTCCATCGCCCG	237458 (Heliothis virescens)
PX016	2246	GACGTGATGAACCTCCATCGCCCGTGG	22474040 (Helicoverpa armigera)
PX016	2247	GAGAACGGTTCCATGGAGAACGT	91829127 (Bombyx mori)
PX016	2248	GAGGAGATGATCCAGACTGGTATCTCTCCGCTAT	237458 (Heliothis virescens) 76554661 (Spodoptera frugiperda)
PX016	2249	GAGGAGATGATCCAGACTGGTATCTCTCCGCTATCGACGTGATG AACTCCAT	27372076 (Spodoptera littoralis)
PX016	2250	GAGGAGGCGCTACGCCCGACGAC	9713 (Manduca sexta)
PX016	2251	GAGTTCITGGCCTACCAAGTGCAGAA	4680479 (Aedes aegypti)
PX016	2252	GCCAGGTCTTCAAGCAGGACTTCGAGGAGAACGG	101403557 (Plodia interpunctella)
PX016	2253	GCCCGTGGTCAGAAGATCCCCAT	67877903 (Drosophila pseudoobscura)
PX016	2254	GCCCGTGGTCAGAAGATCCCCATCTTCTC	6901845 (Bombyx mori)

PX016	2255	GCCCGTGGTCAGAAAGATCCCCATCTTCTCCGCCGC	92950254 (<i>Drosophila ananassae</i>)
PX016	2256	GCCGAGTTCTTGGCCTACCAAGTCCGAGAA	24646340 (<i>Drosophila melanogaster</i>)
PX016	2257	GCCGAGTTCTTGGCCTACCAAGTCCGAGAAACACGTTTGGT	110240379 (<i>Spodoptera frugiperda</i>)
PX016	2258	GCCGCCCGTGAGGAGGTGCCCGGACG	31206154 (<i>Anopheles gambiae</i> str. PEST) 9713 (<i>Manduca sexta</i>) 110240379 (<i>Spodoptera frugiperda</i>)
PX016	2259	GCCTACCAAGTCCGAGAAACACGTTGTTGGTAATCTTGACCCGAC ATGTC	101406307 (<i>Plodia interpunctella</i>)
PX016	2260	GGCAGATCTACCCGCCCGGTGAA	31206154 (<i>Anopheles gambiae</i> str. PEST)
PX016	2261	GGCGAGGAGGCGCTCACGCCCGACGA	31206154 (<i>Anopheles gambiae</i> str. PEST)
PX016	2262	GGTCAGAAAGATCCCCATCTTCTC	60295607 (<i>Homalodisca coagulata</i>)
PX016	2263	GGTTACATGTACACGGATTGGCCAC	92924977 (<i>Drosophila virilis</i>)
PX016	2264	GTGGTGGCGGAGGAGGCGCTCACGCC	112349870 (<i>Helicoverpa armigera</i>)
PX016	2265	GTTACCCGGCGATATTCTGCG	92997483 (<i>Drosophila grimshawi</i>)
PX016	2266	GTTACCCGGCGATATTCTGCGCAC	92950254 (<i>Drosophila ananassae</i>) 92048971 (<i>Drosophila willistoni</i>)
PX016	2267	TACCAGTCCGAGAAACACGTTTGGT	237458 (<i>Heliothis virescens</i>)
PX016	2268	TACGCCATCGGCAAGGACGTGCAGGCCGATGAAGGC	87266757 (<i>Choristoneura fumiferana</i>)
PX016	2269	TCCATCACGCAGATCCCCATCCT	101406307 (<i>Plodia interpunctella</i>)
PX016	2270	TCCGGCAAGCCCCATCGACAAGGG	92460896 (<i>Drosophila erecta</i>) 24646340 (<i>Drosophila melanogaster</i>) 22474040 (<i>Helicoverpa armigera</i>) 237458 (<i>Heliothis virescens</i>)
PX016	2271	TCTACGAGCGCGCGGGCGAGTC	33528180 (<i>Trichoplusia ni</i>)
PX016	2272	TCTCGTCTCATGAAGTCCGCCATCGG	9713 (<i>Manduca sexta</i>)
PX016	2273	TGACTGCTGCCGAGTTCTTGGCCTACCAGTGCAGAGAAACAC GTGTTGGT	27372076 (<i>Spodoptera littoralis</i>)
PX016	2274	TGCACAACAGGCAGATCTACCC	62239897 (<i>Diabrotica virgifera</i>)
PX016	2275	TGCGTATCTTCCCCAAGGAGAT	16900620 (<i>Ctenocephalides felis</i>) 92967975 (<i>Drosophila mojavensis</i>)

PX016	2276	TGCTACGCCCATCGGCAAGGACGTGCAGGC	31206154 (Anopheles gambiae str. PEST) 92953069 (Drosophila ananassae) 92477149 (Drosophila erecta) 24646340 (Drosophila melanogaster) 67898824 (Drosophila pseudoobscura) 55694467 (Drosophila yakuba)
PX016	2277	TGCTCTACCTCGAGTTCCTCACCCAAGTTCGAGAAAGAACTTCA TC	76555122 (Spodoptera frugiperda)
PX016	2278	TGCTCTGTTCTTGAACCTTGGCCAA	4680479 (Aedes aegypti) 92477818 (Drosophila erecta) 24646340 (Drosophila melanogaster)
PX016	2279	TGCTCTGTTCTTGAACCTTGGCCAATGA	55905051 (Locusta migratoria)
PX016	2280	TGTTCTTGAACCTTGGCCAATGA	91090030 (Tribolium castaneum)
PX016	2281	TTC AACGGCTCCGGCAAGCCCAT	76554661 (Spodoptera frugiperda)
PX016	2282	TTC AACGGCTCCGGCAAGCCCATCGACAAGGG	4680479 (Aedes aegypti) 31206154 (Anopheles gambiae str. PEST) 67877903 (Drosophila pseudoobscura)
PX016	2283	TTCGAGGAGAACGGTTCCTCATGGAGAA	92972277 (Drosophila grimshawi)
PX016	2284	TTCGAGGAGAACGGTTCCTCATGGAGAACGT	92950254 (Drosophila ananassae)
PX016	2285	TTCCTCAAGCAGGACTTCGAGGAGAA	83937868 (Lutzomyia longipalpis)
PX016	2286	TTCCTCAAGCAGGACTTCGAGGAGAACGG	92477818 (Drosophila erecta)
PX016	2287	TTCCTCAAGCAGGACTTCGAGGAGAACGGTTC	31206154 (Anopheles gambiae str. PEST)
PX016	2288	TTCCTCAAGCAGGACTTCGAGGAGAACGGTTCATGGAGAAC GT	24646340 (Drosophila melanogaster)
PX016	2289	TTCCTGAACCTTGGCCAATGACCC	9713 (Manduca sexta)
PX016	2290	TTCCTGGCCTACCAGTGCGAGAA	31206154 (Anopheles gambiae str. PEST) 67883622 (Drosophila pseudoobscura) 92231646 (Drosophila willistoni)

Table 4-AD

Target ID	SEQ ID NO	Sequence *	Example Gi-number and species
AD001	2384	AAAGCATGGATGTTGGACAAA	73619372 (Aphis gossypii); 77325485 (Chironomus tentans); 22474232 (Helicoverpa armigera); 37951951 (Ips pini); 60305420 (Mycetophagus quadripustulatus); 84647995 (Myzus persicae)
AD001	2385	AAAGCATGGATGTTGGACAAACT	94432102 (Bombyx mori); 103790417 (Heliconius erato); 55904580 (Locusta migratoria); 101419954 (Plodia interpunctella)
AD001	2386	AAAGGTATTCATTCTTGGTGACCCATGATGGCC GTACTATCCGTTATCTCTGACCCAGTCATTAAAGT	109978109 (Gryllus pennsylvanicus)
AD001	2387	AACTGTGAAGTAACGAAGATTGTTATGCAGCGACT TATCAAAGTTGA	109978109 (Gryllus pennsylvanicus)
AD001	2388	AAGAAGCATTTGAAGCGTTTAAA	3658572 (Manduca sexta)
AD001	2389	AAGGGTAAGGGTGTAATTTAGTAT	109978109 (Gryllus pennsylvanicus)
AD001	2390	AATGTATTCATCATTTGGAAAAGC	55904577 (Locusta migratoria)
AD001	2391	AGAAGCATTTGAAGCGTTTAAA	98994282 (Antheraea mylitta) 73619372 (Aphis gossypii)
AD001	2392	AGAAGCATTTGAAGCGTTTAAATGC	27620566 (Anopheles gambiae)
AD001	2393	AGTACTGGCCCCACAAATTGCG	109978109 (Gryllus pennsylvanicus)
AD001	2394	AGTGCAGAAGAACCCAAAGTACAAGCT	109978109 (Gryllus pennsylvanicus)
AD001	2395	ATCGCCGAGGAGCGGGACAAAGC	3953837 (Bombyx mandarina) 94432102 (Bombyx mori)
AD001	2396	CAAGGACATACCTTTTCCACAAAGATTGAATAATGT ATTCATCATTTGGAAA	109978109 (Gryllus pennsylvanicus)
AD001	2397	CAGAAGAAGCCAAAGTACAAGCT	42764924 (Armigeres subalbatus)
AD001	2398	CATGATGGCCGTACTATCCGTTA	73613065 (Aphis gossypii)
AD001	2399	CATGATGGCCGTACTATCCGTTATCCTGACCC	31365398 (Toxoptera citricida)
AD001	2400	CATTGAAGCGTTTAAATGCTCC	27557322 (Anopheles gambiae)

AD001	2401	CCTAAAGCATGGATGTTGGAC	77324536 (<i>Chironomus tentans</i>)
AD001	2402	CCTAAAGCATGGATGTTGGACAA	58371410 (<i>Lonomia obliqua</i>)
AD001	2403	CCTAAAGCATGGATGTTGGACAAA	60311985 (<i>Papilio dardanus</i>)
			30031258 (<i>Toxoptera citricida</i>)
AD001	2404	CCTAAAGCATGGATGTTGGACAAACT	98994282 (<i>Antheraea mylitta</i>)
AD001	2405	CGTACTATCCGTTATCCTGACCC	37804548 (<i>Rhopalosiphum padi</i>)
AD001	2406	GAATGTTTACCTTTGGTGATTTTCTTCGCAATCG GCT	109978109 (<i>Gryllus pennsylvanicus</i>)
AD001	2407	GCAGAAGAAGCCCAAGTACAAGCT	37953169 (<i>Ips pini</i>)
AD001	2408	GCATGGATGTTGGACAAACTCGG	83935968 (<i>Lutzomyia longipalpis</i>)
AD001	2409	GCTGGTTTCATGGATGTTGTAC	109978109 (<i>Gryllus pennsylvanicus</i>)
AD001	2410	GGCCCCAAGAACCATTTGAAGCGTTTAA	14693528 (<i>Drosophila melanogaster</i>)
AD001	2411	GGTTTCATGGATGTTGTACCCAT	25958683 (<i>Curculio glandium</i>)
AD001	2412	TATGATGTGAAGGCCGTTTCACAAATTCACAGAAT	109978109 (<i>Gryllus pennsylvanicus</i>)
AD001	2413	TCATTGCCAAAGGGTAAAGGGT	77324972 (<i>Chironomus tentans</i>)
AD001	2414	TGGATATTGCCACTTGTAAATCATGGACCACATC AGATTTGAATCTGG	109978109 (<i>Gryllus pennsylvanicus</i>)
AD001	2415	TTAAATGCTCTCTAAAGCATGGATGTTGGACAAACT	109978109 (<i>Gryllus pennsylvanicus</i>)
AD001	2416	TTTGAATCTGGCAACCTGTGTATGAT	60311985 (<i>Papilio dardanus</i>)
AD001	2417	TTTGATATTGTTTCATATCAAGGATAC	109978109 (<i>Gryllus pennsylvanicus</i>)
AD002	2418	AAGAAAATCGAACAAAGAAATC	55902553 (<i>Locusta migratoria</i>)
AD002	2419	CAGCACATGGATGTGGACAAGGT	67899569 (<i>Drosophila pseudoobscura</i>)
AD002	2420	GAGTTCTTTAGTAAAGTATTCGGTGG	110762684 (<i>Apis mellifera</i>)
AD009	2421	CACTACAACTACCACAAGAGC	84226228 (<i>Aedes aegypti</i>)
			18941376 (<i>Anopheles gambiae</i>)
AD009	2422	CAGAACATCCACAACCTGTGACT	29534871 (<i>Bombyx mori</i>)
AD009	2423	GGTGTGGTGTCGTGCGAGGG	83926368 (<i>Lutzomyia longipalpis</i>)
AD009	2424	TGGATCCCTGAATACATAATGA	83926506 (<i>Lutzomyia longipalpis</i>)
AD015	2425	GAGCAGTAGAATTCAAAAGTAGT	99012451 (<i>Leptinotarsa decemlineata</i>)
AD015	2426	GCAATTATATTTATTGATGAA	83936542 (<i>Lutzomyia longipalpis</i>)
AD015	2427	TCACCATATTGTATTGTTGCT	31366806 (<i>Toxoptera citricida</i>)
AD015	2428	TTGTCCTGATGTTAAGTATGG	84114691 (<i>Blomia tropicalis</i>)
AD016	2429	ACGATGCCCAACGACGACATCACCCATCC	101406307 (<i>Plodia interpunctella</i>)

AD016	2430	ATGCCCAACGACGACATCACCCA	53883819 (<i>Plutella xylostella</i>)
AD016	2431	ATGCCCAACGACGACATCACCCATCCTATT	110240379 (<i>Spodoptera frugiperda</i>) 27372076 (<i>Spodoptera littoralis</i>)
AD016	2432	CAGAAGATCCCCATCTTCTCGG	91827264 (<i>Bombyx mori</i>) 22474331 (<i>Helicoverpa armigera</i>) 60295607 (<i>Homalodisca coagulata</i>)
AD016	2433	CGGCTCCATCACTCAGATCCCCAT	67896654 (<i>Drosophila pseudoobscura</i>)
AD016	2434	GCCAACGACCCACCATCGAG	101406307 (<i>Plodia interpunctella</i>)
AD016	2435	GCCCGTGTCCGAGGACATGCTGGG	83937868 (<i>Lutzomyia longipalpis</i>) 75473525 (<i>Tribolium castaneum</i>)
AD016	2436	GGCAGAAGATCCCCATCTTCTC	2286803 (<i>Drosophila melanogaster</i>)
AD016	2437	GTTACCGGCGATATTCTGCG	92997483 (<i>Drosophila grimshawi</i>)
AD016	2438	GTTACCGGCGGATATTCTGCGC	92953552 (<i>Drosophila ananassae</i>) 92042621 (<i>Drosophila willistoni</i>)

Table 5-LD

Target ID	SEQ ID No	Sequences*	Example Gi-number and species
LD001	124	AAGAAGCATTTGAAGCGTTTG	8005678 (<i>Meloidogyne incognita</i>), 9829015 (<i>Meloidogyne javanica</i>)
LD003	125	GTTCTTCTCTTGACGCGTCC	7710484 (<i>Zeldia punctata</i>)
LD003	126	GCAGCTTTACGGATTTTGCCAA	32183696 (<i>Meloidogyne chitwoodi</i>)
LD003	127	TTTCAACTCCTGATCAAGACGT	1662318 (<i>Brugia malayi</i>), 31229562 (<i>Wuchereria bancrofti</i>)
LD006	128	GCTATGGGTAAGCAAGCTATGGG	520506 (<i>Caenorhabditis elegans</i>)
LD007	129	AAAGAATAAAAAATTATTGA	17539725 (<i>Caenorhabditis elegans</i>)
LD007	130	AAGCAAGTGATGATGTTCAAGTGC	7143515 (<i>Globodera pallida</i>)
LD014	131	ATGATGGCTTTCATTGAACAAGA	10122191 (<i>Haemonchus contortus</i>)
LD015	132	AACGCCCCAGTCTCATTAGCCAC	20064339 (<i>Meloidogyne hapla</i>)
LD016	133	TTTTGGCGTCGATTCCTGATG	71999357 (<i>Caenorhabditis elegans</i>)
LD016	134	GTGTACATGTAACCTGGGAAACC	13418283 (<i>Necator americanus</i>)
LD016	135	GTGTACATGTAACCTGGGAAACCACGACG	10819046 (<i>Haemonchus contortus</i>)

Table 5-PC

Target ID	SEQ ID NO	Sequence *	Example Gi-number and species
PC001	435	ATGGATGTTGGACAAATTGGG	7143612 (<i>Globodera rostochiensis</i>)
PC003	436	GCTAAATCCGTAAAGCTGCTCGTGAAC	9831177 (<i>Strongyloides stercoralis</i>)
PC003	437	GAGTAAAGTACACTTTGGCTAAA	28914459 (<i>Haemonchus contortus</i>)
PC003	438	AAATCCGTAAAGCTGCTCGTGAAC	32185135 (<i>Meloidogyne chitwoodi</i>)
PC003	439	CTGGACTCGCAGAGCACATCGACTT	51334250 (<i>Radopholus similis</i>)
PC003	440	CGTCTGGATCAGGAATTGAAA	61115845 (<i>Litomosoides sigmodontis</i>)
PC005	441	TGGTTGGATCCAAATGAAATCAA	5430825 (<i>Onchocerca volvulus</i>)
PC005	442	GTGTGGTTGGATCCAAATGAAATCAA	6845701 (<i>Brugia malayi</i>); 45215079 (<i>Wuchereria bancrofti</i>)
PC014	443	CACATGATGGCTTTTCATTGAACAAGAAGC	10122191 (<i>Haemonchus contortus</i>)
PC014	444	TACGAGAAAAAGGAGAAAGCAAGT	21265518 (<i>Ostertagia ostertagi</i>)
PC016	445	GTCTGGATCATTTCCCTCGGGATAAT	18081287 (<i>Globodera rostochiensis</i>)
PC016	446	CCAGTCTGGATCATTTTCTCGGGATA	108957716 (<i>Bursaphelenchus mucronatus</i>); 108962248 (<i>Bursaphelenchus xylophilus</i>)

Table 5-EV

Target ID	SEQ ID NO	Sequence *	Example Gi-number and species
EV005	563	TTAAAGATGGTCTTATTATTAA	21819186 (<i>Trichinella spiralis</i>)
EV016	564	GCTATGGGTGTCATATGGAAC	54554020 (<i>Xiphinema index</i>)

Table 5-AG

Target ID	SEQ ID NO	Sequence *	Example Gi-number and species
AG001	739	GCTGGATTCATGGATGTGATCA	15666884 (<i>Ancylostoma ceylanicum</i>)
AG001	740	ATGGATGTTGGACAAATTGGG	18081843 (<i>Globodera rostochiensis</i>)
AG001	741	TTCATGGATGTGATCACCATTGA	27002091 (<i>Ascaris suum</i>)
AG005	742	GTCTGGTTGGATCCAAATGAAATCAATGA	2099126 (<i>Onchocerca volvulus</i>)
AG005	743	GGATCCAAATGAAATCAATGA	2099309 (<i>Onchocerca volvulus</i>)
AG005	744	TGATCAAGGATGTTTGATCAT	2130916 (<i>Brugia malayi</i>)
AG005	745	TGGTTGGATCCAAATGAAATCAATGA	6845701 (<i>Brugia malayi</i>)
AG005	746	CCAAGGGTAACGTGTTCAAGAACAAG	29964728 (<i>Heterodera glycines</i>)

AG005	747	TGGTTGGATCCAAATGAAATCAATGA	45215079 (<i>Wuchereria bancrofti</i>)
AG005	748	TGGATCCAAATGAAATCAATGA	61116961 (<i>Litomosoides sigmodontis</i>)
AG014	749	GAAGAAATTAACATTGAAAAGGG	10122191 (<i>Haemonchus contortus</i>)
AG014	750	GAATTTAACATTGAAAAGGGCCG	28252967 (<i>Trichuris vulpis</i>)
AG016	751	GGTACATGTACACCGGATTGGC	54552787 (<i>Xiphinema index</i>)

Table 5-JC

Target ID	SEQ ID NO	Sequence *	Example Gi-number and species
TC014	853	ATCATGGAATATTACGAGAAGAA	6562543 (<i>Heterodera schachtii</i>); 15769883 (<i>Heterodera glycines</i>)
TC015	854	AACGGTCCCGAAATTATGAGTAAATT	108966476 (<i>Bursaphelenchus xylophilus</i>)

Table 5-MP

Target ID	SEQ ID NO	Sequence *	Example Gi-number and species
MP001	1011	GATCTTTTGATATTGTTACATTAA	13099294 (<i>Strongyloides ratti</i>)
MP001	1012	ACATCCAGGATCTTTTGATATTGTTAC	15275671 (<i>Strongyloides ratti</i>)
MP001	1013	TCCTTTGATATTGTTACATTAA	32183548 (<i>Meloidogyne chitwoodi</i>)
MP016	1014	TATTGCTCGTGGACAAAAAT	9832367 (<i>Strongyloides stercoralis</i>)
MP016	1015	TCTGCTGCTCGTGAAGAAGTACCTGG	13418283 (<i>Necator americanus</i>)
MP016	1016	GCTGAAGATTATTGGATATT	20064440 (<i>Meloidogyne hapla</i>)
MP016	1017	GGTTACCCACATAATGAGATTGCTGC	20064440 (<i>Meloidogyne hapla</i>)
MP016	1018	AAGAAATGATTCAAACTGGTATTCAGCTATTGAT	31545172 (<i>Strongyloides ratti</i>)
MP016	1019	TATTGCTCGTGGACAAAAATTTCCAAT	31545172 (<i>Strongyloides ratti</i>)
MP016	1020	GTTTCTGCTGCTCGTGAAGAAGT	31545172 (<i>Strongyloides ratti</i>)
MP016	1021	CGTGGTTTCCCTGGTTACATGTACAC	31545172 (<i>Strongyloides ratti</i>)
MP016	1022	CCTGGTTACATGTACACCGATT	54552787 (<i>Xiphinema index</i>)
MP027	1023	TTTAAAAATTTTAAAGAAAAA	27540724 (<i>Meloidogyne hapla</i>)
MP027	1024	CTATTATGTTGGTGGTGAAGTTGT	34026304 (<i>Meloidogyne arenaria</i>)
MP027	1025	AAAGTTTTTAAAAATTTTAAA	34028558 (<i>Meloidogyne javanica</i>)

Table 5-NL

Target ID	SEQ ID No	Sequence *	Example Gi-number and species
NL001	1438	AGTACAAGCTGTGCAAAAGTGAAGA	18087933 (<i>Globodera rostochiensis</i>), 54547517 (<i>Globodera pallida</i>)
NL001	1439	ATGGATGTTGGACAAAATTGGGTGG	7143612 (<i>Globodera rostochiensis</i>)
NL001	1440	TGGATGTTGGACAAAATTGGGTGG	7235910 (<i>Meloidogyne incognita</i>)
NL001	1441	AGTACAAGCTGTGCAAAAGTGAAGA	111164813 (<i>Globodera rostochiensis</i>)
NL003	1442	AGTCCATCCATCACGCCCGTGT	6081031 (<i>Pristionchus pacificus</i>)
NL003	1443	CTCCGTAACAAGCGTGAGGTGTGG	5815927 (<i>Pristionchus pacificus</i>)
NL003	1444	GACTCGCAGAAGCACATTGACTTCTC	5815618 (<i>Pristionchus pacificus</i>)
NL003	1445	GCAGAAAGCACATTGACTTCTC	6081031 (<i>Pristionchus pacificus</i>)
NL003	1446	GCCAAAGTCCATCCATCACGCC	6081133 (<i>Pristionchus pacificus</i>)
NL003	1447	GCCAAAGTCCATCCATCACGCCCGTGT	1783663 (<i>Pristionchus pacificus</i>)
NL003	1448	TCGCAGAAAGCACATTGACTTCTC	10804008 (<i>Ascaris suum</i>)
NL003	1449	TCGCAGAAAGCACATTGACTTCTCGCTGAA	18688500 (<i>Ascaris suum</i>)
NL003	1450	GCCAAAGTCCATCCATCACGCCCGTGT	91102596 (<i>Pristionchus pacificus</i>)
NL003	1451	GACTCGCAGAAGCACATTGACTTCTC	91102596 (<i>Pristionchus pacificus</i>)
NL003	1452	CTCCGTAACAAGCGTGAGGTGTGG	91102596 (<i>Pristionchus pacificus</i>)
NL004	1453	AAGAACAAGGATATTCGTAAATT	3758529 (<i>Onchocerca volvulus</i>), 6200728 (<i>Litomosoides sigmodontis</i>)
NL004	1454	AAGAACAAGGATATTCGTAAATTCCTTGGAA	21056283 (<i>Ascaris suum</i>), 2978237 (<i>Toxocara canis</i>)
NL004	1455	CCGTGTACGCCCATTTCCCATCAAC	1783477 (<i>Pristionchus pacificus</i>)
NL004	1456	TACGCCCATTTCCCATCAAC	2181209 (<i>Haemonchus contortus</i>)
NL007	1457	CAACATGAATGCATTCCTCAAGC	39747064 (<i>Meloidogyne paranaensis</i>)
NL007	1458	GAAGTACAACATGAATGCATTCC	6721002 (<i>Onchocerca volvulus</i>)
NL007	1459	GCTGTATTTGTGTTGCCGACA	27541378 (<i>Meloidogyne hapla</i>)
NL008	1460	AGAAAAGGTTGTGGGTTGGTA	108958003 (<i>Bursaphelenchus mucronatus</i>)
NL011	1461	GGACTTCGTGATGGATATTACATTCAGGGACAATG	33138488 (<i>Meloidogyne incognita</i>)
NL011	1462	CAACTACAACATTCGAGAAGCC	108984057 (<i>Bursaphelenchus xylophilus</i>)
NL014	1463	GAAGAATTCACATTTGAAAAGGG	11927908 (<i>Haemonchus contortus</i>)

NL014	1464	GAGCAAGAAAGCCCAATGAGAAAGC	108958555 (Bursaphelenchus mucronatus)
NL014	1465	TTTCATTGAGCAAGAAGCCCAATGAGAAAGCCGAAGA	108979738 (Bursaphelenchus xylophilus)
NL015	1466	ATGAGCAAAATTGGCCGGGAGTCGGAG	18090737 (Globodera rostochiensis)
NL015	1467	CACACCAAGAACATGAAGTTGGCTGA	68276872 (Caenorhabditis remanei)
NL015	1468	CAGGAAATCTGTCGAAGTGT	45564676 (Meloiodogone incognita)
NL015	1469	CTGGCGCAGATCAAAAGAGATGGT	18090737 (Globodera rostochiensis)
NL015	1470	TGGCGCAGATCAAAAGAGATGGT	27428872 (Heterodera glycines)
NL016	1471	TATCCCGAGGAATGATCCAGAC	18081287 (Globodera rostochiensis)
NL016	1472	CGTATCTATCCCGAGGAAATGATCCAGACTGGAATTTTC	108957716 (Bursaphelenchus mucronatus)
NL023	1473	TGGATGGGAGTCATGCATGGA	108962248 (Bursaphelenchus xylophilus)
			13959786 (Nippostrongylus brasiliensis)

Table 5-CS

Target ID	SEQ ID NO	Sequence *	Example GI-number and species
CS001	1988	ATACAAGCTGTGCAAGGTGCG	10803803 (Trichuris muris)
CS003	1989	AAGCACATTGACTTCTCGCTGAA	18850138 (Ascaris suum)
CS003	1990	CGCAACAAGCGTGAGGTGTGG	40305701 (Heterodera glycines)
CS003	1991	CGTCTCCAGACTCAGGTGTTCAAG	91102965 (Nippostrongylus brasiliensis)
CS011	1992	TTTAATGTATGGGATACTGCTGG	9832495 (Strongyloides stercoralis)
CS011	1993	CAC TTGACTGGAGAGTTCGAGAAAA	18082874 (Globodera rostochiensis)
CS011	1994	CTCGTGTCACCTACAAAAATGTACC	71182695 (Caenorhabditis remanei)
CS011	1995	CAC TTGACTGGAGAGTTCGAGAA	108987391 (Bursaphelenchus xylophilus)
CS013	1996	TAGGTGAATTTGTTGATGATTA	40305096 (Heterodera glycines)
CS014	1997	AAGAAAAGAGAAACAAGTGGAAC	51871231 (Xiphinema index)
CS016	1998	GTGTACATGTAAACCTGGGAAACCCAG	10819046 (Haemonchus contortus)
CS016	1999	GTGTACATGTAAACCTGGGAAAC	13418283 (Necator americanus)
CS016	2000	GCCAAATCGGTGTACATGTAAAC	54552787 (Xiphinema index)
CS016	2001	AAGTTCTTCTCGAACTTGGTGAGGAAC	111163626 (Globodera rostochiensis)

Table 5-PX

Target ID	SEQ ID NO	Sequence *	Example Gi-number and species
PX001	2291	CTCGACATCGCCACCTGCAAG	11069004 (Haemonchus contortus); 27770634 (Teladorsagia circumcincta)
PX001	2292	GACGGCAAGTCCGACCCGAC	32320500 (Heterodera glycines)
PX001	2293	CCCGGCTGGATTTCATGGATGT	51334233 (Radopholus similis)
PX001	2294	ATCAAGGTGGACGGCAAGGTCCGCAC	108959807 (Bursaphelenchus xylophilus)
PX001	2295	ACAACGTGTTTCATCATCGGCAA	111166840 (Globodera rostochiensis)
PX016	2296	CGTGGTTTCCAGGTACATGTACACGGATTGGC	10819046 (Haemonchus contortus)
PX016	2297	GGTTCCAGGTTACATGTACAC	13418283 (Necator americanus)
PX016	2298	GAGTTCCCTCACCAAGTTCGAGAAGAACTT	111163626 (Globodera rostochiensis)

Table 5-AD

Target ID	SEQ ID NO	Sequence *	Example Gi-number and species
AD015	2439	ATAAATGGTCCTGAAATTATGA	9832193 (Strongyloides stercoralis)
AD016	2440	GTCACATGGAGACGGCGCGCTT	30220804 (Heterodera glycines)

Table 6-LD

Target ID	SEQ ID No	Sequences*	Example Gi-number and species
LD001	136	TAGCGGATGGTGCGGCGTCGTG	54625255 (Phlebiopsis gigantea)
LD003	137	TTCCAAGAAATCTTCAATCTTCAAA	50294437 (Candida glabrata CBS 138)
LD007	138	GACTGCGGTTTTGAACACCCCTTCAGAAGTTCA	110463173 (Rhizopus oryzae)
LD007	139	TGTCAGGCCAAATCTGGTATGGG	110463173 (Rhizopus oryzae)
LD011	140	GGCTTCTCAAAGTTGTAGTTA	48898288 (Aspergillus flavus)
LD011	141	CCATCACGGAGACCACCAAACTT	60673229 (Alternaria brassicicola)
LD011	142	AAAGGCTTCTCAAAGTTGTAGTTA	58157923 (Phytophthora infestans)
LD011	143	TGTGCTATTATCATGTTTGTATGT	110458937 (Rhizopus oryzae)
LD011	144	ACTGCCGGTCAGGAGAAGTTTGG	90638500 (Thermomyces lanuginosus)
LD011	145	AATACAACTTTGAGAAGCCTTTCCT	90549582 (Lentinula edodes), 90381505 (Amorphotheca resinae)

LD011	146	CAGGAGAAGTTTGGTGTCTCCG	90544763 (<i>Gloeophyllum trabeum</i>)
LD011	147	ACCACCAAACTTCTCCTGACC	90368069 (<i>Aureobasidium pullulans</i>)
LD011	148	GGTCAGGAGAAGTTGGTGGTCTCCG	90355148 (<i>Coprinopsis cenerea</i>)
LD016	149	GCAGCAATTTTCATTGTGAGGCAGACCAG	50285562 (<i>Candida glabrata</i> CBS 138)
LD016	150	ATGGAGTTTCATCACGTCATATAGC	68419480 (<i>Phytophthora parasitica</i>)
LD016	151	GGTCTGCCTCACAATGAAATTTGCTGCCAGAT	85109950 (<i>Neurospora crassa</i>)
LD016	152	CTATTGTTTTCGCTGCTATGGGTGTTAACATG GA	50423336 (<i>Debaryomyces hansenii</i>), 90540142 (<i>Gloeophyllum trabeum</i>)
LD016	153	ATGAACCTCCATTGCTCTCGTGGTCAGAAGAT	84573655 (<i>Aspergillus oryzae</i>)
LD016	154	ATAGGAATCTGGGTGATGGATCCGTT	90562068 (<i>Leucosporidium scottii</i>), 90359845 (<i>Aureobasidium pullulans</i>)
LD016	155	TCCTGTTTCTGAAGATATGTTGGG	90388021 (<i>Cunninghamella elegans</i>)
LD016	156	TTTGAAGATTGAAGATTCTTGGAAACG	50294437 (<i>Candida glabrata</i> CBS 138), 110468393 (<i>Rhizopus oryzae</i>), 90388664 (<i>Cunninghamella elegans</i>), 90376235 (<i>Amorphotheca resinae</i>)
LD027	157	TCACAGGCAGCGAAGATGGTACC	90546087 (<i>Gloeophyllum trabeum</i>)
LD027	158	TTCTTTGAAGTTTTTGAATAT	50292600 (<i>Candida glabrata</i> CBS 138)

Table 6-PC

Target ID	SEQ ID NO	Sequence *	Example GI-number and species
PC001	447	CCCTGCTGGTTTCATGGATGTCTAT	110469463 (<i>Rhizopus oryzae</i>)
PC003	448	ATTGAAGATTCTTGGAAAGAAG	50294437 (<i>Candida glabrata</i> CBS 138)
PC003	449	TTGAAGATTCTTGGAAAGAAG	50310014 (<i>Kluyveromyces fragilis</i> NRRL Y-1140)
PC003	450	CTTCTTTCCAAGAAATCTTCAA	622611 (<i>Saccharomyces cerevisiae</i>)
PC003	451	GACTCGCAGAAAGCACATCGACTT	109744873 (<i>Allomyces macrogynus</i>); 59284959 (<i>Blastocladiella emersonii</i>); 90623359 (<i>Corynascus heterothallicus</i>); 29427071 (<i>Verticillium dahliae</i>)
PC003	452	GACTCGCAGAAAGCACATCGACTTC	59298648 (<i>Blastocladiella emersonii</i>); 90565029 (<i>Leucosporidium scottii</i>)
PC003	453	TCGCAGAAAGCACATCGACTTC	47032157 (<i>Mycosphaerella graminicola</i>)
PC003	454	CAGAAGCACATCGACTTCTCCCT	34332427 (<i>Ustilago maydis</i>)

PC005	455	CTTATGGAGTACATCCACAAG	98997063 (<i>Spizellomyces punctatus</i>)
PC005	456	AAGAAGAAGGCAGAGAGGCCA	84572408 (<i>Aspergillus oryzae</i>)
PC010	457	GTGTTCAATAATCTCCTGATGA	50288722 (<i>Candida glabrata</i> CBS 138)
PC010	458	ATTTCCATGGAGAGACCATTCG	70990481 (<i>Aspergillus fumigatus</i>)
PC010	459	GGCAGAATCCCCAAGCTGCC	90631635 (<i>Thermomyces lanuginosus</i>)
PC014	460	AATACAAGGACGCCACCGGCA	30394561 (<i>Magnaporthe grisea</i>)
PC016	461	ATGCCCCAACGACATCACCCA	59281308 (<i>Blastocladiella emersonii</i>)
PC016	462	TGGGTGATGTCGTCGTTGGCAT	38353161 (<i>Hypocrea jecorina</i>)
PC016	463	GGTTCCCGGTTACATGTACAC	34447668 (<i>Cryphonectria parasitica</i>)
PC016	464	ACTATGCCCAACGACGACATCAC	34447668 (<i>Cryphonectria parasitica</i>)
PC016	465	CCGGGCACCTCTCTCGAGCGG	38353161 (<i>Hypocrea jecorina</i>)
PC016	466	CCGACCATCGAGCGCATCATCAC	59281308 (<i>Blastocladiella emersonii</i>)
PC016	467	TTCITGAACCTGGCCAAACGATCC	50285562 (<i>Candida glabrata</i> CBS 138)
PC016	468	TGTTCTTGAACCTGGCCAAACGA	66909391 (<i>Phaeosphaeria nodorum</i>)
PC016	469	GCTATGGGTGTCAACATGGAAACTGC	110463410 (<i>Rhizopus oryzae</i>)
PC016	470	TGCTATGGGTGTCAACATGGA	71006197 (<i>Ustilago maydis</i>)
PC016	471	CTATTGTGTTGCTGCTATGGGTGT	68488910 (<i>Candida albicans</i>)
PC016	472	TACGAGCGCGCGGTCGTGTGGA	90347883 (<i>Coprinopsis cinerea</i>)

Table 6-EV

Target ID	SEQ ID NO	Sequence *	Example Gi-number and species
EV010	565	TTCATAATTACCCAGATGAAAC	50405834 (<i>Debaryomyces hansenii</i>)
EV015	566	CGATCGCCTTGAACAGCGACG	22502898 (<i>Gibberella zeae</i>)
EV015	567	GTTACCATGGAGAACTTCCGTTA	67900533 (<i>Aspergillus nidulans</i> FGSC A4)
EV015	568	GTTACCATGGAGAACTTCCGTTACGCC	70820241 (<i>Aspergillus niger</i>)
EV015	569	ACCATGGAGAACTTCCGTTACGCC	84573628 (<i>Aspergillus oryzae</i>)
EV015	570	ATGGAGAACTTCCGTTACGCC	71002727 (<i>Aspergillus fumigatus</i>)
EV016	571	TCTGAAGATATGTTGGTCTGTGT	90396765 (<i>Cunninghamella elegans</i>)
EV016	572	CAAAAGATTCCTCAATTTCTCTGCA	50306984 (<i>Kluyveromyces lactis</i> NRRL Y-1140)
EV016	573	CCCCACAATGAAATCGCTGCTCAAAT	68001221 (<i>Schizosaccharomyces pombe</i> 972h-)
EV016	574	ATCGTTTTGCGCGCTATGGGTGT	58271359 (<i>Cryptococcus neoformans</i> var.)
EV016	575	TTCAGCAAGATTTTGAAGAGAAATGG	50285562 (<i>Candida glabrata</i> CBS 138)

Table 6-AG

Target ID	SEQ ID NO	Sequence *	Example GI-number and species
AG001	752	CGTAACAGGTTGAAGTACGCCCT	16931515 (<i>Coccidioides posadasii</i>)
AG001	753	AAGGTCGACGGCAAGTCAGGACTGAT	33515688 (<i>Cryptococcus neoformans</i> var.)
AG001	754	CCATTCTTGGTCAACCCACGATG	38132640 (<i>Hypocrea jecorina</i>)
AG001	755	ATCAAGGTAAACGACACCATC	56939474 (<i>Puccinia graminis</i> f. sp.)
AG005	756	TGTACATGAAGGCCAAGGTAACGTGTCAAGAAACAAG	98997063 (<i>Spizellomyces punctatus</i>)
AG005	757	CCAAGGGTAACGTGTCAAGAAACAAG	109744763 (<i>Allomyces macrogynus</i>); 59297176 (<i>Blastocladiella emersonii</i>)
AG005	758	AAGGGTAACGTGTCAAGAAACAAG	109741162 (<i>Allomyces macrogynus</i>)
AG005	759	CAAGAAGAGGCTGAGAAAGGC	67903433 (<i>Aspergillus nidulans</i> FGSC A4)
AG005	760	CAAGAAGAGGCTGAGAAAGGC	4191107 (<i>Emericella nidulans</i>)
AG005	761	AAGAAGAGGCTGAGAAAGGC	66909252 (<i>Phaeosphaeria nodorum</i>)
AG005	762	CAAAACATCCGTAAATTGATCAAGGATGGTTT	21649803 (<i>Conidiobolus coronatus</i>)
AG016	763	TCGCCGCCATGGGTGTCAAC	50554108 (<i>Yarrowia lipolytica</i>)
AG016	764	ATGGGTGTCAACATGGAAACCGC	90639144 (<i>Trametes versicolor</i>)
AG016	765	TGGAACCGCCCGTTTCTTCA	85109950 (<i>Neurospora crassa</i>)
AG016	766	GGTTACATGTACACCGATTG	32169825 (<i>Mucor circinelloides</i>)
AG016	767	GTCAAGATGGGAATCTGGGTGATGGA	38353161 (<i>Hypocrea jecorina</i>)

Table 6-TC

Target ID	SEQ ID NO	Sequence *	Example GI-number and species
TC001	855	AACAGGCTGAAGTATGCCCTTGACC	90545567 (<i>Gloeophyllum trabeum</i>)
TC015	856	TTCATCGTCCGTGGTGCGCATG	46122304 (<i>Gibberella zeae</i> PH-1)
TC015	857	AGTTTACCGGTACCTGGAGG	50310636 (<i>Kluyveromyces lactis</i> NRRL Y-1140)
TC015	858	CCTCCAGGTACCGGTAAACCT	85114224 (<i>Neurospora crassa</i>)
TC015	859	CCTCCAGGTACCGGTAAACCTT	50290674 (<i>Candida glabrata</i> CBS 138)
TC015	860	ATTAAAGTTTACCGGTACCTGGAGG	3356460 (<i>Schizosaccharomyces pombe</i>)
TC015	861	GGTGTCTTCTCTCTTAATCAA	21649889 (<i>Conidiobolus coronatus</i>)
TC015	862	ATCAACGGTCCCGAAATTATG	82610024 (<i>Phanerochaete chrysosporium</i>)

Table 6-MP

Target ID	SEQ ID NO	Sequence *	Example Gi-number and species
MP002	1026	AATTTTGTAGAAAAAATTTG	68026454 (Schizosaccharomyces pombe 972h-)
MP010	1027	GTCACCATATTAGCTAGGAAT	48564349 (Coccidioides posadasii)
MP016	1028	AAGAAATGATTCAAACTGGTAT	90396765 (Cunninghamella elegans)
MP016	1029	AAGAAATGATTCAAACTGGTATTC	110463410 (Rhizopus oryzae)
MP016	1030	CATGAACCTCTATTGCTCGTGG	50285562 (Candida glabrata CBS 138)
MP016	1031	GCTGCTATGGGTGTTAATATGGA	90348219 (Coprinopsis cinerea)
MP016	1032	TGCTATGGGTGTTAATATGGAAC	90396964 (Cunninghamella elegans)
MP016	1033	CCTACTATTGAGCGTATCATTAC	90524974 (Geomyces pannorum)
MP016	1034	GAAGTTTCGTGCTGCTGGAAGTACCTGG	90396313 (Cunninghamella elegans)
MP016	1035	GTTTCTGCTGCTGCTGGAAGAAGT	32169825 (Mucor circinelloides)
MP016	1036	GTGTACATGTACACGGAACCCACG	45392344 (Magnaporthe grisea)
MP016	1037	CCTGGTTACATGTACACCGATT	32169825 (Mucor circinelloides)
MP016	1038	GGTTACATGTACACCGATT	47067814 (Eremothecium gossypii)
MP016	1039	CCTATTTTAACATATGCCCTAACGA	90396313 (Cunninghamella elegans)
MP027	1040	ACTCTCCATCACCACATACATA	60673889 (Alternaria brassicicola)

Table 6-NL

Target ID	SEQ ID No	Sequence *	Example Gi-number and species
NL001	1474	CCAAGGGCAAGGGGTGTGAAGCTCA	30418788 (Magnaporthe grisea)
NL001	1475	TCTCTGCCCAAGGGCAAGGGTGT	22500578 (Gibberella zeae), 46128672 (Gibberella zeae PH-1), 70662858 (Gibberella moniliformis), 71000466 (Aspergillus fumigatus)
NL001	1476	TCTGCCCAAGGGCAAGGGTGT	14664568 (Fusarium sporotrichioides)
NL001	1477	TCTCTGCCCAAGGGCAAGGGT	50550586 (Yarrowia lipolytica)
NL001	1478	TCTCTGCCCAAGGGCAAGGGTGT	71000466 (Aspergillus fumigatus) 92459259 (Gibberella zeae)
NL001	1479	CTGCCCAAGGGCAAGGGGTGTGAAG	90545567 (Gloeophyllum trabeum)
NL003	1480	ATGAAGCTCGATTACGCTTGG	24446027 (Paracoccidioides brasiliensis)
NL003	1481	CGTAAGGCCGCTCGTGAGCTG	10229753 (Phytophthora infestans)

NL003	1482	CGTAAGGGCCGCTCGTGAGCTGTTGAC	58082846 (Phytophthora infestans)
NL003	1483	GACTCGCAGAAAGCACATTGACTT	21393181 (Pratylenchus penetrans), 34330401 (Ustilago maydis)
NL003	1484	TGAAGCTCGATTACGTCCTGG	46346864 (Paracoccidioides brasiliensis)
NL003	1485	TGGCCAAGTCCATCCATCAGCCCGTGT	58113938 (Phytophthora infestans)
NL004	1486	CGTAACCTCCTGGGCGAGAAG	58127885 (Phytophthora infestans)
NL003	1487	ATGAAGCTCGATTACGTCCTGG	90366381 (Aureobasidium pullulans)
NL003	1488	TCGGTTTGGCCAAAGTCCATCCA	90353540 (Coprinopsis cinerea)
NL003	1489	GACTCGCAGAAAGCACATTGACTT	71012467 (Ustilago maydis)
NL003	1490	GACTCGCAGAAAGCACATTGACTTCTC	90616286 (Ophiostoma piliferum)
NL004	1491	TACGCCCATTTCCCCATCAAC	15771856 (Gibberella zeae), 29426217 (Verticillium dahliae), 30399988 (Magnaporthe grisea), 34330394 (Ustilago maydis), 39945691 (Magnaporthe grisea 70-15), 46108543 (Gibberella zeae PH-1), 70660620 (Gibberella moniliformis)
NL004	1492	CGGTACGCCCATTTCCCCATCAAC	90615722 (Ophiostoma piliferum)
NL004	1493	TACGCCCATTTCCCCATCAAC	90367524 (Aureobasidium pullulans)
			90372622 (Cryptococcus laurentii)
			109654277 (Fusarium oxysporum f. sp.)
			90535059 (Geomyces pannorum)
			46108543 (Gibberella zeae PH-1)
NL004	1493	TACGCCCATTTCCCCATCAAC	90566138 (Leucosporidium scottii)
			39945691 (Magnaporthe grisea 70-15)
			110115733 (Saitoella complicata)
			110081735 (Tuber borchii)
			71021510 (Ustilago maydis)
NL004	1492	CGGTACGCCCATTTCCCCATCAAC	50554252 (Yarrowia lipolytica)
NL004	1494	TACGCCCATTTCCCCATCAACTG	90640952 (Trametes versicolor)
NL004	1495	CGGTACGCCCATTTCCCCATCAAC	90615722 (Ophiostoma piliferum)
NL005	1496	AAAAGGTCAAGGAGGCCAAGA	14662414 (Fusarium sporotrichioides)
NL005	1497	TTCAAGAACAAAGCGTGTATTGATGGA	90395504 (Cunninghamella elegans)
NL005	1498	TTCAAGAACAAAGCGTGTATTGATGGAGT	90542553 (Gloeophyllum trabeum)
NL006	1499	CCTGGAGGAGGAGACGACCAT	70998503 (Aspergillus fumigatus)
NL006	1500	TCCCATCTCGTATGACAAATTGG	68471154 (Candida albicans)

NL006	1501	ATGGTCGTCTCCTCCTCCAGG	7098503 (<i>Aspergillus fumigatus</i>)
NL006	1502	TCCCATCTCGTATGACAAATTGG	68471154 (<i>Candida albicans</i>)
NL007	1503	CAAGTCATGATGTTCAAGTCAAC	50425488 (<i>Debaryomyces hansenii</i>)
NL007	1504	TGACGCTTCACGGCCTGCAGCAG	70984614 (<i>Aspergillus fumigatus</i>)
NL007	1505	CAAGTCATGATGTTCAAGTCAAC	10229203 (<i>Phytophthora infestans</i>)
NL010_2	1506	CAATTCCTTGCAAGTGTCAACAA	70984614 (<i>Aspergillus fumigatus</i>)
NL010_2	1507	TCAACAACACAGTCTGATGAAAC	68478799 (<i>Candida albicans</i>)
NL010_2	1508	TTCTTGCAAGTGTTCACAAC	21649260 (<i>Conidiobolus coronatus</i>)
NL011	1509	AAGAAGTTCCTCAACTGGCAC	47031965 (<i>Mycosphaerella graminicola</i>)
NL011	1510	ACAAGAAGTTCCTCAACTGGCA	68132303 (<i>Trichophyton rubrum</i>)
NL011	1511	ACCTACAAGAAGTTCCTCAACT	68132303 (<i>Trichophyton rubrum</i>)
NL011	1512	ACCTACAAGAAGTTCCTCAACTGGCAC	68132303 (<i>Trichophyton rubrum</i>)
NL011	1513	CAACTACAACCTTCGAGAAAGCC	22500425 (<i>Gibberella zeae</i>), 34331122 (<i>Ustilago maydis</i>), 46108433 (<i>Gibberella zeae</i> PH-1), 47029512 (<i>Mycosphaerella graminicola</i>), 56236507 (<i>Setosphaeria turcica</i>), 62926335 (<i>Fusarium oxysporum</i> f. sp.), 70674996 (<i>Gibberella moniliformis</i>), 70992714 (<i>Aspergillus fumigatus</i>)
NL011	1514	CAAGAAGTTCCTCAACTGGCAC	68132303 (<i>Trichophyton rubrum</i>)
NL011	1515	CACCTACAAGAAGTTCCTCAAC	68132303 (<i>Trichophyton rubrum</i>)
NL011	1516	CCTACAAGAAGTTCCTCAACTG	68132303 (<i>Trichophyton rubrum</i>)
NL011	1517	CTACAAGAAGTTCCTCAACTGG	68132303 (<i>Trichophyton rubrum</i>)
NL011	1518	GCAACTACAAGTTCGAGAAAGCC	22505588 (<i>Gibberella zeae</i>)
NL011	1519	TACAAGAAGTTCCTCAACTGGC	68132303 (<i>Trichophyton rubrum</i>)
NL011	1520	TCACCTACAAGAAGTTCCTCA	68132303 (<i>Trichophyton rubrum</i>)
NL011	1521	TCACCTACAAGAAGTTCCTCAA	68132303 (<i>Trichophyton rubrum</i>)
NL011	1522	TCACCTACAAGAAGTTCCTCAACT	30405871 (<i>Magnaporthe grisea</i>)
NL011	1523	TCACCTACAAGAAGTTCCTCAACTGGCAC	13903501 (<i>Blumeria graminis</i> f. sp.), 3140444 (<i>Emericella nidulans</i>), 34331122 (<i>Ustilago maydis</i>), 49096317 (<i>Aspergillus nidulans</i> FGSC A4)
NL011	1524	TGGGACACAGCTGGCCAGGAAA	14180743 (<i>Magnaporthe grisea</i>), 39950145 (<i>Magnaporthe grisea</i> 70-15)

NL011	1525	TTGAGAAAGCCGTTCCCTGTGG	38056576 (Phytophthora sojae), 45244260 (Phytophthora nicotianae), 58091236 (Phytophthora infestans)
NL011	1526	TTGAGAAAGCCGTTCCCTGTGGTTGGC	58090083 (Phytophthora infestans)
NL011	1527	TGGACACAGCTGGCCAGGAAA	39950145 (Magnaporthe grisea 70-15)
NL011	1528	TATTACATTCAAGGACAAATGCG	110134999 (Taphrina deformans)
NL011	1529	TCACCTACAAGAAGCGTTCCCAACTGGCAC	84573903 (Aspergillus oryzae) 90355199 (Coprinopsis cinerea) 90624693 (Corynascus heterothallicus) 90638500 (Thermomyces lanuginosus)
NL011	1530	ACCTACAAGAAGCGTTCCCAACTGGCAC	113544700 (Cordyceps bassiana) 85114463 (Neurospora crassa)
NL011	1531	TACAAGAAGCGTTCCCAACTGGCA	110269748 (Hypocrea lixii)
NL011	1532	TACAAGAAGCGTTCCCAACTGGCAC	110458937 (Rhizopus oryzae)
NL011	1533	AGGAAGAAGAACCCTTCAGTACT	90557551 (Leucosporidium scottii)
NL011	1534	AAGAAGAACCCTTCAGTACTACGA	113551594 (Cordyceps bassiana)
NL011	1535	AAGAAGAACCCTTCAGTACTACGACATC	90036917 (Trichophyton rubrum)
NL011	1536	AAGAACCCTTCAGTACTACGACATC	90624693 (Corynascus heterothallicus)
NL011	1537	GGCTTCGGAAGTTGTAGTTGC	89975123 (Hypocrea lixii)
NL011	1538	CAACTACAACCTTCGAGAAGCC	70992714 (Aspergillus fumigatus) 90368808 (Aureobasidium pullulans) 90629512 (Corynascus heterothallicus) 109656121 (Fusarium oxysporum f. sp.) 90532849 (Geomyces pannorum) 110272576 (Hypocrea lixii) 47029512 (Mycosphaerella graminicola) 85114463 (Neurospora crassa) 90617165 (Ophiostoma piliferum) 90036917 (Trichophyton rubrum)
NL011	1539	GGCTTCGGAAGTTGTAGTTG	92233975 (Gibberella zeae)
NL013	1540	CCCGAGATGGTGGTGGCTGGTACCA	49069733 (Ustilago maydis)
NL013	1541	GGTACCACTCGCACCCGGGCTT	58134950 (Phytophthora infestans)
NL013	1542	GTGGGCTGGTACCACTCGCACCCGGGCTTCGG CTGCTGGCTGTGGG	38062327 (Phytophthora sojae)
NL013	1543	TGGTACCACTCGCACCCGGGCTT	58084933 (Phytophthora infestans)

NL013	1544	CCCGAGATGGTGGTGGGCTGGTACCA	71006043 (<i>Ustilago maydis</i>)
NL015	1545	ATCCACACCAAGAACATGAAG	10181857 (<i>Aspergillus niger</i>), 22505190 (<i>Gibberella zeae</i>), 30394634 (<i>Magnaporthe grisea</i>), 33507832 (<i>Cryptococcus neoformans</i> var.), 3773467 (<i>Emericella nidulans</i>), 39940093 (<i>Magnaporthe grisea</i> 70-15), 46122304 (<i>Gibberella zeae</i> PH-1), 47032030 (<i>Mycosphaerella graminicola</i>), 49106059 (<i>Aspergillus nidulans</i> FGSC A4)
NL015	1546	CACACCAAGAACATGAAGTTGG	21649889 (<i>Conidiobolus coronatus</i>)
NL015	1547	GCCTTCTTCTTCTCATCAACGG	46122304 (<i>Gibberella zeae</i> PH-1)
NL015	1548	TTGGAGGCTGCAGAAAGCAGCT	90369178 (<i>Cryptococcus laurentii</i>)
NL015	1549	GCCTTCTTCTTCTCATCAACGG	46122304 (<i>Gibberella zeae</i> PH-1)
NL015	1550	ATCCACACCAAGAACATGAAG	70820941 (<i>Aspergillus niger</i>) 58260307 (<i>Cryptococcus neoformans</i> var.) 85691122 (<i>Encephalitozoon cuniculi</i> GB-M1) 46122304 (<i>Gibberella zeae</i> PH-1) 39940093 (<i>Magnaporthe grisea</i> 70-15) 85082882 (<i>Neurospora crassa</i>) 50555821 (<i>Yarrowia lipolytica</i>)
NL015	1551	CACACCAAGAACATGAAGTTGGC	110272618 (<i>Hypocrea lixii</i>)
NL016	1552	CATGAACTCGATTGCTCGTGG	30418452 (<i>Magnaporthe grisea</i>), 39942327 (<i>Magnaporthe grisea</i> 70-15)
NL016	1553	CCACCATCTACGAGCGCGCCGGACG	39942327 (<i>Magnaporthe grisea</i> 70-15), 45392344 (<i>Magnaporthe grisea</i>)
NL016	1554	CATGAACTCGATTGCTCGTGG	90367610 (<i>Aureobasidium pullulans</i>) 39942327 (<i>Magnaporthe grisea</i> 70-15)
NL016	1555	CATGTCGGTGAGGATGACGAG	90562068 (<i>Leucosporidium scottii</i>)
NL016	1556	CCACCATCTACGAGCGCGCCGGACG	39942327 (<i>Magnaporthe grisea</i> 70-15)
NL019	1557	CAGATTTGGACACGCGCGCCGAGGCG	9834078 (<i>Phytophthora sojae</i>)
NL019	1558	GACCAGGAGTCGTTCAACAAC	9834078 (<i>Phytophthora sojae</i>)
NL019	1559	TGGGACACGGCGCGCCGAGGAG	38056576 (<i>Phytophthora sojae</i>), 40545332 (<i>Phytophthora nicotianae</i>), 58083674 (<i>Phytophthora infestans</i>)
NL019	1560	TGGGACACGGCGCGCCGAGGAGCG	29426828 (<i>Verticillium dahliae</i>), 38057141 (<i>Phytophthora sojae</i>)
NL019	1561	TGGGACACGGCGCGCCGAGGCGGTT	70981934 (<i>Aspergillus fumigatus</i>)
NL019	1562	TTCTGGAGACGTCGGCGAAGAACGC	90643518 (<i>Trametes versicolor</i>)

NL019	1563	CAGATTTGGACACGGCCGGCCAGGAGCG	90616605 (<i>Ophiostoma piliferum</i>)
NL019	1564	TGGGACACGGCCGGCCAGGAG	110272626 (<i>Hypocrea lixii</i>)
NL019	1565	TGGGACACGGCCGGCCAGGAGCG	50550714 (<i>Yarrowia lipolytica</i>)
NL019	1566	TGGGACACGGCCGGCCAGGAGCGGTT	70981934 (<i>Aspergillus fumigatus</i>)
NL019	1567	TGGGACACGGCCGGCCAGGAGCGGTTCCG	50553761 (<i>Yarrowia lipolytica</i>)
NL022	1568	CAGGCAAGAATTTCTGCCCCA	58124185 (<i>Phytophthora infestans</i>)
NL022	1569	GGCAAGTCTTCGGTCTGTACAC	58124872 (<i>Phytophthora infestans</i>)
NL023	1570	GGATGACCAAAAACGTAATCT	46137132 (<i>Gibberella zeae</i> PH-1)
NL023	1571	AGAATACGTTTTTGGTCATCC	46137132 (<i>Gibberella zeae</i> PH-1)

Table 6-CS

Target ID	SEQ ID NO	Sequence *	Example Gi-number and species
CS003	2002	TGGTCTCCGCAACAAGCGTGGA	46356829 (<i>Paracoccidioides brasiliensis</i>)
CS003	2003	GGTCTCCGCAACAAGCGTGAG	71012467 (<i>Ustilago maydis</i>)
CS003	2004	TGGTCTCCGCAACAAGCGTGAGGT	5832048 (<i>Botryotinia fuckeliana</i>)
CS003	2005	TGGTCTCCGCAACAAGCGTGAGGT	40545704 (<i>Sclerotinia sclerotiorum</i>)
CS003	2006	GGTCTCCGCAACAAGCGTGAGGT	21907821 (<i>Colletotrichum trifolii</i>); 90623359 (<i>Corynascus heterothallicus</i>); 94331331 (<i>Pyronema omphalodes</i>); 29427071 (<i>Verticillium dahliae</i>)
CS003	2007	TGGTCTCCGCAACAAGCGTGAGGTGG	27439041 (<i>Chaetomium globosum</i>); 47032270 (<i>Mycosphaerella graminicola</i>)
CS003	2008	CGCAACAAGCGTGAGGTGTGG	71000428 (<i>Aspergillus fumigatus</i>); 67537265 (<i>Aspergillus nidulans</i> FGSC A4); 70825441 (<i>Aspergillus niger</i>); 84573806 (<i>Aspergillus oryzae</i>); 3773212 (<i>Emmericella nidulans</i>); 90632673 (<i>Thermomyces lanuginosus</i>); 34332427 (<i>Ustilago maydis</i>)
CS006	2009	TCCCCCTCTCGTATGACAAATTGGT	68011927 (<i>Schizosaccharomyces pombe</i> 972h-)
CS007	2010	ATTAGCTTTGACAAAGAATA	50305206 (<i>Kluyveromyces lactis</i> NRRL Y-1140)
CS007	2011	GAGCACCCCTTCAGAAAGTTCAACA	90553133 (<i>Lentinula edodes</i>)
CS011	2012	TGGGATACTGCTGGCCCAAGAA	90385536 (<i>Amorphotheca resinae</i>); 68475609 (<i>Candida albicans</i>); 50304104 (<i>Kluyveromyces</i>)

CS011	2013	AAGTTTGGTGCTCCGAGATGGTTACTA	lactis NRRL Y-1140); 85105150 (<i>Neurospora crassa</i>)
CS011	2014	CAATGTGCCATCATCATGTTCCGA	90355199 (<i>Coprinopsis cinerea</i>)
CS011	2015	CATCATCATGTTCCGATGTAAC	15276938 (<i>Glomus intraradices</i>)
CS011	2016	CACTTGACTGGAGAGTTGAGAA	28268268 (<i>Chaetomium globosum</i>)
CS011	2017	TGAAGGTTCTTTTCTGTGGAA	90368808 (<i>Aureobasidium pullulans</i>); 34331122 (<i>Ustilago maydis</i>)
CS013	2018	GGATGGTACCACTCGCATCCTGG	6831345 (<i>Pneumocystis carinii</i>)
CS015	2019	AACGAGAGGAAGAAGAAG	109651225 (<i>Fusarium oxysporum</i> f. sp.)
CS015	2020	AGGGCTTCTTCTTCTTCTCTCTC	39944615 (<i>Magnaporthe grisea</i> 70-15)
CS015	2021	TAGGGCTTCTTCTTCTTCTCTC	14662870 (<i>Fusarium sporotrichioides</i>)
CS015	2022	GAGATGGTCGAGTTGCCTCTA	85112692 (<i>Neurospora crassa</i>)
CS016	2023	GCTGAAGACTTTTGGACATC	71005073 (<i>Ustilago maydis</i>)
CS016	2024	CCTCACCAAGTTCGAGAAAGACTTC	30418452 (<i>Magnaporthe grisea</i>)
CS016	2025	GTCGTGGTGAGGAAGCCCTG	90566317 (<i>Leucosporidium scottii</i>)
CS016	2026	TCCTCACCGACGACAGCCTTCATGGCC	84573655 (<i>Aspergillus oryzae</i>)
CS016	2027	GATGTTTCCAAACCAGCTGTACGCC	29427786 (<i>Verticillium dahliae</i>)
CS016	2028	GGCGTACAGCTGGTTGGAAACATC	90368806 (<i>Aureobasidium pullulans</i>)
CS016	2029	TGATGTTTCCAAACCAGCTGTACGCC	29427786 (<i>Verticillium dahliae</i>)
CS016	2030	ATGGCAGACTTCATGAGACGAGA	46107507 (<i>Gibberella zeae</i> PH-1)
CS016	2031	ATGCCCCAACGACGACATCACCCA	29427786 (<i>Verticillium dahliae</i>)
CS016	2032	TGGGTGATGTCGTCGTTGGGCAT	59281308 (<i>Blastocladiella emersonii</i>)
CS016	2033	ACTATGCCCCAACGACGACATCAC	38353161 (<i>Hypocrea jecorina</i>)
CS016	2034	GGTTACATGTACACCGATTG	34447668 (<i>Cryphonectria parasitica</i>)
CS016	2035	CCCAGGTTACATGTACACCGATT	32169825 (<i>Mucor circinelloides</i>)
CS016	2036	ACACCACGTTGGCCTTGACT	47067814 (<i>Eremothecium gossypii</i>)
CS016	2037	GCCATGGGTGTGAACATGGAGAC	68488910 (<i>Candida albicans</i>)
CS016	2038	GACGACCACGAGGACAACCTTGCCATCGTGTTCG	82608508 (<i>Phanerochaete chrysosporium</i>)
CS016	2039	AAGATCCCCCATTTTCTCGGCTGC	59277641 (<i>Blastocladiella emersonii</i>)
CS016			90348219 (<i>Coprinopsis cinerea</i>)

Table 6-PX

Target ID	SEQ ID NO	Sequence *	Example Gi-number and species
PX001	2299	CTCATCAAGGTGGACGGCAAGGT	85080580 (<i>Neurospora crassa</i>)
PX001	2300	TCGGTGGGACCTTGCCGTCCACCTTGA	70768092 (<i>Gibberella moniliformis</i>)
PX001	2301	GACGGCAAGGTCCGCACCGAC	109745014 (<i>Allomyces macrogynus</i>); 60673542 (<i>Alternaria brassicicola</i>); 90368699 (<i>Aureobasidium pullulans</i>); 59299145 (<i>Blastocladiella emersonii</i>); 27438899 (<i>Chaetomium globosum</i>); 90623992 (<i>Corynascus heterothallicus</i>); 89975695 (<i>Hypocrea lixii</i>); 99039195 (<i>Leptosphaeria maculans</i>); 39970560 (<i>Magnaporthe grisea</i>); 47731115 (<i>Metarhizium anisopliae</i>); 90036859 (<i>Trichophyton rubrum</i>); 29427127 (<i>Verticillium dahliae</i>)
	2302	GACGGCAAGGTCCGCACCGACCC	70823112 (<i>Aspergillus niger</i>); 90633197 (<i>Thermomyces lanuginosus</i>)
PX001	2303	AAGTCCGCACCGACCCACCTACCC	71015993 (<i>Ustilago maydis</i>)
PX001	2304	CGCTTCAACCATCCACCGCATCAC	90639458 (<i>Trametes versicolor</i>)
PX001	2305	CGAGGAGGCCAAGTACAAGCTG	78177454 (<i>Chaetomium cupreum</i>); 27438899 (<i>Chaetomium globosum</i>)
PX001	2306	GAGGCCAAGTACAAGCTGTGCAAGT	109745014 (<i>Allomyces macrogynus</i>)
PX001	2307	GCCAAGTACAAGCTGTGCAAG	45923813 (<i>Coccidioides posadasii</i>)
PX001	2308	CCCGACCCGCTCATCAAGGTCAACGAC	78177454 (<i>Chaetomium cupreum</i>)
PX001	2309	CGACATCGTCCACATCAAGGAC	82603501 (<i>Phanerochaete chrysosporium</i>)
PX001	2310	CCGCACAAGCTGCGCGAGTGCCCTGCCGCTC	109745014 (<i>Allomyces macrogynus</i>)
PX010	2311	TTCGACCAAGGAGGCGGCGCGGT	90542152 (<i>Gloeophyllum trabeum</i>)
PX010	2312	CACCACCCGCGCGCCTCCTG	84578035 (<i>Aspergillus oryzae</i>)
PX010	2313	TGCAGGTCTTCAACAACCTGCCCGACGAC	39978050 (<i>Magnaporthe grisea</i>)
PX010	2314	TCAACAACCTGCCCGACGAGAC	90618424 (<i>Corynascus heterothallicus</i>)
PX015	2315	CATGCGCGCGTCCGAGTCAAGGTGGT	59282860 (<i>Blastocladiella emersonii</i>)
PX015	2316	GCATTCCTTCTCTCATCAACGG	68323226 (<i>Coprinopsis cinerea</i>)
PX015	2317	ATCAACGGCCCCGAGATCATGTC	85082882 (<i>Neurospora crassa</i>)
PX015	2318	TGGCAAGGCGGTTCGAGGAGGC	71002727 (<i>Aspergillus fumigatus</i>)
PX016	2319	CCTCACCAAGTTCGAGAAAGAACTTC	90566317 (<i>Leucosporidium scottii</i>)

PX016	2320	GAGGAGATGATCCAGACTGGTAT	90639144 (<i>Trametes versicolor</i>)
PX016	2321	GAGGAGATGATCCAGACTGGTATCTC	58271359 (<i>Cryptococcus neoformans</i>)
PX016	2322	ATGAATCCATCGCCCGTGGTCAGAAGATCCC	90545177 (<i>Gloeophyllum trabeum</i>)
PX016	2323	GTCAGAAAGATCCCCATCTTCTCCGCC	9651842 (<i>Emericella nidulans</i>)
PX016	2324	CAGAAAGATCCCCATCTTCTCCGCC	70825597 (<i>Aspergillus niger</i>); 90611576 (<i>Ophiostoma piliiferum</i>); 90639144 (<i>Trametes versicolor</i>)
PX016	2325	CAGAAATCCCCATCTTCTCCGCC	67540123 (<i>Aspergillus nidulans</i>)
PX016	2326	CAGAAATCCCCATCTTCTCCGCCCGCGG	59283275 (<i>Blastocladiella emersonii</i>)
PX016	2327	AAGATCCCCATCTTCTCCGCCCGCGGTCT	34447668 (<i>Cryphonectria parasitica</i>)
PX016	2328	CCCATCTTCTCCGCCCGCGGTCTGCC	90621827 (<i>Corynascus heterothallicus</i>)
PX016	2329	GGTCTGCCCCACAACAGAGATTGCTGC	90367610 (<i>Aureobasidium pullulans</i>); 66909391 (<i>Phaeosphaeria nodorum</i>)
PX016	2330	TTCGCCGCCATGGAGTCAACATGGAGAC	90562163 (<i>Leucosporidium scottii</i>)
PX016	2331	ACCGCCAGGTTCTTCAAGCAGGA	47067814 (<i>Eremothecium gossypii</i>)
PX016	2332	CTGTCTTGAACCTTGGCCCAATGA	90545177 (<i>Gloeophyllum trabeum</i>)
PX016	2333	GGTTACATGTACACGGATTGG	34447668 (<i>Cryphonectria parasitica</i>); 90545177 (<i>Gloeophyllum trabeum</i>); 39942327 (<i>Magnaporthe grisea</i>); 82608506 (<i>Phanerochaete chrysosporium</i>); 71006197 (<i>Ustilago maydis</i>)
PX016	2334	GGCAAGCCCATCGACAAGGGGCC	59283275 (<i>Blastocladiella emersonii</i>)
PX016	2335	ATGGGGTGGGTGATGTCGTGTTGGCATGGTCA	38353161 (<i>Hypocrea jecorina</i>)
PX016	2336	ACCATGCCCAACGACGACATCACCCACCC	59281308 (<i>Blastocladiella emersonii</i>)
PX016	2337	TGCACAACAGGCAGATCTACCC	107889579 (<i>Encephalitozoon cuniculi</i>)
PX016	2338	CCGTCGCTATCTCGTCTCATGAA	48521040 (<i>Coccidioides posadasii</i>)

Table 6-AD

Target ID	SEQ ID NO	Sequence *	Example Gi-number and species
AD001	2441	CCCGCTGGTTTCATGGATGTT	58259586 (<i>Cryptococcus neoformans</i>)
AD001	2442	GACAACATCCATGAACACGCGGG	21649877 (<i>Conidiobolus coronatus</i>)
AD001	2443	TTCATGGATGTTGTACCATTTG	90616000 (<i>Ophiostoma piliiferum</i>)
AD001	2444	GAAGAAGCCCAAGTACAAGCTCTG	110469512 (<i>Rhizopus oryzae</i>)
AD001	2445	AAGAAGCCCAAGTACAAGCTCTG	110469518 (<i>Rhizopus oryzae</i>)

AD001	2446	GCCAAAGTACAAGCTCTGCAAGGT	98996590 (<i>Spizellomyces punctatus</i>)
AD001	2447	GCCAAAGTACAAGCTCTGCAAGGTCA	109743129 (<i>Allomyces macrogynus</i>)
AD001	2448	AGTACAAGCTCTGCAAGGTCA	71000466 (<i>Aspergillus fumigatus</i>); 67537247 (<i>Aspergillus nidulans</i>); 70823112 (<i>Aspergillus niger</i>); 40886470 (<i>Emicella nidulans</i>)
AD015	2449	TATGGACCCCTGGAACTGGTAAACCC	46349704 (<i>Paracoccidioides brasiliensis</i>)
AD016	2450	TGCCCCGTGTCGAGGACATGCTGGCCG	109743322 (<i>Allomyces macrogynus</i>)
AD016	2451	TGCCCCGTGTCGAGGACATGCTGGCCGCG	59283275 (<i>Blastocladiella emersonii</i>)
AD016	2452	CGTGCCGAGGACATGCTGGCCGCGCA	90612905 (<i>Ophiostoma piliferum</i>)
AD016	2453	ATGGGCGTCAACATGGAGACGGC	59277641 (<i>Blastocladiella emersonii</i>)
AD016	2454	TGGAGACGGCGCGCTTCTTCA	90611376 (<i>Ophiostoma piliferum</i>)
AD016	2455	TTCCTCAACCTGGCCAAACGACCCAC	90611376 (<i>Ophiostoma piliferum</i>)
AD016	2456	ACCATCGAGCGCATCATCCCCGCGCTCGC	59281308 (<i>Blastocladiella emersonii</i>)
AD016	2457	TCCACCATCTACGAGCGCGCTGG	90368806 (<i>Aureobasidium pullulans</i>)
AD016	2458	CTGACGATGCCCAACGACGACATCAC	90611301 (<i>Ophiostoma piliferum</i>)
AD016	2459	ATGCCCAACGACGACATCACCCA	59281308 (<i>Blastocladiella emersonii</i>)
AD016	2460	TGGGTGATGTCGTCGTTGGGCAT	38353161 (<i>Hypocrea jecorina</i>)

Table 7-LD

Target ID	SEQ ID NO and DNA Sequence (sense strand) 5' → 3' of fragments and concatemer constructs
LD014_F1	SEQ ID NO: 159 TCTAGAATGTTGAATCAGGCTCGATTGAAAGTATTGAAGGTTAGGGAAGATCACGTTTCGTACCGTACTAGAGGAGGCGCGTAAA CGACTTGGTCAGGTCACAAACGCCCGGG
LD014_F2	SEQ ID NO: 160 TCTAGAAAGATCACGTTTCGTACCGTACTAGAGGAGGCGCGTAAACGACTTGGTCAGGTCACAAACGCCCGGG
LD014_C1	SEQ ID NO: 161 TCTAGAATGTTGAATCAGGCTCGATTGAAAGTATTGAAGGTTAGGGAAGATCACGTTTCGTACCGTACTAGAGGAGGCGCGTAAA CGACTTGGTCAGGTCACAAACGATGTTGAATCAGGCTCGATTGAAAGTATTGAAGGTTAGGGAAGATCACGTTTCGTACCGTACTA GAGGAGGCGCGTAAACGACTTGGTCAGGTCACAAACGATGTTGAATCAGGCTCGATTGAAAGTATTGAAGGTTAGGGAAGATCA CGTTCGTACCGTACTAGAGGAGGCGCGTAAACGACTTGGTCAGGTCACAAACGCCCGGG
LD014_C2	SEQ ID NO: 162 TCTAGAAAGATCACGTTTCGTACCGTACTAGAGGAGGCGCGTAAACGACTTGGTCAGGTCACAAACGAGATCACGTTTCGTACCGT

<p> ACTAGAGAGGCGGTAAACGAC TTGGTCAGGTCAAAAACGAAGATCACG TTCTGACCGTACTAGAGGAGGCGGCTAAACGAC TT GGTACAGGTCAAAAACGAAGATCACG TTCTGACCGTACTAGAGGAGGCGGCTAAACGAC TTGGTCAGGTCAAAAACGAAGATCACG TTCGTACCGTACTAGAGGAGGCGGCTAAACGAC TTGGTCAGGTCAAAAACGCCCCGGG </p>
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Table 8-LD

Target ID	Primers Forward 5' → 3'	Primers Reverse 5' → 3'	dsRNA DNA Sequence (sense strand) 5' → 3'
LD001	SEQ ID NO: 164 GCGTAATACGACTC ACTATAGGGCCCC AAGAAGCATTTGAA GGC SEQ ID NO: 166 GGCCCCAAGAAGCA TTTGAAGCG	SEQ ID NO: 165 CCTTTGGGGCCAGT TTGCATC SEQ ID NO: 167 GCGTAATACGACTC ACTATAGGCCTTTG GGGCCAGTTTGCAT C	SEQ ID NO: 163 GGCCCCAAGAAGCATTTGAAGCGTTTGAATGCCCCAAAAGCATGGATGTTGG ATAAATTGGGAGAGTGTTTTTCGCACCTCGCCCATCTACAGGACCTCACAAATTG CGAAGTCTTTGCCCTTGGTGATCTCTCTACGTAACCGATTGAAGATGACTTT GACTAACGCGGAAGTTACTAAGATTGTTATGCAAAAGTTAATCAAAGTACGATG GAAAAGTGAGGACCGACTCCAATTACCTGCTGGTATTATGGATGTTATTAC ATTGAAAAAAGTGGTGAATTTTTCCGACTCATCTATGATGTTTAAAGGACGATTT GCAGTGCACTCGTATTACTGCTGAGGAAGCAAAGTACAAACTATGCAAAAGTCAG GAGGATGCAAACTGCCCCCAAAGG
LD002	SEQ ID NO: 169 GCGTAATACGACTC ACTATAGGGTCCAC GTCCAAGTTTTTATG GGC SEQ ID NO: 171 GTCCACGTCCAAGT TTTTATGGGC	SEQ ID NO: 170 AAGCGATTAGAAAA AAATCAGTTGC SEQ ID NO: 172 GCGTAATACGACTC ACTATAGGAAAGCGA TTAGAAAAAAATCAG TTGC	SEQ ID NO: 168 GTCCACGTCCAAGTTTTTATGGGCTTTCTTAAAGAGCTTCAGCTGCATTTTTCAT AGATTCCAATACTGTGGTGTTCTGACTAGCTCCCTCCAGAGCTTCTCGTTGAA GTTCAATAGTAGTTAAAGTGCCATCTATTTGCAACTGATTTTTTTCTAATCGCTT
LD003	SEQ ID NO: 174 GCGTAATACGACTC ACTATAGGGCCAGG CGACCTTATGAAA GGC SEQ ID NO: 176 GCGTAATACGACTC ACTATAGGGGTGAC	SEQ ID NO: 175 GGTGACCAACCAACCG AATGGAG SEQ ID NO: 177 GCGTAATACGACTC ACTATAGGGGTGAC	SEQ ID NO: 173 GGTGACCAACCAACCGAATGAGATTGAGCGAGAAGTCAATATGCTTCTGGGA ATCAAGTCTCACAATGAAGCTTGGAAATATTACGACCTGCTTACGAACCTGTA TATGCTTTGACGGACCAACGACACGAGCATGATGGATTGATTTTGCAGGCCCC AACTTGAAAACCTTGTTTGGAGACGTCGTTCCAAAGAAATCTTCAATCTTCAAA CCCAAGACGTAATCAAGCTTCATACGGTTTCATCCAACTCCAAATACGCAC CAACCGAAGAAAGAGCATTTGCCCTTCAAAACAACCTGCGCTGATCTTTCTCTT

LD006	<p>CCCAGGCGACCTTA TGAAAAAGGC</p> <p>SEQ ID NO: 179 GCGTAATACGACTC ACTATAGGGGTGTT GGTTGCTTCTGGTG TG</p> <p>SEQ ID NO: 181 GGTGTGGTTGCTT CTGGGTG</p>	<p>CACCACCGAATGGA G</p> <p>SEQ ID NO: 180 GCTTCGATTCCGGCA TCTTTATAGG</p> <p>SEQ ID NO: 182 GCGTAATACGACTC ACTATAGGGCTTCG ATTCGGCATCTTTAT AGG</p>	<p>CCAAAGTCAGAAAGTTCTCTGGCAGCTTTACGGATTTTTGCCAAGGTATACTTGG ACTCGCCACACTTCACGTTTGTCTTAAGACCATAATCTCCTATGATTTTCAAC TCCTGATCAAGACGTGCCCTTTTCATAAGGTCGCCTGGG</p> <p>SEQ ID NO: 178 GGTGTGGTTGCTTCTGGTGTGGTGAATACATCGACACTCTTGAAGAAGAAA CTGTCAATGATTGCGATGAATCCTGAGGATCTTCGGCAGGACAAAGAATATGCT TATTGTACGACCTACACCCACTCGGAAATCCACCCGCCATGATCTTGGGCG TTTGGCGCTTATTATACCTTTCCCGATCATAACCCAGAGCCCAAGGAACACC TACCAGAGCGCTATGGGTAAAGCAAGCTATGGGGTCTACATTACGAATTTCCA CGTGCGGATGGACACCCCTGGCCACGTCGTATCTACCCGACAAACCTCTG GTCACACAGGCTCTATGGAGTATCTGCGGTTACAGAGAAATACCAAGCCGGGA TCAACAGTATAGTTGCTATTGCTTGTATCTGTTTATGTTTCCGATCCGTGTTTTAT TTATCTGAACCGCTCTGCTGTGGAAGAGGATTTTCCGATCCGTGTTTTAT CGTTCCTATAAAGATGCCGAATCGAAGC</p>
LD007	<p>SEQ ID NO: 184 GCGTAATACGACTC ACTATAGGACTGG CGGTTTTGAACACC C</p> <p>SEQ ID NO: 186 GACTGGCGGTTTTG AACACCC</p>	<p>SEQ ID NO: 185 CCTTCAATGTCCAT GCCACG</p> <p>SEQ ID NO: 187 GCGTAATACGACTC ACTATAGGCTTTCA ATGTCCATGCCACG</p>	<p>SEQ ID NO: 183 GACTGGCGGTTTTGAACACCCCTTCAGAAGTTCAGCAGCAATGTATCCTCAAG CTGTCAATGGCATGGACATTTTATGTCAAGCCAAATCTGGTATGGGCAAAACG GCAGTGTGTTTCTGGCGACACTGCAACAATTTGAACCCAGCGGACAATGTTG TTTACGTTTTGGTGATGTGCACACTCGTGAACCTGCTTCCAAATCAGCAAA GAGTACGAGAGGTTCAATAATATATGCCAGTGTCAAGGTGGCGTCTTTT CGGAGGAATGCCTATTGCTAACGATGAAGAAGTATTGAAAACAAATGTCCAC ACATTGTTGTGGGACGCTGGCGTATTTTGGCGTTGTCAAGTCTAGGAA GCTAGTCTCAAGAACCCTGAACACTTCAATCTTGTGATGAGTGCATATAAATGT TAGAAGTGTGGATATGAGGAGAGACGTCAGGAAATCTACAGAAACACCC TCACACCAAGCAAGTATGATGTTTCAAGTCCACACTCAGCAAGAAATCAGG CCGGTGTGCAAGAAATTCATGCAAGATCCAATGGAGGTGTATGTAGACGATG AAGCCAAATGACGTTGACGGATTACAACAGCATACGTTAACTCAAAGAA AATGAAAAGAAATAAAAATATTGAGTTGCTCGATGTTCTCGAATTTAATCAG GTGGTCAATTTTGTGAAGTCCGTTCAAAGGTGTGTGGCTTTGGCACAGTTGCT GACTGAACAGAAATTTCCAGCCATAGGAAATTCACAGAGGAATGGACCAGAAA GAGAGGTTGCTCGGTATGAGCAGTTCAAAGATTTCCAGAAAGAGAAATATTGCT AGCTACGAATCTCTTTGGGCGTGGCATGGACATTGAAAGG</p>
LD010	<p>SEQ ID NO: 189 GCGTAATACGACTC ACTATAGGCTTGT GCCCCCGAATGC</p>	<p>SEQ ID NO: 190 CTATCGGGTTGGAT GGAACCTG</p>	<p>SEQ ID NO: 188 GCTTGTGCCCCCGAATGCCCTTATAGGGTTGATTACCTTTGGGAAGATGGTC CAAGTGCACGAAGTAGTACCGAGGGCTGCAGCAAAATCTACGTTTCCGAG GGACGAAAGACCTCACAGCTAAGCAAGTTCAAGAGATGTTGGAAGTGGGCAG</p>

	<p>SEQ ID NO: 191 GCTTGTGCCCCCG AATGC</p>	<p>SEQ ID NO: 192 GCGTAATACGACTC ACTATAGGCTATCG GGTTGGATGGAAC CG</p>	<p>AGCCGCAGTAAGTGCTCAACCTGCTCCTCAACAACCCAGGACCAACCCATGAGG CCTGGAGCACTCCAGCAAGCTCCTACGCCACCAGGAAGCAGGTTCTTTCAAC CCATCTGAAATGCGACATGAACCTCACTGATCTATTGGAGAGTTGCAAGA GACCATGGCCTGCAACCAAGGAAATGCGCCCTTAGATCGACCGGACACA GCTTATCGATAGCCATTGGGTGGAGTGGAGTGCACATACGCCAATACTGGTGC CAGGGTCATGCTATTGTTGGAGGACCTTCTCTCAAGGCCCTGCTCAAGT TTGAATGATGATCTGAAGCAACCTATCAGATCTCACCACGACATCCAAAAAGA CAATGCCAAATACATGAAGAAACAAATCAAGCACTATGATAATTTAGCGATGA GAGCAGCAACGAATGGCCACTGCGTTGACATATATTCATGCGCTTTGGATCA GACAGGATTGATGGAGATGAACAGTGTGTAATTCACAGGGGGACATATG GTCATGGCGACTCGTTCAATCTCCCTGTTCAAGCAACGTTCCAGCGCAT ATTTTCGAAGATCAGAAAAACGAGCTGAAGATGGCATTAAATGGTACTCTGG AGGGTCAAGTGTCCAGGGAGTTGAAATTCAGGGCGTATTGGATCTTGTGT TTGTTGAATGTGAAGATCCTTTGGTTCCGACACCCGAAATAGGAATGGTA ACACGGTCCAGTGGAATGTGACGGTAACTCCAAGTACTACCATGGCCTT GTTCTCGAGGTGTCACCAACATCCGCTCCCATCAAGGGGGAAGG GGCTGCATACAGTTCATCAGCAATATCAGCATGCTAGTGGCCAGAAAGGA TCCGAGTAACGACAGTTGCTAGAACTGGCCGATGCTCCGCTAATATACAT CATGTCAAGTGTGATTCGATCAGGAGCGAGCGAGTGAATGGCGAGGA TGGCAGTTTACAGAGCGGAATCAGACGATAGCCCTGATTTTGAATGGGT CGATAGGATGTTGATACGCTGTGCCAGAAATTCGGCGAATATAACAAGGAC GACCCGAATTCGTTCCGCTTGGCGAAACTTCAGCCTCTACCCGCGATTCA TGACCATTTGAGAAGGTCACAGTTCCTGCAGGTGTTTAACTTCTCCCGAC GAAACGTCCTTCTACAGGACATGCTTATGCGGAAGACCTCAGCAGTCCG TGATCATGATCCAGCCGATCTACAGCTACAGTTTCAATGGACCACCCAGAA CCTGTGCTTTTGGATACGAGTTCATCCAAACCCGATAG</p>
LD011	<p>SEQ ID NO: 194 GCGTAATACGACTC ACTATAGGGCCATA GGAAGGCTTCTCA AAG</p> <p>SEQ ID NO: 196 GCCATAGGAAAGGC TTCTCAAAG</p>	<p>SEQ ID NO: 195 GGAAAAACGACATT TGTGAAACGTC</p> <p>SEQ ID NO: 197 GCGTAATACGACTC ACTATAGGGGAAA ACGACATTTGTGAAA CGTC</p>	<p>SEQ ID NO: 193 GCCATAGGAAAGGCTTCTCAAAGTTGTAGTTGGCAGAGATATCATAG TACTGCAATTCCTTCTCTATGAAAGACAATCTTTTCGCTTTTACTTTCTGT CTTTGATGTCAACCTTGTTCGCAAGTACTATCGGATATTTTACAGACTC TGACAAGATCTGTGCCAATTTGTACATCTTGTATGTAACTCTGGAAGTTA CATCAACATGATAAGCACACTGTCCCTGAATGTAATCCATCACGGAGA CCACCAAACTTCTCTGACCGGACGTGCTCCATACATTGAACCGAATAGGGC CCCTGTTTGTATGGAAGACCAAGGATGGACTTCACTCCCAAGTAGCTACA TATCTTTTTTCAAATTCACCAGTCAATGACGTTTCAACAAATGTCTGTTTTCC</p>
LD014	<p>SEQ ID NO: 199</p>	<p>SEQ ID NO: 200</p>	<p>SEQ ID NO: 198</p>

	<p>GCGTAATACGACTC ACTATAGGTTTCATT GAACAAGAGGCCAAA CG</p> <p>SEQ ID NO: 201 TTTCATTGAACAAGA GGCAAAACG</p>	<p>GCGAAATCAGCTCC AGACGAGC</p> <p>SEQ ID NO: 202 GCGTAATACGACTC ACTATAGGGCGAAA TCAGCTCCAGACGA GC</p>	<p>TTTCATTGAACAAGAGGCAACGAAAGGCGAGAAGAAATCGATGCCAAGGCC GAGGAAGAATTTAATATTGAAGAAGGGCGCCCTTGTTCAAGCAACACGTCTCAA GATTATGGAATATTATGAGAAGAAAGAGAAACAGGTCGAACTCCAGAAAAGAAA TCCAATCGTCTAACATGTTGAATCAGGCTCGATTGAAAGTATTGAAAGGTTAGG GAAGATCACGTTCTGACCGTACTAGAGGAGCGCGTAAACGACTTGGTCAGG TCACAAACGACAGGGAATAATTCCTCAATCTGGAAGCCTCATTTTGCAG GGATTATCAGCTTTTTGAGAAAGATGTACCATTCGAGTTCGGCCCCAGGA CCGAGAACTGGTCAAAATCCATCATTCACCACCGTCACGAAACAGTATAAGATG CCACCGGTAAGGACATCCATCTGAAAATTGATGACGAAATCCATCTGTCCCAA GAAACACCGGGGAATCGACCTGCTGGCGCAGAAAAACAAAATCAAGATCA GCAATACTATGAGGCTCGTCTGGAGCTGATTTCCG</p>
LD014_F1	<p>SEQ ID NO: 204 GCGTAATACGACTC ACTATAGGATGTTGA ATCAGGCTCGATTG</p> <p>SEQ ID NO: 206 ATGTTGAATCAGGC TCGATTG</p>	<p>SEQ ID NO: 205 CGTTTGTGACCTGA CCAAAGTC</p> <p>SEQ ID NO: 207 GCGTAATACGACTC ACTATAGGCGTTTGT GACCTGACCAAGTC</p>	<p>SEQ ID NO: 203 ATGTTGAATCAGGCTCGATTGAAAGTATTGAAGGTTAGGGAAGATCACGTTTCG TACCGTACTAGAGGAGGCGCGTAAACGACTTGGTCAGGTCACAAACG</p>
LD014_F2	<p>SEQ ID NO: 209 GCGTAATACGACTC ACTATAGGAAGATC ACGTTCTGTACCGTA C</p> <p>SEQ ID NO: 211 AAGATCACGTTTCGT ACCGTAC</p>	<p>SEQ ID NO: 210 CGTTTGTGACCTGA CCAAAG</p> <p>SEQ ID NO: 212 GCGTAATACGACTC ACTATAGGCGTTTGT GACCTGACCAAG</p>	<p>SEQ ID NO: 208 AAGATCACGTTTCGTACCGTACTAGAGGAGGCGCGTAAACGACTTGGTCAGGT CACAAACG</p>
LD014_C1			<p>SEQ ID NO: 213 AATGTTGAATCAGGCTCGATTGAAAGTATTGAAGGTTAGGGAAGATCACGTTTC GTACCGTACTAGAGGAGGCGCGTAAACGACTTGGTCAGGTCACAAACGATGT TGAATCAGGCTCGATTGAAAGTATTGAAGGTTAGGGAAGATCACGTTTCGTACC GTACTAGAGGAGGCGCGTAAACGACTTGGTCAGGTCACAAACGATGTTGAAT CAGGCTCGATTGAAAGTATTGAAGGTTAGGGAAGATCACGTTTCGTACCGTACT</p>

LD014_C2				AGAGGAGGCGGTAAACGACTTGGTCAGGTCACAAAGCG SEQ ID NO: 214 AAAGATCAGGTTCTGTAACCGTACTAGAGGAGGCGGTAAACGACTTGGTCAGG TCACAAACGAAGATCAGTTCGTACCGTACTAGAGGAGGCGGTAAACGACT TGGTCAGGTCACAAACGAAGATCAGTTCGTACCGTACTAGAGGAGGCGCGT AAACGACTTGGTCAGGTCACAAACGAAGATCAGTTCGTACCGTACTAGAGG AGGCGGTAAACGACTTGGTCAGGTCACAAACGAAGATCAGTTCGTACCGT ACTAGAGGAGGCGGTAAACGACTTGGTCAGGTCACAAACGCG SEQ ID NO: 215 CGCCGGAGAGTTTTTGTACGCTTCTTCAAAGCTTTGCGCAAGTTACTCTCAG ACTGCCAGCGAGTTGCTCATGATCTCCGGCCGTTTATCAAGAAGAAAGAA CGCCCCAGTCTCATTAGCCACGGCGAGCAATCAGGGTCTTACCCGTACCA GGGGGACCACATACAGCAGTATACCCCTAGGGGCTTACGCGCCGATAG
LD015	SEQ ID NO: 216 GCGTAATACGACTC ACTATAGGCGCGG AGAGTTTTTGTACG	SEQ ID NO: 217 CTATCGGCGTGAAG CCCC SEQ ID NO: 219 GCGTAATACGACTC ACTATAGGCTATCG GCGTGAAGCCCC		SEQ ID NO: 220 GGCATGTCATATAGGAATCTGGTGATGGATCGGTTACGTCCTTCAACACG GCCGGCACGTTATAGATGGTAGCTAAATCGGTGTACATGTAACTGGGAAA CCAGGACGACCGGACCTCTCTCTGGCAGCAGATACCTCACGCAAGCTT CTGCATACGAAAGACATATCTGTCAAGATGACCAAGACGTCTTCTCACATTGG TAAGCCAAAGATTTCGGCAGCTGTCAAAGCCAGACGAGGTAAATCTTTTC AATGGTAGGATCGTTGGCCAAATTCAGAACAGGACAGACATCTCCATAGAAC CGTCTCTCGAAATCCTGTTTGAAGAACCTAGCTGTTTCCATGTTAACACCCA TAGCAGCGAAACAAATAGCAAAAGTTATCTTCATGATCATCAAGTACAGATTTAC CAGGAATCTTGACTAAACCAAGCCCTGTCTACAGATCTGGCAGCAATTTCAATTG TGAGGACAGACCGCTGCAGAGAAATGGGGATCTTCTGACCCAGGCAATGG AGTTCATCAGCTCAATAGCTGTAAATACCCGCTGGATCTTCTCAGGATAG ATACGGGACCAAGGATTGATTGGTTGACCCCTGGATGTCAGCAAGTCTTCAG CCAAATTTGGGGACCTTTGTGATGGTTTCTGATCCATTGAAACACAGT CCCAACATATCTCAGAAACAGGAGTCTCAAATATCTCCTGTGAATTCACAA GCGGTGTTTTTGGCGTCGATTCTGATGTGCCCCCGAACACTTGAACCCACAG CTTTTGACCCACTGACTTCCAGAACTTGTCCCGAACGTATAGTGCCATCAGCC AGTTTGAGTTGTACGATTTCATTGTACTTGGGGAACCTTAAACATCTTCGAGGATT ACC
LD016	SEQ ID NO: 221 GCGTAATACGACTC ACTATAGGGGCATA GTCAATATAGGAATC TGGGTG SEQ ID NO: 223 GGCATAGTCAATATA GGAATCTGGGTG	SEQ ID NO: 222 GGTAATCCTCGAAG ATGTTAAGTTCC SEQ ID NO: 224 GCGTAATACGACTC ACTATAGGGGTAAT CCTCGAAGATGTTA AGTTCC		

LD018	<p>SEQ ID NO: 226 GCGTAATACGACTC ACTATAGGGGAGTC GCAGAAATACGAGA GCAC</p> <p>SEQ ID NO: 228 GGAGTCGCAGAAAT ACGAGAGCAC</p>	<p>SEQ ID NO: 227 GTAGAGGCTCCACC GTCAATCGC</p> <p>SEQ ID NO: 229 GCGTAATACGACTC ACTATAGGGTAGAG GCTCCACCGTCAAT CGC</p>	<p>SEQ ID NO: 225 GGAGTCGAGAAATACGAGAGCACCTTCTCGAACCAACCAAGCCTCCTTGAGG GTAAACAAGCCAGTCTGAGACTCGGACACTACACTTTGTTGGCGGAGA ACCCTCAAGGCTGCATAGTGTCTGCTACTTACTTAGCCATAGAACCGGTAACC ACCCAGGAAGGGTTGATCCACGAGTCCACCTTCAAGCAGCAACAGACCGGAAA TGGAGCAAAATCGACACCAAGCAAGACCTTGGCGCCTAACTTCGTCAGGGTTTG CGGGATAGAGAGTGACCGAGGGCAAGATGACCCGCTTCGACTGTCGGGT CACTGGTCTCCTTATCCAGAGTGTACATGGTACATAAACGGTCGACAAGTCA CCGACGACCACCAACCAAGATTTTGGTTAACGAATCCGGAACCATGCCCT GATGATCACCAACCGTGAGCAGGAACGACTCAGGAGTAGTGACCTGCGTCGC CAGGAACAAGACGGGAGAAACCTCCTTCCAGTCAACCTTAAACGTCAATCGAA AAGGAACAGGTAGTCCGCGCCCAAGTTCTGTGGAGAGATTACACAGTCAACG TGGCAGGAAGGAGAACCAAGTGTCTCTGCGCGCTAGAGCTGTTGGACGCGCGG TGCCGCGAATCACTTGGCAGAGGGACGGGCGCCCTAGCCAGCGGGGCC GACGTTGCGCATCGCGATTGACGGTGGAGCCTCTAG</p>
LD027	<p>SEQ ID NO: 231 GCGTAATACGACTC ACTATAGGGGAGC AGACGATCGGTTGG</p> <p>SEQ ID NO: 233 GGGAGCAGACGATC GGTTGG</p>	<p>SEQ ID NO: 232 TCGGACAGACTCGT TCATTTCCC</p> <p>SEQ ID NO: 234 GCGTAATACGACTC ACTATAGGTCGGAC AGACTCGTTCAATTC CC</p>	<p>SEQ ID NO: 230 GGGAGCAGACGATCGGTTGGTTAAATCTGGGACTATCAAAACAAACGTTGT GTCCAACCTTGAAGGACACGCCCAAAACGTAACCGGGTTGTTCCACC CTGAACCTACCTGTGGCTCTCACAGGCAGCGAAGATGGTACCGTTAGAGTTTG GCATACGAATACACACAGATTAGAGAATTGTTGAATTATGGGTTGAGAGAG TGTGGACCATTTGTTGCTTGAAGGTTTGAATATGTTTCTCTGGGGTATGAC GAGGGCAGTATATTAGTGAAGTTGGAAGAGAAACCGGCAGTTAGTATGG ATGCCAGTGGCGGTAAATAATTTGGGCAAGGCACCTCGGAATTACAACAAGC TAATTTGAAGGCGCTGCCAGAAAGTGGAGAAATAGAGATGGGAGCGTTTA CCTGTCTCTGTAAAGATATGGAGCATGTGAATATACCTCAAAACAATCCA ACATAATCCGAATGGAAGATTGTTGTAGTATCGGAGACGGCGGAATATATCA TTTACACAGCGATGGCTCTACGGAACAAGGCTTTTGAAGCGCTCAAGAGTTT GTCTGGGCTCAGGACTCCAGCGAGTATGCCATTCCGAGTCTGGTCCACAA TTCGGATATCAAAAACTTCAAAGAAAGGAACATTCGAAGTCGGATTTCAGC GCGGAAGGAATCTACGGGGTTTCTCTTGGGGATTAAATCGGTGTCGGTT TAACGTTTACGATTGGAAACTTTGGACTTGGTGGAGCGGATTGAATACAA CCGAGGGCGGTTTATTGGTCTGACAGTGGAAAATTAGTCTGTCTCGCAACGG AGGACAGCTACTTCATCCTTTCTTATGATTCGGAGCAAGTTCAAGAGGCCAGG GAGAACAAATCAAGTCGCAGAGGATGGCGTAGAGGCCGCTTTCGATGTGTTGG GGAAATGAACGAGTCTGTCCGA</p>

gfp	SEQ ID NO: 236 GCGTAATACGACTC ACTATAGGAGATAC CCAGATCATATGAAA CGG	SEQ ID NO: 237 CAATTTGTGTCCAAG AATGTTTCC	SEQ ID NO: 235 AGATACCCAGATCATATGAAACGGCATGACTTTTTCAGAGTGCCATGCCCGA AGGTTATGTACAGGAAAGAACTATATTTTCAAAGATGACGGAACTACAAGA CACGTAAGTTTAAACAGTTCGGTACTAACTAACCATACATATTTAAATTTTCAG GTGCTGAAGTCAAGTTTGAAGGTGATACCCCTGTTAATAGAAATCGAGTTAAAA GGTATTGATTTTAAAGAAGATGGAACACATTCTTGGACACAAATG
	SEQ ID NO: 238 AGATACCCAGATCA TATGAAACGG	SEQ ID NO: 239 GCGTAATACGACTC ACTATAGGCAATTTG TGTCCAAGAATGTTT CC	

Table 8-PC

Target ID	Primers Forward 5' → 3'	Primers Reverse 5' → 3'	dsRNA DNA Sequence (sense strand) 5' → 3'
PC001	SEQ ID NO: 474 GCATGGATGTTGGA CAAATTGGG	SEQ ID NO: 475 GCGTAATACGACTC ACTATAGGAGATTCA AATTTGATGTAGTCA AGAATTTTAG	SEQ ID NO: 473 GCATGGATGTTGGACAAATTTGGGGGTGCTTCGCCCTCGTCCATCCACCGGG CCTCACAAGTTGCGCAATCCCTGCTTTAGTGATTTCTTCGTAAACAGGCTGAA GTATGCCCTTACAAACAGTGAAGTCACTAAATTTGTCATGCAAGGTTGATCAAAG TTGATGGTAAAGTGAGGACTGATTCTAATTACCCCTGCTGTTTTCATGGATGTCATT ACTATTGAGAAAGACTGGTGAATTTTCCGCTGATCTATGATGTTAAAGGAAGATT TGCTGTGACCCGTATTACAGCTGAAGAGGCAAAATACAAAGTTGTGTAAGTAAGG AGAGTCCAAACTGGTCCCAAGGAATCCCATTTTGGTAACACATGATGGCAGAA CCATTGTTACCCCTGACCCCAACATCAAAGTGAATGACACAAATTCAAATGGAATTT GCTACATCTAAATTTCTTGACTACATCAAAATTTGAATCT
	SEQ ID NO: 476 GCGTAATACGACTC ACTATAGGCGATGG ATGTTGGACAAATTG GG	SEQ ID NO: 477 AGATTCAAATTTGAT GTAGTCAAGAATTTT AG	
PC003	SEQ ID NO: 479 CCCTAGACGTCCCT ATGAAAAGGCCC	SEQ ID NO: 480 GCGTAATACGACTC ACTATAGGTTGACA CGGCCAGGTCGGC CACC	SEQ ID NO: 478 CCCTAGACGTCCCTATGAAAAGGCCCGTCTGGATCAGGAATTTGAAAATTTATCGGC GCCTTTGGTTTACGAAACAAACCGTGAAGTGTGGAGTAAAGTACACTTTGGCTA AAATCCGTAAGCTGCTCGTGAACCTGCTACCCCTAGAAAGAAAAGAGCCTAAAAG ATTGTTGAAGGTAATGCACCTCTACGTCGTTTGGTGGCGAATTTGGTCTCTGGATG AGAACAGGATGAAGCTTGATTATGTTTGGTCTGAAAATTTGAAGATTTCTTGGAA AGAAAGGCTCCAAACTCAGGTGTTCAAATCTGGTCTGGCAAGTCAATTCATCATG CTAGAGTACTGATTAGGCAGAGACACATCCGGTGCAGAGCAGGTGGTGAACA TCCCTCGTTTCATCGTGGGCTGGACTCGCAGAAAGCACATCGACTTCTCCCTGAA GTGCGCCCTTCGGGGGTGGCCGACCTGGCCGTGTCAA
	SEQ ID NO: 481 GCGTAATACGACTC ACTATAGGCCCTAG ACGTCCTATGAAA AGGCC	SEQ ID NO: 482 TTGACACGGCCAGG TCGGCCACC	

PC005	<p>SEQ ID NO: 484 ATCCTAATGAAATCA ACGAAATCGCC</p> <p>SEQ ID NO: 486 GCGTAATACGACTC ACTATAGGATCCTAA TGAATCAACGAAAT CGCC</p>	<p>SEQ ID NO: 485 GCGTAATACGACTC ACTATAGGTTCCCTA CGTTCCCTGGCCTG CTTC</p> <p>SEQ ID NO: 487 TTCCCTACGTTCCCT GGCCTGCTTC</p>	<p>SEQ ID NO: 483 ATCCTAATGAAATCAACGAAATCGCCAAACACCAACTCAAGACAAAACATCCGTAAG CTCATCAAGGATGGTCTTATCATCAAGAACCCAGTGGCAGTACACTCTAGGGCCC GTGTACGCAAGAACACTGAAGCTAGAAGGAAGGAGGCAATGTGGATTGGAAA GAGGAAGGGTACGGCAATGCCGTATGCCCTCAAAGGAACCTGTGGTGACGCG CATGGCGTCTCTCAGGCGCTCTCTCAAAGATACAGGGAGGCCAAGAAATCGA CGCCATCTTTACCACGCCCTGTACATGAAGCGAAGGGTAACGTTCAGGAAC AAGAGGTCCTTATGGAGTACATCCACAAGAAAGGCAGAGAAAGGCCAGGGCC AAGATGCTGCTGACCAGGCTAACGCCAGGAGATTGAAGGTGAAGCAGGCCAGG GAACGTAGGGAA</p>
PC010	<p>SEQ ID NO: 489 GCTCAGCCTATTAC CGCCCAACGC</p> <p>SEQ ID NO: 491 GCGTAATACGACTC ACTATAGGGCTCAG CCTATTACGCCCA ACGC</p>	<p>SEQ ID NO: 490 GCGTAATACGACTC ACTATAGGATGGAA AATGAGTATCTGGA AGAAAG</p> <p>SEQ ID NO: 492 ATGGAAATGAGTAT CTGGAAGAAAG</p>	<p>SEQ ID NO: 488 GCTCAGCCTATTACCGCCCAACCGGTTGATTGGATTGATCACGTTCCGAAAAATG GTGCAAGTCCAGCAACTGGGTACCGAAGGCTGCAGCAAGTTCGTGTTCTGT GGAACGAAAGATCTCACCGCCCAAGCAAGTCCAGGAGATGTGGGCATTGGAAAA GGGTACCAAAATCCCAACAACAGCCAGGCAACCTGGCGGCCAGGGCAGCAAT CCCCAAGCTGCCCTGTACCAACCGGGGAGCAGATTCTTGCAGCCGTGTCAAAA TGCACATGAACCTTGACAGATCTGATCGGGAGTTGCAGAAAGACCCCTGGCCCC GTACATCAGGGCAAAAGACCTCTTAGATCCACAGGCGCAGCATTTGCCATCGCTG TCGGCCTCTTAGAATGCACCTATCCGAATACGGGTGGCAGATCATGATATTCTTA GGAGACCATGCTCTCAGGTCGCCGCCAGGTGTGAACGACGATTGAAGCAG CCCATCAGGTCCCATCATGACATACACAAGACAATGCCAAGTACATGAAGAAG CTATCAAAACATTACGATCACTTGGCAATGCGAGTGCACCTGCCACCAAGCCATTGCAT CGACATTTACTCTCGCCCTGGATCAGACGCGGACTGATGGAGATGAAGCAGTG CTGCAATCCACCGAGGGCAGATGGTTCATGGCGATTCTCAATTCTCTCTA TTCAAAACAAACCTCCAGCGAGTGTCTCAAAGACCCGAAAGACGACCTCAAGA TGGCGTTCAACGCCACCTTGAGGTGAAGTGTCCAGGGAGTTAAAGTCCAAAG GGGCGATCGGCTCGTGTCTCTTGAACGTTAAAGCCCTCTGGTTCCGATAC GGAACTAGGCATGGGAATACGTGCAGTGGAACTTTGCACGTTGGCGCCGAG CTCTACTGTGGCGTGTCTTCGAGGTGTTAACCCAGATTTCGGCGCCCATACCA CAGGGAGGCAGGGGCTGCATCCAGTCTATCACCAGTATCAGCACGCGAGCGG GCAAAGGAGGATCAGAGTGACCACGATTGCTAGAAATTTGGCGGACGCTACTGC CAACATCCACCACATTAGCGCTGGCTTCGACCAAGAAAGCGCGGCGAGTTGTGAT GGCCCGAATGGCCGGTTACAAGGCGGAATCGGAGAGACTCCCGACGTGCTCA GATGGGTGGACAGGATGTTGATCAGGCTGTGCCAGAAGTTCCGAGAGTACAAATA AAGACGATCCGAATTCGTTCAAGTTGGGGAGAACTTCAGTCTGTATCCGCGATT CATGTACCATTTGAGACGGTCCGAGTTTCTGCAGGTGTTCAATAATTTCTCCTGATG AAAGTGCGTTTTATAGGCACATGCTGATGCGTGAGGATTGACTCAGTCTTTGATC</p>

PC014	<p>SEQ ID NO: 494 CTGATGTTCAAAAC AAATCAACACATG</p> <p>SEQ ID NO: 496 GCGTAATACGACTC ACTATAGGCTGATG TTCAAAACAAATCA AACACATG</p>	<p>SEQ ID NO: 495 GCGTAATACGACTC ACTATAGGTGAGCG ATCAGATCCAACTA GCCTCC</p> <p>SEQ ID NO: 497 TGAGCGATCAGATC CAACCTAGCCTCC</p>	<p>ATGATCCAGCCGATTTTGACAGTTACAGTTACAGCTTCAACGGGCCCGCCGAGCCTGTGT TGTTGGACACAAGCTCTATTAGCCGGATAGAAATCCTGCTCATGGACACTTTCTTC CAGATACTCATTTTCCAT</p> <p>SEQ ID NO: 498 CTGATGTTCAAAACAAATCAACACATGATGGCTTTTCAATTGAACAAGAAGCCAAAT GAGAAAGCAGAAGAAATTTGATGCCAAGGAGGAGGAGGAAATCAACATTTGAAAAAG GGCGTTTGCTCAGCAACAGAGACTCAAGATCAGTCTCTAATATGTTGAATCAGGCTC GAAGCAAGTCGAACCTCAAAAGAAAAATTCAGTCTCTAATATGTTGAATCAGGCTC GTTGAAGGTGCTGAAAGTGAGAGAGGACCATGTCAGAGCAGTCTCTGAGGATG CTCGTAAAGTCTTGGTGAAGTAACCAAGACCAAGGAAATATCTCCAAATTTTG GAGAGCTAATCTCAAGGACTGTTCCAGCTGTTGAGAGGAGGAGTACGCTC CGCGTGAGACCGCAAGACAGGACCTGGTCAAGTCCATCCTGCCCAACGTCGCT GCCAAATACAAGGACGCCACCGGCAAGACATCTACTCAAGGTGACGATGAG TCGCACCTGTCTCAGGAGATCACGGAGGCTCGATTTGCTCGCTCAGAAAGAAC AAGATCAAGATCAGCAACACGATGGAGGCTAGGTTGGATCTGATCGCTCA</p>	<p>SEQ ID NO: 499 ACTGGTCATTCTTGA GGATGTCAAGT</p> <p>SEQ ID NO: 501 GCGTAATACGACTC ACTATAGGACTGGT CATTCTTGAGGATGT CAAGT</p>	<p>SEQ ID NO: 500 GCGTAATACGACTC ACTATAGGTGGGC ATAGTCAAGATGGG GATCTGC</p> <p>SEQ ID NO: 502 TTGGGCATAGTCAA GATGGGGATCTGC</p>	<p>ACTGGTCATTCTTGAAGGATGTCAAGTTTCCAAAAATCAATGAAATTTGCCAGCTCA AATTGGCAGATGGAATCTACGATCTGGACAAGTTTGGAAATCAGTGGATGATCAAA GGCAGTTGTTCCAGTATTTGAAGGCACATCAGGTATTGATGCTAAGAACACGGTG TGTGAGTCACTGGAGATATTCTAAGCAATCCAGTATCAGAGATATGCTGGGAC GTGCTTCAATGGATCAGGAAACCCATTGATAAAGTCCCGGATCCTGGCTGA GGACTACCTCGACATCCAAGGACAGCCGATCAACCCGTTGGTCCGTTATTTATCCC GAGGAAATGATCCAGACTGGGATCAGGCCATCGACGTGATGAATCTATCGCCA GAGGCGAGAAGATCCGATCTTCTCCCGCTGGGCTGCCCCACAAATGAGATTG CAGCCAGATTTGTAGGCAAGCTGGCTTGGTCAAAAGTACCTGGCAAGTCTGTGCT GGATGACCATGAAGACAATTTGCTATTGTTGTTGCTGCTATGGGTCAACATG GAACTGCCAGGTTCTCAAGCAGGACTTCGAAGAGAACGGCTCGATGGAGAAC GTGTGCTGTTCTTGAACCTTGGCCAAACGATCCGACCATCGAGCGCATCACGCG CGCGTTTGGCTCTGACGGCCCGCAATCTTGGCCCTACCACTGCGAGAGAACGACG TGCTGGTCACTTGACCGACATGTCGTGTCACGCGGAGGCGTTGCGTGAGGTGT CTGCCGCTCGAGAAGAAAGTCCCGGCGCTAGGGTTTCCCGGTTACATGTACA CCGATCTGCCACCATTTACGAGCGCGCGGTGCTGTGGAGGGCCGCAACGCGC TCCATCAGCGCAGATCCCCATCTTGACTATGCCCAA</p>
PC016	<p>SEQ ID NO: 499 ACTGGTCATTCTTGA GGATGTCAAGT</p> <p>SEQ ID NO: 501 GCGTAATACGACTC ACTATAGGACTGGT CATTCTTGAGGATGT CAAGT</p>	<p>SEQ ID NO: 500 GCGTAATACGACTC ACTATAGGTGGGC ATAGTCAAGATGGG GATCTGC</p> <p>SEQ ID NO: 502 TTGGGCATAGTCAA GATGGGGATCTGC</p>	<p>ACTGGTCATTCTTGAAGGATGTCAAGTTTCCAAAAATCAATGAAATTTGCCAGCTCA AATTGGCAGATGGAATCTACGATCTGGACAAGTTTGGAAATCAGTGGATGATCAAA GGCAGTTGTTCCAGTATTTGAAGGCACATCAGGTATTGATGCTAAGAACACGGTG TGTGAGTCACTGGAGATATTCTAAGCAATCCAGTATCAGAGATATGCTGGGAC GTGCTTCAATGGATCAGGAAACCCATTGATAAAGTCCCGGATCCTGGCTGA GGACTACCTCGACATCCAAGGACAGCCGATCAACCCGTTGGTCCGTTATTTATCCC GAGGAAATGATCCAGACTGGGATCAGGCCATCGACGTGATGAATCTATCGCCA GAGGCGAGAAGATCCGATCTTCTCCCGCTGGGCTGCCCCACAAATGAGATTG CAGCCAGATTTGTAGGCAAGCTGGCTTGGTCAAAAGTACCTGGCAAGTCTGTGCT GGATGACCATGAAGACAATTTGCTATTGTTGTTGCTGCTATGGGTCAACATG GAACTGCCAGGTTCTCAAGCAGGACTTCGAAGAGAACGGCTCGATGGAGAAC GTGTGCTGTTCTTGAACCTTGGCCAAACGATCCGACCATCGAGCGCATCACGCG CGCGTTTGGCTCTGACGGCCCGCAATCTTGGCCCTACCACTGCGAGAGAACGACG TGCTGGTCACTTGACCGACATGTCGTGTCACGCGGAGGCGTTGCGTGAGGTGT CTGCCGCTCGAGAAGAAAGTCCCGGCGCTAGGGTTTCCCGGTTACATGTACA CCGATCTGCCACCATTTACGAGCGCGCGGTGCTGTGGAGGGCCGCAACGCGC TCCATCAGCGCAGATCCCCATCTTGACTATGCCCAA</p>	<p>SEQ ID NO: 503 CAAGCTAACTTGAAGTACTACCAGAAAGGAGCTGAAATCAGAGATGGAGAACGTT TGCCAGTCAAGTAAAGGACATGGGAGCATGCGAGATTTACCCACAAACAATCCA</p>	<p>SEQ ID NO: 503 GCGTAATACGACTC ACTATAGGTTTTGGGA</p>	<p>SEQ ID NO: 504 CAAGCTAACTTGA GTACTACGAAAGG</p>
PC027	<p>SEQ ID NO: 504 CAAGCTAACTTGA GTACTACGAAAGG</p>	<p>SEQ ID NO: 505 GCGTAATACGACTC ACTATAGGTTTTGGGA</p>	<p>SEQ ID NO: 505 GCGTAATACGACTC ACTATAGGTTTTGGGA</p>	<p>SEQ ID NO: 505 GCGTAATACGACTC ACTATAGGTTTTGGGA</p>	<p>SEQ ID NO: 505 GCGTAATACGACTC ACTATAGGTTTTGGGA</p>	<p>SEQ ID NO: 505 GCGTAATACGACTC ACTATAGGTTTTGGGA</p>

SEQ ID NO: 506 GCGTAATACGACTC ACTATAGGCAAGCT AACTTGAAAGTACTA CCAGAAGG	ATTGAAGGCAATACT CGATCAG SEQ ID NO: 507 TTTTGGAATTGAAGG CAATACTCGATCAG	ACACAACCCCAATGGGCGGTTTGTAGTGGTTTGTGGTGATGGAGAATACATAATA TACACGGCTATGGCCCTTCGTAACAAAGCAATTTGGTAGCGCTCAAGAAATTTGTATG GGCAGGACTCGAGTGAATATGCCATCCGGAATCCGGATCCACCATTCGAATC TTCAAGAAATTTCAAGAAANAAGAAATTTCAAGTCCGACTTTGGTCCGAAGGAAT CTATGGTGGTTTCTCTGGGTGTAATCAAGTCCGACTTTGGTCCGTTCTATGACT GGAAACGCTTGAGTTAGTAAGGCGCATTGAATACAGCCTAGAGCTACTACTG GTCAGATAGTGCAAGTTGGTATGCCCTTGTACCGAAGATAGCTATTTTCATATTGT CCTATGACTCTGACCAAGTCCAGAAAGCTAGAGATAACAACCAAGTTGCTGAAGA TGGAGTGGAGGCTGCCCTTTGATGTCTAGGTGAATAAATGAATCCGTAAGAAACA GGTCTTTGGGTAGGAGACTGCTTCATTTACACAAACGAGTCAACCGTATCAACTA CTTTGTGGGTGGTGAATTTGGTAACATTTGCACATCTGGACCGTCTCTATATGTCC TGGGCTATGTACCTAGAGATGACAGTTATACCTTGGTTGATAAAGAGTTAGGAGTA GTCAGCTATCNAATTGCTATTATCTGTACTCGAATATCAGACTGCAGTCAATGCGAC GAGACTTCCCAACGGCTGATCGAGTATTGCCCTTCAATTCACAAA
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Table 8-EV

Target ID	Primers Forward 5' → 3'	Primers Reverse 5' → 3'	dsRNA DNA Sequence (sense strand) 5' → 3'
EV005	SEQ ID NO: 577 GACAAAACATCCGC AAACTG SEQ ID NO: 579 GCGTAATACGACTC ACTATAGGACAAA ACATCCGCAAACTG	SEQ ID NO: 578 GCGTAATACGACTC ACTATAGGCTCCTT GCATCAGCTTGATC SEQ ID NO: 580 CTCCTTGATCAGC TTGATC	SEQ ID NO: 576 GACAAAACATCCGCAAACTGATTAAAGATGGTCTTATTATTAAGAGCCTGTGCGG GTGCATTCGTGACCGTGTACGCAAAATACTGAAGCCCGCAGGAAAGGTGCTC ATTGTGGATTTGGTAAAGGAAAGGAACTGCAAAATGCTAGGATGCCAGAAAGGA ATTATGGATTCAACGTATGAGAGTTCTCAGAAAGGTTATTGAAGAAATATAGGGAAG CTAAGAAAATTGATAGGCATTTATACCATGCTTTATATATGAAGCTAAGGGAAT GTATTCAAGAAATAGAGAGTAAATGATGGACTATATCCATATAAAGAAAGGCGGAGAA AGCAGGTACAAAGATGCTCAATGATCAAGCTGATGCAAGGAG
EV009	SEQ ID NO: 582 CAGGACTGAAGAAT CTATAATAGG SEQ ID NO: 584 GCGTAATACGACTC ACTATAGGCAAGGAC	SEQ ID NO: 583 GCGTAATACGACTC ACTATAGGCTGGAA AGATGGGTAATACTT C SEQ ID NO: 585	SEQ ID NO: 581 CAGGACTGAAGAATCTATAATAGGAACAACCCAGGAATGGGTTTATAGGCCAATG CCCGACAACACGAAGAAAGTACCTTGATTTGGTTACAGGGTCTTAATAAACAA CTACGAAAATGGAATGAATCTCTCATATTTAGACAAGTATTACACTCCCG GAAAATAGAAAAGGGAATATCCAGTAAAGCGCTTTCATACGGAGAAAATTG ATTAGGGGACAAAGTATGTAGTGTAGTGTAGGGAATGGGAGCCGTGCACCCCG GAAATCATTTTGATTACCTCAGAAATGCGCCTTGATATTTCTGAAGCTGAACAG

	TGAAGAATCTATAAT AGG	CTGGAAGATGGGT AATACTTC	GATATATGGATGGGAACCGGAGTACTACAACGATCCAAATGATCTCCAGATGAT ATGCCGACGAGTTGAAGGACCATATACGTTATAATATCACCAATCCAGTGGAGA GAAATACCGTCTGGTGAACATGCGCAGGTGAAATCCGGCAGACGTGGAGTACTT GGCCCTGTGAAGTATTACCCATCTTTCCAG
EV010	SEQ ID NO: 587 CCAATGGAGACTTG AAGATGTC SEQ ID NO: 589 GCGTAATACGACTC ACTATAGGCCAATG GAGACTTGAAGATG TC	SEQ ID NO: 588 GCGTAATACGACTC ACTATAGGCTTCCCT CATCAACATGTGC SEQ ID NO: 590 CTTCCCTCATCAACA TGTGC	SEQ ID NO: 586 CCAATGGAGACTTGAAGATGTCTTCAACGCCATATTAGAAGTGAAGTGTCTAGA GAATTAAGTACAAAGGAGGTATAGTCTTGTCTCTCTAAATGTCAAAATCC TCTTGTCTCTGATTAGAAATAGGCATGGTAACACAGTTCAGTGGAACTGTGTA GCTTAAGTCCAAGCACTACGGTTGCCCTTATTTTCGAAGTTGTTAATCAGCATGCA GCACCAATTCCTCAAGGGGACGTGGATGCATTCAGTTTATTAATCAATATCAGC ATTCAAGTGGTCAAGAAAAAATAAGGGTAACATACTAAGCAAGAAATGGCGGA TGCCACTGCAAAATATTCACCATATTAGCGCTGGCTTGACGAACAACTGCGGCT GTTTTAATGGCGAGGATCGCTGTATATAGAGCAGAACTGATGAGAGTTCAAGATG TTCTCAGATGGGTGACAGAAATGTTGATACGATTGTGTCAGAAATTTGGAGAATAT AACAAAGATGACCAACAGCTTCAGGGCTCAGTGAAACTTCAGCTTATATCCACA GTTTATGATATCATCTACGTGCTGCCAAATTTCTACAAGTGTCAATAATTCACCAGA TGAACCTTCATCTATAGGCACATGTTGATGAGGGAAG
EV015	SEQ ID NO: 592 GTTAAGCCTCCAAG GGGTATTC SEQ ID NO: 594 GCGTAATACGACTC ACTATAGGGTTAAG CCTCCAAGGGGTAT TC	SEQ ID NO: 593 GCGTAATACGACTC ACTATAGGGAGCAC AAAGAGCCCAAGTC AG SEQ ID NO: 595 GAGCACAAAGAAGC CAAGTCAG	SEQ ID NO: 591 GTTAAGCCTCCAAGGGTATTCTCTTTACGGGCTCCCGCACGGGGAACG CTGATCGCCAGGCGGTGCCAACGAACTGGTGGCTTCTTCTCCTCATCAATG GGCCCGAGATTATGAGCAAGCTGGCCGGAGAATCCGAGAGCAATCTTAGAAAGG CTTTTGAAGAGGCTGATAAAACTCTCCTGCAATCATCTTTATCGACGAATTAGAC GCAATCGCTCCCAAGCGGAGAAGACTCATGGTGAGGTAGAGAGCGCATCGTC TCCCAACTGTTGACTTTGATGGACGGCATGAAGAAAGTTCCCATGTGATCGTGA TGGCGGCCACGAACAGGCCCAATTCATCGACCCCTGCACTCAGACGTTTCGGCC GATTGACAGAGAGATCGACATCGGTATCCCGACGCTACTGGAAGATTAGAAGT ACTCAGAAATACACACCAACCAATGAAATTTGGCTGACGATGTAGATTTGGAACAGA TTGCCGACAGAGACTCACGGTCATGTAGGTGCTGACTTGGCTTTTGTGCTC
EV016	SEQ ID NO: 597 GGTGATCCTTGATA GTGTTAAG SEQ ID NO: 599 GCGTAATACGACTC ACTATAGGGGTGAT CCTTGATAGTGTAA	SEQ ID NO: 598 GCGTAATACGACTC ACTATAGGCCCTCAG CATAAGATGACATG SEQ ID NO: 600 CCTCAGCATAAGAT GACATG	SEQ ID NO: 596 GGTGATCCTTGATAGTGTAAAGTTTCCAAAATTTAACGAAATTTGTACAGCTCAAGTT ATCAGATGGAACAGTTAGGTCTGGACAAGTTTGGAAAGTCAGTGGACAGAAGGCG GTTGTCCAAGTTTGAAGGCACCTCCGGAATGATGCTAAAACACCTTTATGTGA ATTTACAGGAGATATCTTAAAGAACTCCAGTGTCTGAAGATATGTTGGTGTGTGT TTAATGGATCTGGAAGCCTATCGATAAGGGCCCAATCTTAGCTGAAGATTTT CTTGACATTCAGGTCAACCTATAAATCCTTGGTCTGTCGATCTATCCAGAAGAAAT GATCCAGACTGGTATTTCTGCGATTGATGTGATGAATCCATTGCCAGAGGACAAA

	G		AGATTCCAATTTTCTCTGCAGCTGGTTTACCCCAACAATGAAATGGCTGCTCAAATC TGTAACAAGCTGGTCTTGTCAAAATCCAGGAAATCTGTCTTAGATGATCATGA AGACAACCTTGTCTATCGTTTCGCCGCTATGGTGTAATGGAACAGCCAGAT TCTTCAAGCAAGATTTTGAAGAGAAATGGCTCTATGAAATGTGCTTATTTTG AACTTGGCCAATGATCCTACCAATTGAAAGAAATTATAACACCCCGTTTGACTTTAAC AGCGGCTGAATTTATGGCATATCAATGTGAGAAGCATGTGTTAGTCATATTGACTG ACATGTCATCTTATGCTGAGG
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Table 8-AG

Target ID	Primers Forward 5' → 3'	Primers Reverse 5' → 3'	dsRNA DNA Sequence (sense strand) 5' → 3'
AG001	SEQ ID NO: 769 GCGTAATACGACTC ACTATAGGGCATGG ATGTTGGACAAATTG G SEQ ID NO: 771 GCATGGATGTTGGA CAAATTGG	SEQ ID NO: 770 GATTTCCAGTTGGAT GGTGTCG SEQ ID NO: 772 GCGTAATACGACTC ACTATAGGGATTTCC AGTTGGATGGTGTC G	SEQ ID NO: 768 GCATGGATGTTGGACAAATTTGGGGGGTGTGTTGCCCCCAAGGCCCTCCACCCGGG CCACACAAGCTCAGGGAGTCCCTTCCATTAGTATTCTTTCGTAACAGGTTGAA GTACGCCCTGACAAACTGTGAGGTGACCAAGATCGTTATGCAGAGACTTATTAAG GTCGACGGCAAGTCAGGACTGATCCTAACTATCCTGCTGGATTCATGGATGTGA TCACCATTTGAAAAAAGTGGTGAATTTCTCCGTTTGATCTATGATGTTAAGGGAAGA TTCACTATTACAGGATCACTGCTGAAGAAGCAAAATACAAATTTGTCAAAAGTCCG CAAGGTGCAAAACCGGACCAAAAGGTTTCCATTCTTGGTCACCCACGATGGTAGG ACCATTAGTACCCTGACCCCAATGATCAAGGTAAACGACACCATCCAACTGGAAA TC
AG005	SEQ ID NO: 774 GCGTAATACGACTC ACTATAGGCAACAC CAACTCGAGGCAAA AC SEQ ID NO: 776 CAACACCAACTCGA GGCAAAAC	SEQ ID NO: 775 CCTTTTCCTTCTGG CGTTAG SEQ ID NO: 777 GCGTAATACGACTC ACTATAGGCCCTTTTG CCTTCTGGCGTTAG	SEQ ID NO: 773 CAACACCAACTCGAGGCAAAACATCCGTAAATTGATCAAGGATGTTTGATCATT AGAAACCGGTGGCAGTGCACTCTAGGGCTCGTCCGTAAACACACAGAAGCTC GCAGGAAGGGAAGGCACCTCGGTTTCGGTAAGAGGAAGGTACAGCGAACGCTC GTATGCCCTCAAAAGGAACATATGGATCCAAAGGATCGCTGTCTTGAGGCGTCTCCT GAAAAAATACAGGGAAGCCAAAAGATCGACAGGCATCTGTACCCCGCTGTAC ATGAAGGCCAAGGGTAACGTGTTCAAGAACAAAGAGAGTGTGATGGAATACATCC ACAAGAAGAAGGCTGAGAAGGCCCGTCCCAAGATGTTGGCCGACCAAGCTAACG CCAGAAGGCCAAAAGG
AG010	SEQ ID NO: 779 GCGTAATACGACTC ACTATAGGCAAACTT TCCAAAGGGTGTTTC	SEQ ID NO: 780 GAAGGATGCCCTGGT CATCTTTG	SEQ ID NO: 778 CAAACCTTCCAAAGGGTGTTCGCGAAGGACCAAGATGGACATTTGAAGATGGCTT TCAACGGTACTTTGGAGGTGAAGTGTCTAGGGAATTAAGTTCAAGCGCGGTAT TGGCTCATGCGTGTGCTGCTAAATGTAAAAAGTCCTTTGGTAGCGGACACGGAAATA

	G SEQ ID NO: 781 CAAACCTTCCAAAG GGTGTTCCG	SEQ ID NO: 782 GCGTAATACGACTC ACTATAGGGAAGGA TGCCTGGTCATCTTT G	GGCATGGGAAACACCCGTGCAATGGAAGATGTGCACCTTCAACCCTAGCAGCAG ATGGCGCTGTTTTTCGAGGTGGTCAATCAGCATTCGGCCCCCATCTCCTCAAGGTG GTAGAGGATGTATACAGTTTATTACACAATATCAGCACTCGAGTGGCCAAAGGAG GTAAGGGTGACGACGATAGCAGAAATTTGGCGGACGATCGCGGAATATTCA CCACATCAGCCGCGGTTTCGATCAGGAACGTTGCCGCGGTGATTATGGCCCCGGAT GGCTGTTTATAGAGCGGAGACCGATGAGATGCCGATGTTTTAAGATGGGTCCGAT CGGATGCTGATTCTGTTGTGTCAAAAGTTTGGAGAATATAACAAAGATGACCAGG CATCCTTC
AG014	SEQ ID NO: 784 GCGTAATACGACTC ACTATAGGGAAG GCCGAGGAAATTGA TG SEQ ID NO: 786 GAAAAGGCCGAGGA AATTGATG	SEQ ID NO: 785 CAACTGTTGCGAAA TCAGGTCC SEQ ID NO: 787 GCGTAATACGACTC ACTATAGGCAACTG TTGCGAAATCAGGT CC	SEQ ID NO: 783 GAAAAGGCCGAGGAAATTTGATGCCAAGGCGGAAGAAGAAATTTAACATTGAAAAGG GCCGCCCTTGTGCAACAACAAGATTGAAGATCATGGAATACTATGAGAAGAAGGA GAAGCAAGTCGAACTACAAAAGAAATTTCAATCCTCCAACATGCTGAACCAAGCC CGTCTTAAGGTTCTGAAAGTCGCGAAGATCATGTTAGAGCTGATTGGATGAGG CTCGCAAGAAGCTTTGGTGAAGTCAACGAGGATCAAGGCAAAATATGCCAGATTCT GGAATCTTTGATCCTTCAGGGACTCTACCAGCTTTTCGAGGCAAACTGACCCGTA CGCGTCCGCCCAAGACAGAACCTTAGTCCAATCAGTGTGCCAACCATCGCAA CCAAATACCGTGACGTACCGCCGAGATGTACACCTGTCCATCGATGACGAAAC TCAACTGTCCGAATCCGTAAACCGGCGGAATCGAACTTTTGTGCAAAACAAACAAA ATTAAGGCTCTGCAACACCCCTGGAGGCACGTTTGGACCTGATTTCGCAACAGTTG
AG016	SEQ ID NO: 789 GCGTAATACGACTC ACTATAGGGTGTTC AACGGATCAGGAA ACC SEQ ID NO: 791 GTGTTCAACGGATC AGGAAAACC	SEQ ID NO: 790 CGACCGGCTCTTTC GTAAATG SEQ ID NO: 792 GCGTAATACGACTC ACTATAGGCGACCG GCTCTTTTCGTAAATG	SEQ ID NO: 788 GTGTTCAACGGATCAGGAAACCCATTGACAAAGGTCTCCAATCTTAGCCGAAG ATTTCTTGGACATCCAAGTCAACCCATCAACCCATGGTCGGTATCTACCCCGGA AGAAATGATCCAGACCGGTATCTCCGCCATCGACGTGATGAACCTCATCGCGCGT GGCAAAAATCCCATTTTCTCCGCGCGCGTTTACCGCACAAACGAAATCGCCG CCCAATCTGTAGACAGCGCGTTTAGTCAAACTGCCGGCAATCGGTAATCGA CGATCAGGAGACAAATTCGCCATCGTGTTCGCCGCCATGGGTGTCACATGGAA ACCGCCGTTTCTTCAAGCAGGACTTCGAAGAAACGGTTCCATGGAGAACGTGT GTCTCTTCTTGAATTTGGCCCAACGATCCACCATCGAGAGAAATCATCACGCCCG TTTGCTCTGACCGCGCGCAATTTTGGCTTATCAATCGAGAAACACGTGCTG GTTATCTTAACTGATGTCTTCTACGCCGAGGCTTTCGCCGTTACATGTACACCGATTG CAGAGAAGAAGTACCCGAGCGTGTGGTTCGCCCGGTTACATGTACACCGATTG GCCACCATTTACGAAAGAGCCGGTCCG

Table 8-TC

Target ID	Primers Forward 5' → 3'	Primers Reverse 5' → 3'	dsRNA DNA Sequence (sense strand) 5' → 3'
TC001	SEQ ID NO: 864 GCGTAATACGACTC ACTATAGGCTGCCA AACAGGCTGAAGTA TGC	SEQ ID NO: 865 GGTGTGCCCATTTG CATCCT	SEQ ID NO: 863 CTGCGAAACAGGCTGAAGTATGCCTTGACCAACTCAGAAGTGACGAAGATTGTTA TGCAAGATTGATTAAAGTTGACGGAAAAGTTAGACAGACCCCAACTACCCCGC GGTTTCATGGATGTTGTGACTATTGAGAAAACCTGGGAAATCTTCCGCTTGATTT ATGATGTTAAGGGAAGGTTCACAATCCATCCGCTTACTGGAGAAGAGGCCAAATA TAAATTGTCAAGTGAAGAAAGTACAGACAGGCCCCCAAGGCCATTCCTTCTTG GTGACCCGCGACGACGACCTATCAGATACCCAGACCCCATGATCAAAAGTGAAT GACACCAATCAATTGGAGATTGCCACTTCGAAAATCTTGATTTATCAAAATTTGAG TCCGGTAATTTGTATGATTACTGGAGGTCTGAATTTGGGGCGTGTGCGGTACAG TGGTGAGCCGAGAACGTCAACCCAGGTTCTTCGACATCGTTTCATATTAAAGGATGC AAATGGGCACACC
	SEQ ID NO: 866 CTGCGAAACAGGCT GAAGTATGC	SEQ ID NO: 867 GCGTAATACGACTC ACTATAGGCGTGTG CCCATTTGCATCCT	SEQ ID NO: 868 CATCCATGTTGAGGTGGGCATTTTTGAGGGCGTCCGCTGCGTTTTTCATCGTTTT GAGTACGGCTGTGTGGTGTGGCCCTCGAGGGCCTCCCGCTGCATCTCGAT GGTCTGAGGGTGCCATCGATCTGCTGGAGCTGCTTTTCGTAGCGTTTTCTTCCTC TTGATGGCCTGGATGGCGCTGTTCAACAAG
TC002	SEQ ID NO: 869 GCGTAATACGACTC ACTATAGGCATCCAT GTTGAGGTGGCA	SEQ ID NO: 870 CTTTGTGAACAGCG GCCATC	SEQ ID NO: 871 GCGTAATACGACTC ACTATAGGCTTTGTG AACAGCGGCCATC
	SEQ ID NO: 871 CATCCATGTTGAGG TGGCA	SEQ ID NO: 872 GCGTAATACGACTC ACTATAGGCTTTGTG AACAGCGGCCATC	SEQ ID NO: 873 ATGTCCTGTAATCTGAGGTTCCTCATTGGGCGATTGTCTACCGTGAAAAATCA AAATTTGGAAAATGTGTCCATGAGAAGGATCCGATCGGGTTGAATGGAACCTAGT GTCGAGGAGGACGGGTTGAGGGGGCCGTTGAACTATACTGTACAAAATCGG CTGGATCATAAATGAGACTTTGGGTGAGGTCTCCCGCATCAGCATGTGGCGGTAG AACGAGGTCTGCTGCGGAGTTGTTGAAAACCTTGGAGGAATTGGGAGCGGCGC AAATGGTACAT
TC010	SEQ ID NO: 874 GCGTAATACGACTC ACTATAGGATGTAC CATTTGCGCGGCTC	SEQ ID NO: 875 ATGTCCTGGTACTT GAGGTTCTCTC	SEQ ID NO: 877 GCGTAATACGACTC ACTATAGGATGTCTC GGTACTTGAGGTTT CTCC
	SEQ ID NO: 876 ATGTACCATTTGCG CCGCTC	SEQ ID NO: 878 GCGTAATACGACTC ACTATAGGATGTCTC GGTACTTGAGGTTT CTCC	SEQ ID NO: 879 CAACAGCGCTTGAAGATCATGGAATATTACGAGAAGAGGAGAAACCGGTGGAAT
TC014	SEQ ID NO: 879 GCGTAATACGACTC	SEQ ID NO: 880 ACAAGGCGGTACGA	SEQ ID NO: 880 CAACAGCGCTTGAAGATCATGGAATATTACGAGAAGAGGAGAAACCGGTGGAAT

	ACTATAGGCAACAG CGCTTGAAGATCAT GG SEQ ID NO: 881 CAACAGCGCTTGAA GATCATGG	ATTTCTGG SEQ ID NO: 882 GCGTAATACGACTC ACTATAGGACAAGG CCGTACGAAATTTCT GG	TGCAGAGAAAAATTCAGTCGTCAAAACATGCTGAACCAAGCCCGTTTGAAGTATTA AAAGTGGTGAAGACACAGTCCACAATGTCTGGATGACGCCCGCAACCGTCTG GGCGAAATCACCAATGACCAAGGAGATATTCACAACATTTTGGAGTCTCTTATCCT CCAGAGTCTTACCAGTACTTGGGAATCAGTATGAGTTTGGAGAACAAATAG TGGTGAGAGTCAGGCAACAGGACGAGGATATAATCCAGGGCATCTCCAGTTGT TGGACGAAATACAGGACGCCACTGGTAAAGACGTTTCATCTTAAATCGACGAT GAGAGCCACTTGCCATCCGAAACCCAGGAGGAGTGGTTTGTATGCGCAAAAG GGTAAATCAAGATTGACAACACCTTGGAGGCTCGTTTGGATTTAATTGCACAGCA ACTTGTGCCAGAAATTCGTACGGCCCTTGT
TC015	SEQ ID NO: 884 GCGTAATACGACTC ACTATAGGCGATAC AGTGTGCTGAAAG GGAAG SEQ ID NO: 886 CGATACAGTGTGTC TGAAAGGGAAG	SEQ ID NO: 885 TCGGATTCGCCGGC TAATTTAC SEQ ID NO: 887 GCGTAATACGACTC ACTATAGGTCGGAT TCGCCGGCTAATTT AC	SEQ ID NO: 883 CGATACAGTGTGCTGAAAGGGAAGCGGGGAAAGAGACCGTCTGCAATTGTGCT GGCCGACGAAACTGCCCGATGAGAAGATCCGGATGAACAGGATCGTCAGGAA TAATCTACGGGTAGGCTCTCTGACGTCTGTGGATCCAGCCCTGTCCCGACGTC AAATACGGGAAGAGGATCCACGTTTGGCCATCGATGACACGGTCAAGGGCTC GTCGAAATCTCTCGAGGTGTAATAAACCCATACCTCTCGAAGCTTATCGACC AATCCACAAGCGGACGTTTTCATCGTCCGTGGTGGCATCGAGCCGTTGAATTC AAAGTGGTGAACCGGAACCGTACCATATTGTATCGTCCCCCGATACCGTCA TCCATTGTGACGGCGATCCGATCAACAGGAGAAGAGGAGGAAAGCCCTTGAACG CCGTCGGCTACGACGATATCGCGGTTGTCGCAAAACATCGCACAAATCAAAGA AATGTCGAATTACCTCTACGCCACCCGTCGCTCTTCAAGGCCATTGGCGTGAAA CCACCACGTGGTATCCTCTTGTACGGACCTCCAGGTACCGGTAAACCTTTAATCG CACGTGCAGTGGCCAAACGAAACCGGTCTTCTTCTTCTTAAATCAACGGTCCCGA AATTATGAGTAAATTAGCCGGCGAATCCGA

Table 8-MP

Target ID	Primers Forward 5' → 3'	Primers Reverse 5' → 3'	dsRNA DNA Sequence (sense strand) 5' → 3'
MP001	SEQ ID NO: 1042 GCGTAATACGACTC ACTATAGGGTTTAAA CGCACCCAAAGCAT GG SEQ ID NO: 1044	SEQ ID NO: 1043 CAATACCAACACGC CCTAAATTGC SEQ ID NO: 1045 GCGTAATACGACTC ACTATAGGCAATAC	SEQ ID NO: 1041 GTTTAAACGCACCCAAAGCATGGATGTTGGACAAATCGGGGGGTGCTTCGCTCC ACGTCCAAGCACCGGTCCACACAAACTTCGTGAATCACTACCGTTATTGATCTTCT TGGTAATCGTTTGAAGTATGCACCTACTGTGCGGAAAGTCAACCAAGATTGTCATG CAAAGATTAATCAAGTTGATGGCAAAAGTCGTAACCCACCTAATTATCCAGCCG GTTTATGGATGTTATATCTATCCAAAAGACCAAGTGAAGCTTTAGATTGATCTATG ATGTGAAAGGTGCTTTCACCATCCACAGAAATTAATCCTGAAGAAGCAAAATACAAG TTGTGTAAAGTAAAGAGGGGTACAAACTGGACCCAAAGGTGTGCCATTTTAACTAC

	GTTTAAACGCACCC AAAGCATGG	CAACACGCCCTAAA TTGC	TCATGATGGCCGTACTATTGCTACCCCTGACCCTAACATCAAGGTTAATGACACTA TTAGATACGATATTGCATCATCTAAATTTTGGATCATATCCGTTTTGAAACTGGAA ACTTGTGCATGATAAAGTGGAGGTCGCAATTTAGGGCGTGTGGTATTG
MP002	SEQ ID NO: 1047 GCGTAATACGACTC ACTATAGGGGTGGC AAAAAGGAAGAGAA GG SEQ ID NO: 1049 GGTGGCAAAAAGGA AGAGAAGG	SEQ ID NO: 1048 GCTGATTTAAGTGC ATCTGCTGC SEQ ID NO: 1050 GCGTAATACGACTC ACTATAGGGCTGAT TTAAGTGCATCTGCT GC	SEQ ID NO: 1046 GGTGGCAAAAAGGAAGAGAGAGGGACCACATCAACCGAAGATCGGATACAAAAAGCTT CGATCCACTGAAGAGATGCTGATAAAGAAACAAGAAATTTTAGAAAAAATTTGA ACAAGAAGTAGCGATAGCCAAAAAATGGTACAACCTAATAAACGAGCTGCATTG CAAGCATTGAAGCGTAAGAAACGGTACGAACAACAATAGCCCAAATTGATGGTA CCATGTTAACTATTGAACAACAGCGGGAGGCATTAGAAGGTGCCAACACAAATAC AGCAGTATTGACTACCATGAAAACCTGCAGCAGATGCACCTTAAATCAGC
MP010	SEQ ID NO: 1052 GCGTAATACGACTC ACTATAGGCAGACC CTGTTCAGAATATG SEQ ID NO: 1054 CAGACCCGTGTTGAG AATATG	SEQ ID NO: 1053 GCATTGGGAATCGA GTTTTGAG SEQ ID NO: 1055 GCGTAATACGACTC ACTATAGGGCATTG GGAATCGAGTTTTG AG	SEQ ID NO: 1051 CAGACCCCTGTTCAGAATATGATGCATGTTAGTGTGCTGCTTATGATCAAGAAGCATCT GCCGTTTTAATGGCTCGTATGGTAGTGAACCGTGTGAAACTGAGGATAGTCCAG ATGTGATGGCTGGGTGATGCTAGCTACGCTATACGCTTGTCAAAAATTTGGTGAT TATCAAAAAGATGATCCCAATAGTTCCGATGCCAGAAAACCTCAGTTTATATCCCA CAGTTTCATGTATCATTTAAGAAAGGTCCTCAATTTCTACAAGTTTTTAATAATAGTCTT GATGAAACATCATATTATAGGCACATGTTGATGCGTGAAGATGTTACCCAAAGTTT AATCATGATACAGCCCAATTTCTGTATAGCTATAGTTTTAATGGTAGGCCAGAACCTG TACTTTTGGATACCAAGTAGTATTCACCTGATAAAATATTATGATGGACACATTTT TCCATATTTTGATATTCATGGAGAGACTATTGCTCAATGGAGAGCAATGGATTAT CAAAATAGACCAGAGATAGTAACCTCAAGCAGTTGCTTCAAGCCCCCGTTGATG ATGCTCAGGAAATTTCTCAAAACTCGATTCCCAATGC
MP016	SEQ ID NO: 1057 GCGTAATACGACTC ACTATAGGGTTTTCA ATGGCAGTGGAAAG C SEQ ID NO: 1059 GTTTTCAATGGCAGT GGAAAGC	SEQ ID NO: 1058 CGTGGTGTAAATGAT ACGCTC SEQ ID NO: 1060 GCGTAATACGACTC ACTATAGGGCTGGT GTAATGATACGCTC	SEQ ID NO: 1056 GTTTTCAATGGCAGTGGAAAGCCGATAGATAAAGGACCTCCTATTTTGGCTGAAG ATTATTTGGATATTGAAGGCCAACCTATTAAATCCATACCTCCAGAACATATCCCAAG AAATGATTCAAACTGGTATTTTCAGCTATTGATATCATGAACCTATTGCTCGTGAGC AAAAATCCAAATATTTTCAGCTGCAGGTTTACCACATAATGAGATTGCTGCTCAAA TTTTGAGACAAGCTGGTCTCGTTAAAAAACCTGGTAAATCAGTTCTTGACGATCAT GAAGACAATTTTGGCTATAGTATTTGCTGCTATGGTGTAAATATGGAACAGCCAG ATTCTTTAAACAAGATTTGAGGAAAATGGTTCAATGGAGAAATGTTTGTGTTCTT GAATTTAGCTAATGATCCTACTATTGAGCGTATCATACACCACG
MP027	SEQ ID NO: 1062 GCGTAATACGACTC	SEQ ID NO: 1063 CCAAAAATACCATCT	SEQ ID NO: 1061

	ACTATAGGGCTCGT TTGTTTCCATCCAGA AC SEQ ID NO: 1064 GCTCGTTGTTTCCA TCCAGAAC	GCTCCACC SEQ ID NO: 1065 GCGTAATACGACTC ACTATAGGCCAAAA ATACCATCTGCTCCA CC	GCTCGTTGTTTCCATCCAGAACTCCCATCGTGTAACTGGCTCAGAAAGATGGTA CCGTGAGAAATTTGGCATTCTGGTACTATTCGATTAGAAATCATATAAATATGGG TTAGAAGGTGATGGACAATCTGTTGCTTACGGGATCTAATAATGTAGCTCTAGG TTATGATGAAGGAAGTATAATGGTTAAAGTTGGTGTGAAGCCAGCAATGTCAA TGGATGTTGATGGGGTAAATTTGTTGGCACGTCATAGTGAATTTCAACAAGCT AACCTTAAGCGATGCTTCAAGCAGAAAGGAGCCGAAATCAAGAGTGGTGAACGTT TACCAATACAAGTTAAAGACATGGTAGCTGTGAATTTATCCACAGTCAATATCT CATAATCCGAATGGTAGATTTTAGTAGTATGTTGGTATGGAGAGTATATATAT ACATCAATGGCTTTGCGTAAATAAGCAATTTGGCTCCGCTCAGGATTTTGATGGTC TTCTGATTTCTGAGTATGCCATTAGAGAAATTTCTTACAAATCAAAAGTTTTAAAAA TTTTAAAGAAAAAAGTCTTTTAAACCAGAAAGGTGGAGCAGATGGTATTTTTGG
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Table 8-NL

Target ID	Primers Forward 5' → 3'	Primers Reverse 5' → 3'	dsRNA DNA Sequence 5' → 3'
NL001	SEQ ID NO: 1573 GCGTAATACGACTCA CTATAGGGAATCAT GGATGTTGGACAAAT TGG SEQ ID NO: 1575 GAAATCATGGATGTT GGACAAATTGG	SEQ ID NO: 1574 ACTGAGCTTCACA CCCTTGCCC SEQ ID NO: 1576 GCGTAATACGACT CACTATAGGACTG AGCTTACACCCCT TGCCC	SEQ ID NO: 1572 GAAATCATGGATTTGGACAAATTTGGTGGTGTGTATGCACCCCGACCCAGCACA GGTCCACACAAGCTGCGAGAATCTCTCCACTTGTCATATTTTTCGTAATCGGCT CAAGTACGCTTTAACTAACTGTAAGTGAAGAAATTTGTATGCAGCGTCTCATCA AGGTTGACGGCAAAGTGAGGACTGACCCCACTATCTCGAGGTTTTATGGACGT TGTTCAAATCGAAAAGACAAACGAGTTCTTCCGTTTGTATGATGTTAAGGGAC GTTTCACCATCCACAGGATCACAGCTGAAGAGCTAAGTACAAGCTGTGCAAAAGT GAAGAGGGTTCAGACAGGACCCCAAGGGCATTCATTTTGACCACTCAGCATGGA CGCACCATCAGGTATCCAGACCCCTTAGTAAAGTCAATGACACCATCCAATTGG ACATTGCCACATCCAAATCATGGACTTCATCAGATTGACTCTGGTAACCTGTGT ATGATCACTGGAGTGTAACTTGGGTCGTGGGCACTGTCGTGAACAGGGAG CGACACCCGGGCTCTTCGACATCGTGCACATCAAGGACGTGTTGGACACACTT TTGCCACTAGGTTGAACAACGTTTTCATCATCGGCAAGGGTAGTAAAGCATACGT GTCTCTGCCCAAGGGCAAGGGTGTGAAGCTCAGT
NL002	SEQ ID NO: 1578 GCGTAATACGACTCA CTATAGGGATGAAAA GGGCCCTACAACCTGG C	SEQ ID NO: 1579 CTGATCCACATCC ATGTGTTGATGAG SEQ ID NO: 1581	SEQ ID NO: 1577 GATGAAAAGGGCCCTACAACCTGGGAAGCCATTGAGAACTACGCGAAACAGAG GAAATGCTGATAAAGAAACAAGACTTTTGTAGAAAAGAAAATTGAAGTTGAAATTGG AGTTGCCAGGAAGAAATGGAACAAAAACAAAGAGCCGCGATCCAGGCACTCAAA AGGAAGAAAGAGGTATGAAAAGCAATTCAGCAGATCGATGGAACGTTATCAACAA TTGAGATGCAGAGAGAGGCCCTCGAAGGAGGCCAACACGGAATACGGCCGTACTGC

	SEQ ID NO: 1580 GATGAAAAGGGCCCT ACAACTGGC	GCGTAATACGACT CACTATAGGCTGA TCCACATCCATGT GTTGATGAG	AACTATGAAGAACGCGCAGCAGATGCTCTCAAAGCGGCTCATCAACACATGGATGT GGATCAG
NL003	SEQ ID NO: 1583 GCGTAATACGACTCA CTATAGGTCGCGTC GTCCTTACGAGAAGG C	SEQ ID NO: 1584 TTGACGCGACCAG GTCGGCCAC SEQ ID NO: 1586 GCGTAATACGACT CACTATAGGTTGA CGCGACCAGGTGG GCCAC	SEQ ID NO: 1582 TCCGCGTCGTCCTTACGAGAAGGCACGCTCTCGAACAGGAGTTGAAGATCATCGG AGAGTATGGACTCCGTAAACAGCGTGAGGTGTGGAGAGTCAAAATACGCCCTGGC CAAGATTCTGAAGCGCGCTCGTAGCTGTGACTCTGGAAGAGAAGGACCAGAA ACGTTTGTGTTGAAGGTAACGCCCTGCTGCGTCGCCCTGGTGGTATTGAGTGTG GACGAAGGAAGAATGAAGCTCGATTACGCTCTGGGTTTAAATAATTGAAGATTTCT TGAACGTCGCTACAGACTCAGGTGTACAACTCGGTTTGCCCAAGTCCATCCAT CACGCCGTGTACTCATCAGACAAAGACATATCAGAGTGGCAAAACAAGTAGTGA ACATTCGAGCTTTGTGTGCGCTGGACTCGCAGAACACATGACTTCTCGCT GAAGTCGCCGTTTCGGCGGTGGCCGACCTGGTCGGGTCAA
NL004	SEQ ID NO: 1588 GCGTAATACGACTCA CTATAGGGGAGTTGG CTGCTGAAGAACTG SEQ ID NO: 1590 GGAGTTGGCTGCTGT AAGAACTG	SEQ ID NO: 1589 CTGTTGTTGACTGT TGGATGAGG SEQ ID NO: 1591 GCGTAATACGACT CACTATAGGCTGT TGTTGACTGTTGG ATGAGG	SEQ ID NO: 1587 GGAGTTGGCTGTGAAGAACTGTCTGCTCTCACATCGAAACATGCTGAAGGGA GTCAACAAAGGGATTCTCTGTACAAGATGCGTGCGGTACGCCCATTTCCCATCA ACTGTGTGACGACCGAGAACAACTCTGTGATCGAGTGCCTAACCTCTCTGGGCG AGAAGTACATCCGACGGGTGAGGTGGCGCCGCGTCACTGTTACCAACTCGA CAAGCAGAAAGACGAGCTCATCGTCAAGGAAACAGCATAGAGGACGTGTCAA GATCAGCTGCCCTCATCCAACAGTCAACAACAG
NL005	SEQ ID NO: 1593 GCGTAATACGACTCA CTATAGGCGCAACA CAAATTCACGTCAAAG C SEQ ID NO: 1595 CGCAACACAAATTCA CGTCAAAGC	SEQ ID NO: 1594 CCTTCGCTTCTTG GCCTCCTTGAC SEQ ID NO: 1596 GCGTAATACGACT CACTATAGGCTT CGCTTCTTGGCCT CCTTGAC	SEQ ID NO: 1592 CGCAACACAAATTCAAGCATCAGGAAGCTGATCAAAAGACGGTCTTATC ATCAAGAAACCGGTTGCGAGTACATTACGTCGCTCGGTTCTGTAACAACTGAAG CCAGGAGGAAAGGCGAGACATTGTGGCTTTGGTAAGAGGAAAGTACAGCCAAAG CCCGTATGCCACAAAGGTTCTATGGTGAATCGTATGCGTGTCTTGAGAAGACT GTTGAAAAAATACAGACAAAGATAAGAAAAATCGACAGGCTGTACCATCACCTTT ACATGAAGGCTAAGGTTAAGTATTCAAGAACAAAGCGTGTATTGATGGAGTTCAAT CATAAGAAAGAGGCCGAGAAAGCAAGATGAAGATGTTGAACGACCAAGGCTGAA GCTCGCAGACAAAGGTCAAGGAGGCCCAAGAAAGCGGAAGG
NL006	SEQ ID NO: 1598	SEQ ID NO: 1599	SEQ ID NO: 1597

	<p>CGGTAATACGACTCA CTATAGGGTGCTTGT GTCAAGTGGTGTGG</p> <p>SEQ ID NO: 1600 GTGCTTGTGTCAAGT GGTGTGG</p>	<p>CGAGATGGGATAG CGTGAGG</p> <p>SEQ ID NO: 1601 GCGTAATACGACT CACTATAGGCGAG ATGGGATAGCGTG AGG</p>	<p>GTGCTTGTGTCAAGTGGTGTGGGAGTACATTGACACCCCTGGAGGAGGAGAGG ACCATGATAGCGATGTCGCCGGATGACCTGCGTCAGGACAGGAGTATGCCTAC TGTACCACCTACACGCACTGCGAGATCCACCCGGCCATGATCTCGGTGTGTGC GCCTCTATTATTCCTTCCCGCATCACAAACCAAGTCCAGGAACACCTATCAGA GCGCTATGGGAAACAGGCGATGGCGGTGTACATCACCAACTTCCACGTGCGAA TGGACACGCTGGCTCACGTGCTTCTACCCGACAAAGCCACTGGTCAACCACTC TGCCCATCGCCTGCTACACTGGATACAAACAGGAGGACATCTCAACGC CTCCGCTGTCGAGCGGATCTTCAGATCGGTTTTCTCCGATCTTACAAGAT GCAGAACTCGAAGCGTATTGGCGACCAAGGAGCAATTCGAGAAGCCACCCAGA CAGACGTGTCAGGGAATGAGGAATGCCATTTATGACAAATGGACGATGATGGCA TCATTGCTCCCGGTCTGAGAGTGTCTGGTGACGATGTGGTTATTGGCAAAACCAT AACACTGCCCGGATAATGATGACGAGCTGGAGGTACACAAAGAGGTTACGGAAG AGAGATGCCAGTACTTCTCGTAACTAACAGTGAGACGGGAATCGTGACCAAGTCA TGTTAACCTTGAACCTGAGGGTTACAAGTTCTGCAAAATTCGAGTCAGGTCTGTG CGTATCCCGCAGATTGGCGATAAGTTCGCTCCCGACATGGCCAAAAGGAACGT GTGGAATACAGTATCGTCAAGAGGACATGCCCTTTTACAAGCGGAGGGAATCGCAC GGATATTATTCAATCCTCACGCTATCCCATCTCG</p>
NL007	<p>SEQ ID NO: 1603 GCGTAATACGACTCA CTATAGGTGAGAGCA ATCCTTGACTGTGG</p> <p>SEQ ID NO: 1605 TGAGAGCAATCCTTG ACTGTGG</p>	<p>SEQ ID NO: 1604 CCACGGTGAATAG CCACTGC</p> <p>SEQ ID NO: 1606 GCGTAATACGACT CACTATAGGCCAC GGTGAATAGCCAC TGC</p>	<p>SEQ ID NO: 1602 TGAGAGCAATCCTTGACTGTGGTTTTGAACATCCATCTGAAGTACAACATGAATGC ATTCCTCAAGCTGTACTTGGAAATGGACATATTGTGTCAGCGAAATCCGGTATGG GAAAACCTGCTGATTGTGTGGCGACATTACAGCAAAATTGAACCAACTGACAAC CAAGTCAGTGTATTGGTCAATGTGTATACCAAGAGAGCTTGCAATCCAAATCAGCAA AGAGTATGAACGATTTTCGAAATGTATGCCAAATATCAAGGTGGAGTTTTCTTCG GCGGACTGCCGATTGAGAGGGATGAGGAGACGTTGAAATTTGAACCTGCTCCACAT CGTGGTTGGAACACCCGACGAAATTTTGGCGTTGGTACGCAACAAAGAGCTGGA CCTCAAGCATCTCAAGCACTTTGTCCTTGACGAATGTGACAAAATGTTGGAACTGT TAGATATGCGAAGAGATGTGAGGAAATATTCGAAACACGCCGACAGCAAAACA AGTCATGATGTTCAAGTCAACTCTCAGCAAGAAATTCGTCAGTCTGCAAGAAAT TCATGCAAGATCCGATGGAAGTGTACGTTGATGACGAGGCCAAGCTGACGCTTCA CGGCTGCGAGCAGCACTATGTCAAACCTCAAGAAAACGAAAGAAAAGTTA TTTGAATTACTTGACATACTTGAATTCACCCAGGTTGTTATTTGTGAAGTCAGTG CAGCGCTGCATGGCCCTATCGCAACTCCTTAACAGAGCAGCAACTTCCCTGCAGTG GCTATTCACCCGTGG</p>
NL008	<p>SEQ ID NO: 1608 GCGTAATACGACTCA</p>	<p>SEQ ID NO: 1609 GAGCGAGTCTACA</p>	<p>SEQ ID NO: 1607 GATGCTGGAGACCTGGAGGGTGTATTAGATGTTTCAAACAGTTTTGCAGTTCCATTT</p>

	CTATAGGGATGCTGG AGACCTGGAGGTG SEQ ID NO: 1610 GATGCTGGAGACCTG GAGGTG	AAATTGCCG SEQ ID NO: 1611 GCGTAATACGACT CACTATAGGGAGC GAGTCTACAAAATT GCGG	GATGAGGACGACAAAGAAAGAAATGTTTGGTCTTAGACCATGATTACTTGGAAAA CATGTTCCGGGATGTTCAAGAAAGTTAATGCTAGAGAAAAAGTTGTGGTTGGTAC CATACTGGACCCAACTCCACCAAAACGATGTTGCAATCAATGAGTTGATTGGTGG TTACTGTCCAAACTGTGCTTAGTCTAATCGATGCCAAGCCTAAAGATTGGGTC TACCTACAGAGGCATACAGAGTCGTTGAAGAAATCCCATGATGATGGATCGCCAAAC ATCAAAACATTTGAACATGTGATGAGTGGGAGATTGGGCGAGAGAGCTGAGGAG ATTGGCGTTGAACATCTGTTGAGAGACATCAAGATACAAACAGTCGGGTCACGTGT CACAGCGCGTCACAAATCAGCTGATGGCTTGAAGGGCTTGCATCTGCAATTACA GGATATCGGAGACTATTTGAATCAGGTTGTCGAAGGAAAGTTGCCAATGAACCAT CAAATCGTTTACCAACTGCAAGACATCTTCAACCTTCTACCCGATATCGGCCACGG CAATTTGTAGACTCGCTC
NL009	SEQ ID NO: 1613 GCGTAATACGACTCA CTATAGGGCGACTAT GATCGACCGCC SEQ ID NO: 1615 GCGACTATGATCGAC CGCC	SEQ ID NO: 1614 GTGTAAGGGTAGA AGTAGCCCCG SEQ ID NO: 1616 GCGTAATACGACT CACTATAGGGTGT AAGGGTAGAAGTA GCCCCG	SEQ ID NO: 1612 GCGACTATGATCGACCGCCGGGACGCGGTGTCAGGTGTCGACGTCGACGTCAAG AACTGGTTCCCTGCACCTCTGAGAACAAATTTCAACTACCATCAATCGAGCCCCTTG TGTTTTCTCAAACCTGAACAAGATAATTGGTTGGCAACGGAGTACTACAATGAGA CTGAAGGCTTTCCAGATAATATGCCAGGTGACCTCAAGCGACACATTTGCCCAACA GAAGAGTATCAACAAAGCTGTTATGCAAAACAATCTGGATAACTTCCGGAAGGAGAG GGTCTCTAGACAAGGAGAAATGCAGGGGAGATCCAGTACATCCCTAGACAGGGA TTTCCGGGCTACTTCTACCCCTTACAC
NL010	SEQ ID NO: 1618 GCGTAATACGACTCA CTATAGGGCTTGTGT TCCCGTTGGATGTC SEQ ID NO: 1620 GCTTGTGTTCCCGTT GGATGTC	SEQ ID NO: 1619 GCAACTCCAGTAG ATCGGAGAGGTC SEQ ID NO: 1621 GCGTAATACGACT CACTATAGGGCAA CTCCAGTAGATCG GAGAGGTC	SEQ ID NO: 1617 GCTTGTGTTCCCGTTGGATGCTCTGTATCAACCTTTGAAGGAGAGACCTGATCTAC CGCCTGTACAGTACGATCCAGTCTTTGTACTAGGAATACTTGTCTGTCGAATCTG AATCCATTGTGCCAAGTCGACTATCGAGCCAAGCTATGGGTCTGCAACTTTTGT CCAGAGGAATCCTTTCCCCCTCAATATGCAGCTATTTCCGAGCAGCATCAACCA GCAGAACTGATACCTTCATTTCCACCATCGAATACATCATCCAGAGCGCAAC GATGCCGCCGATGTTGCTGCTGGTGGTGGACACATGCTGGACGACGAGGAGCT GGAGCTTTGAAGGACTCACTGCAGATGCTGCTGCTGCTGCCGCCCAATGC ACTCATCGGTCTCATCAGTTCGGCAAAATGGTGCAGGTGCAGAGCTTGGCTGC GACGCTGCTCGAAGAGCTACGTGTTCCGTGGCGTGAAGGACCTGACTGCCAAG CAGATCCAGGACATGTTGGGCATTGGCAAGATGCCGCCGCTCCACAGCCCCATG CAACAGCGCATTTCCCGGCCGCTCCCTCCGACCTGTCAACAGATTTCTTCAGC CTGTCGGAAAGTCGATATGAGTTTAACTGATCTGCTTGGGAATTGCAAAAGAGA TCCATGGAATGTGGCTCAGGGCAAGAGACCTCTCCGATCTACTGGAGTTGC
NL011	SEQ ID NO: 1623	SEQ ID NO: 1624	SEQ ID NO: 1622

	CCACTTTCAAGTGY GTRYTRGTCGG SEQ ID NO: 1625 GTTGCCACCCCTTGGA GTTGAAG	GTCCATTGTGACC TCGGGAGG SEQ ID NO: 1626 GCGTAATACGACT CACTATAGGGTCC ATTGTACCTCGG GAGG	GTTGCCACCCCTTGAGTTGAAGTTCACCCCTTGATTTACACACAAACAGAGGTG TGATTAGGTTCAATGTGTGGACACAGCTGGCCAGGAAAAGTTCCGGTGGACTTCG TGATGGATATTACATTACAGGGACAATGCGCCATCATTTATGTTGACGTAACGTCAA GAGTCACCTACAAGAACGTTCCCAACTGGCACAGAGATTTAGTGAGGGTTTGCGA AAACATTCCTTACTATGCGGCAACAAAGTAGACATCAAGGACAGGAAAAGTC AAGCCAAAGAGCATAGTCTCCATAGGAAGAAACCTTCAGTACTACGACATCA GTGCGAAAAGCAACTACAATTCGAGAACCCGTTCTGTGTTGGCAAAGAAAGCT GATCGGTGACCCCAACCTGGAGTTGCTGCCATGCCCGCCCTCCTCCCAACCCGA GGTCACAATGGAC
NL012	SEQ ID NO: 1628 GCGTAATACGACTCA CTATAGGCGCAGACA CGCAGGCACAGGTAG SEQ ID NO: 1630 GCAGCAGACGCAGGC ACAGGTAG	SEQ ID NO: 1629 GAATTCCTCTTGA GTTTGCCAGCTTG SEQ ID NO: 1631 GCGTAATACGACT CACTATAGGGAAT TTCCTCTTGAGTTT GCCAGCTTG	SEQ ID NO: 1627 GCAGCAGACGCAGGCACAGGTAGACGAGGTGTCGATATAATGAAAACAAACGTT GAGAAAGTATTGGAGAGGGATCAAAAACATCAGAAATTGGATGATCGAGCAGATG CTCTACAGCAAGGCGCTTCACAGTTTGAACAGCAAGCTGGCAAACTCAAGAGGAA ATTG
NL013	SEQ ID NO: 1633 GCGTAATACGACTCA CTATAGGCGCAGAGC AAGTCTACATCTCTC SEQ ID NO: 1635 CGCAGAGCAAGTCTA CATCTCTC	SEQ ID NO: 1634 GGCAACGGCTCTC TTGGATAG SEQ ID NO: 1636 GCGTAATACGACT CACTATAGGGGCA ACGGCTCTCTTGG ATAG	SEQ ID NO: 1632 CGCAGAGCAAGTCTACATCTCTCACCTGGCCCTTATTGAAAATGCTTAAGCAGCGTC GCGCCGGTGTCCCATGGAAGTTATGGCCCTAATGCTGGCGAATTTGTAGACG ACTACACTGTGCGTGTCTATTGATGTTTCGCTATGCCACAGAGTGGAACTGGGAGT GAGTGTGGAGGCTGTAGACCCGCTGTTCCAAAGCGAAGATGTTGGACATGCTAAA GCAGACAGGACGCGCCGAGATGGTGGTGGGCTGGTACCCTCGCACCCCGGCT TCGGCTGCTGGCTGTCGGGTGTCGACATCAACACGCGCAGGAGAGCTTCGAGCAAC TATCCAAGAGAGCGCGTTGCC
NL014	SEQ ID NO: 1638 GCGTAATACGACTCA CTATAGGCATTGAGC AAGAAGCCCAATGAG SEQ ID NO: 1640	SEQ ID NO: 1639 GAGCGGACTCTA ATCTCGG SEQ ID NO: 1641 GCGTAATACGACT	SEQ ID NO: 1637 CATTGAGCAAGAACCCCAATGAGAAAGCCGAAGAGATCGATGCCAAGCGCCGAGGA AGAATTCAACATTGAAAAGGGAAGGCTCGTACAGCACCCAGCGCCTTAAATCATG GAGTACTATGACAGGAAAGAGAGCAGGTGAGCTCCAGAAAAAATCCAATCGT CAAAACATGCTGAACCAAGCGCGTCTGAAGGCACTGAAGGTGCGCGAAGATCACG TGAGAAAGTGTGCTCGAAGATCCAGAAAACGTTCTGGAGAAAGTAACCAAGAAACC AGCCAAAGTACAAGGAAGTCTCTCCAGTATCTAATTGTCCAAGGACTCCTGCAGCTG

	CAATTGAGCAAGAAGC CAATGAG	CACTATAGGGAGC GCGACTCTAATCT CGG	CTAGAATCAAACGCTAGTACTCGCGCTGCGCGAGGCTGACGTGAGTCTGATCGAG GGCATTGTTGGCTCATCGCGCAGAGCAGTACGCGAAGATGACCGGCAAGAGGTTG GTGGTGAAGCTGGACGCTGACAACCTCTGCGCGCGAGACGTGTGGAGGCGTC GAGTTGTTGCGCCGCAACGCGCGCATCAAGATCCCAACACCTCGAGTCCAGG CTCGACCTCATCTCCCAAGCAACTTGTCGCCGAGATTAGAGTCGCGCTC
NL015	SEQ ID NO: 1643 GCGTAATACGACTCA CTATAGGCTGCGAGT GCGCTTGTCGG SEQ ID NO: 1645 CTGCGAGTGCGCTTG TCCG	SEQ ID NO: 1644 GGCCAAAGCGCCT AAGCGC SEQ ID NO: 1646 GCGTAATACGACT CACTATAGGGGCC AAAGCGCCTAAGC GC	SEQ ID NO: 1642 CTGCGAGTGGCTTGTCGACATTGTCTCGATCCAGCCTTGCCAGACGTCGAAGT ATGGAAGCGTATCCATGTGCTGCCCATTTGATACCGTTGAGGGTCTTACAGG AAATCTGTTGGAAGTGATTGGAAGCCATACCTCTGGAAGCATACAGGCCAATTC ACAAAGGATGATGCATTCATTGTTGCGGAGGTATGAGAGCGGTGGAATCAAGGT GGTTGAAACAGATCCATCGCCCTACTGCTGCTGCGCCAGACACCGTCATCCAT TGTGAGGGAGACCCCATCAACGTGAGGATGAAGAAGACGAGCAACGCGAGTC GGCTACGACGACATTGGAGGCTGCAGAAAGCAGCTGGCGCAGATCAAGAGATG GTGGAGTTGCGCTGAGACATCCAGTCTGTTCAAGGCGATCGGCGTGAAGCCG CCACGAGGCATCCTGCTGACGGACACCGGAACCGGAAAGACGTTGATAGCG CGCGCGTCCCAACGAAACGGGCGCTTCTTCTCTCATCAACGGACCCGAG ATTATGAGCAAAATGGCCGGCGAGTCGGAGAGTAACCTGCGCAAGCTTTCGAG GAAGCGGACAAAACGACACCGGCCCATCATCTTCATCGATGAGCTGGACGCAATC GCGCAAAAACGCGAGAAAGACGACGCGGAGGTGGAGCGACGATCGTGTCCGA GCTGCTGACGCTGATGGAGGTTCTCAAGCAGAGCTCGACGTGATTGTATGGC CGCCACCAATCGGCCCAACTCGATCGATGCGCGCTTAGCGCTTTGGCC
NL016	SEQ ID NO: 1648 GCGTAATACGACTCA CTATAGGACGCCAG TATCAGAAGACATGC SEQ ID NO: 1650 GACGCCAGTATCAGA AGACATGC	SEQ ID NO: 1649 GATGGAGCGGTTG CGACC SEQ ID NO: 1651 GCGTAATACGACT CACTATAGGGATG GAGCGTTGCGAC C	SEQ ID NO: 1647 GACGCCAGTATCAGAAGACATGCTTGGTGTGTTCAACGGAAGTGTAAGCCC ATCGACAAAGGACCTCCCATTTCTGCTGAGGATTATCTCGACATTCGAAGTCAAC CATCAATCCTTGGTGGGTATCTATCCCGAGGAAATGATCCAGACTGGAATTTCA GCCATCGACGTCATGAATCGATTGCTCGTGCCAGAAAATCCCCATCTTTTCAG CTGCCGGTCTACCTCACAACGAAATGCTGCTCAAAATCTGAGACAGGCTGGTCT TGTCAACTGCCAGGAAAGTCACTTCTCGATGACTCTGAGGACAACTTTGCTATTG TATTCGCAGCCATGGGAGTCAACATGGAACGCTGCTGATTCTTCAACAGGATTTG GAGGAGAACGGCTCTATGAGAACGTTGCTGCTTCTTGAACCTGGCGAACGAC CCGACGATCGAGCGTATCATCACACCGCTGGCGCTGACGCGCGCCGAGTTG CTGGCCTACAGTGCAGAAAGCACGTCGTCGTCATCTCACGACATGAGCTCC TACGCCGAGGGCGCTGCGAGAGGTGTCGCCCGCCGCGAGGAGGTGCCCGGCC GTGCTGTTTCCCGGTTACATGTACACCGATCTGGCCACCATCTACGAGCGCGC CGGACGAGTCGAGGGTTCGCAACGGCTCCATC
NL018	SEQ ID NO: 1653	SEQ ID NO: 1654	SEQ ID NO: 1652

	<p>GCGTAATACGACTCA CTATAGGGCAATGC CTGTGCCACGC</p> <p>SEQ ID NO: 1655 GCAAATGCCTGTGCC ACGC</p>	<p>GCAATACAGCCGA CCACTCCG</p> <p>SEQ ID NO: 1656 GCGTAATACGACT CACTATAGGGCAA TACAGCCGACCAC TCCG</p>	<p>GCAAATGCCTGTGCCACGCCCCACAAAATAGAAAGCACACAACAGTTTATTCCGATCC GAGAAACAACATACCTGAATGGATTCACACCACTTGAGGAGGACTTCAAAGTAG ACACTTTCGAATACCGTCTCTCGCGAGGTGTCGTTCCGCGAATCTCTGATCAG AAACTACTTGCAGGAGGCGGACATGCAGATGTCGACGGTGGGACCGAGCATT GGGTCCCTCCCTCGGCGCACACATCCAGAGAGCCGCGCAACTCAAAAATCCA GGAGGGGGGATGCCGTCTTTCCATCAAGCTCAGCGCCAAACCCCAAGCCTCG GCTGGTCTGTTCAAGAACGGTCAGCGCATCGGTGACAGCCGAGAAACACCCAGGC CTCCTACTCCAATCAGACCGCCACGCTCAAGGTCAACAAAGTCAGCGCTCAAGAC TCGGCCACTACACGCTGCTGCTGAAATCCGAAAGGATGACTGTGTCCTCAG CTTACCTAGCTGTCGAATCAGCTGGCACTCAAGATACAGGATACAGTGAGCAATA CAGCAGACAAGAGGTGGAGACGACAGAGGGGTTGGACAGCAGCAAGATGCTGG CACCGAATTTGTTCCGCTGCCGCGCATCGCAGCGAGCGAGCGAAGGCAAGATGA CGCGGTTTGAATGCCGCGTGACGGGCGACCCCTACCCGGACGTGGCCTGGTTC ATCAACGGCCAAACAGGTGGTACGACGCGCACCAAGATCCTCGTCAACGAG TCTGGCAACCACTCGCTCATGATCACCGGCGTCACTCGCTTGACCCACGGAGTG GTCGGCTGTATTGC</p>
NL019	<p>SEQ ID NO: 1658 GCGTAATACGACTCA CTATAGGGCTTCAGA TTTGGGACACGGC</p> <p>SEQ ID NO: 1660 GCTTCAGATTTGGGA CACGGC</p>	<p>SEQ ID NO: 1659 GAAGCCTGCTCC ACATTGG</p> <p>SEQ ID NO: 1661 GCGTAATACGACT CACTATAGGGAAC GCCTGCTCCACAT TGG</p>	<p>SEQ ID NO: 1657 GCTTCAGATTTGGGACACGGCCGCGGAGGAGCGGTTCCGACGATCACATCGAG CTACTACCGGGGCGCCACGGCATCATTTGGTGACGACTGCACCCGACCCAGGA GTGCTTCAACAACCTCAACACAGTGGCTCGAGGAGATTGACCGCTACGCCCTGTGAT AATGTCAACAACCTGCTCGTCCGCAACAAGTGTGATCAGACCAACAACAAAGGTGCG TCGACTATACACAGGCTAAGGAATACGCCGACCAAGTGGGCAATTCGGTTCCCTGGA GACGTCGGCGGAAGAACCGGACCAATGTGGAGCAGGCGGTTTC</p>
NL021	<p>SEQ ID NO: 1663 GCGTAATACGACTCA CTATAGGCGTCAGTC TCAATTCTGTACCCG</p> <p>SEQ ID NO: 1665 CGTCAGTCTCAATTCT GTCACCG</p>	<p>SEQ ID NO: 1664 CTTCTAGTTTCATCC AGGTCGCG</p> <p>SEQ ID NO: 1666 GCGTAATACGACT CACTATAGGCTTCT AGTTCATCCAGGT CGCG</p>	<p>SEQ ID NO: 1662 CGTCAGTCTCAATTCTGTACCCGATATCAGCACCACGTTTCATTCTCAAGCCACAAG AGAACGTGAAGATAACGCTTGAGGGCGCACAGGCCCTGTTTCATTTCAACACGAACG ACTTGTGATCTCACTGAAGGGGAGAGAACTCTATGTTCTAACTCTCTATTCCGATA GTATGCGCAGTGTGAGGAGTTTTCATCTGGAGAAAGCTGCTGCCAGTGTCTTGAC TACTTGTATCTGTGTTGTGAGGAGAACATCTGTTCTTGGTTCCCGTCTTGGAA ACTCACTGTTGCTCAGGTTTACTGAGAAGGAATTGAACCTGATTGAGCCGAGGGC CATCGAAAGCTCACAGTCCAGAAATCCGGCCCAAGAAAGCTGGATACTTTG GGAGATTGGATGGCATCTGACGTCACTGAAATACCGGACCTGGATGAACACTAGAAG</p>

NL022	<p>SEQ ID NO: 1668 GCGTAATACGACTCA CTATAGGCTCAGGAG AGGACGTTGCACAC</p> <p>SEQ ID NO: 1670 CTCAGGAGAGGACGT TGCACAC</p>	<p>SEQ ID NO: 1669 CAGACGGAAGCAC TTGCCG</p> <p>SEQ ID NO: 1671 GCGTAATACGACT CACTATAGGCAGA CGGAAGCACTTGC CG</p>	<p>SEQ ID NO: 1667 CTCAGGAGAGGACGTTGCACACTGATATACTGTTCCGTTTGGTGAAGATGTCGC CCGATTAGACCTGACTTGAAGCTGCTCATATCAAGCGCCACACTGGATGCTCAG AAATTCCGAGTTTTTCGACGATGCACCCATCTTACGAGATCCGGGCCGCTAGATT TCCGGTGGACATCTACTACACAAGGCGCCGAGGCTGACTACGTTGACGCGCATG TGTCGTTTCGATCCTGCAGATCCACGCCACTCAGCCGCTGGGAGACATCCTGGTC TTCCTACCGGTGAGGAGATCGAAACCTGCCAGGAGCTGCTGCAGGACAGA GTGCGAGGCTGGTCTCGTATCAAGGAGCTGCTCATATTGCCGCTATTCCCA ACCTACCCAGTGATGCGAGGCAAGATTTTCTGCCCACTCCACCAATGCTAG AAAGGTAGTATTGCCACAATATTGCAGAAACCTCATTGACCATCGACAATATAA TCTACGTGATTGATCCTGGTTTTTGTAAAGCAGAACTTCAATTCAAGGACTGGA ATGGAATCGCTTGTGTAGTGCCTGTTTCAAGGCATCGCCAATCAGCGAGCAG GGCGGGCGGACGGGTGGCGGCCGCGCAAGTGCTTCCGCTCG</p>
NL023	<p>SEQ ID NO: 1673 GCGTAATACGACTCA CTATAGGCTCCTCGG ACGGGAGGTCC</p> <p>SEQ ID NO: 1675 GTCCTCGGACGGGAG GTCC</p>	<p>SEQ ID NO: 1674 GCAATGTTGTCTT GAGCCAGC</p> <p>SEQ ID NO: 1676 GCGTAATACGACT CACTATAGGGCAA TGTTGCTCTTGAG CCAGC</p>	<p>SEQ ID NO: 1672 GTCCTCGGACGGGAGGTCACGTTTACCGGATTCGGTTTGGAAACCTGCC ATCGGTCCGTTGCGATTCCGTAACCGGTTCCCGTCGACCCGTGGCACGGCGTT CTGGATGCGACCCGCTTCCCAACAGCTGCTACCAGGAACGGTACGAGTATTC CCGGCTTCGAGGAGAGGAAATGTGGAATCCGAATACGAATTTGTCGAAGATT GTCTGATTTGAACATATGGTGCCGACCGTTGAGAAATCCGACACAGAGCCAA CAGCGAGAGAAATAACCAAGAGCGAAGTCCCGTGCTGATCTGGATCTACCG GGGGGTTACATGAGCGGCACAGCTACACTGGACGTGTACGATGCTGACATGGT GGCCGCCACGAGTGACGTCTCGTCCCTCCATGCAGTACCGAGTGGGTGCGTT CGGCTTCTCTACCTCGCACAGGACTTGCCCTCGAGGCAGCGAGGAGCGCCCG GCAACATGGGCTCTGGACCAAGGCCCTTGCCATCCGCTCGCTCAAGGACAACA TTGC</p>
NL027	<p>SEQ ID NO: 1678 GCGTAATACGACTCA CTATAGGAGAAAGACG GCACGGTGCG</p> <p>SEQ ID NO: 1680 AGAAGACGGCACCGGT GCG</p>	<p>SEQ ID NO: 1679 CAATCCAGTTTTTA CAGTTTCGTGC</p> <p>SEQ ID NO: 1681 GCGTAATACGACT CACTATAGGCAAT CCAGTTTTTACAGT TTCGTGC</p>	<p>SEQ ID NO: 1677 AGAAGACGGCACGGTGCGTATTTGGCACTCGGGCACCTACAGGCTGGAGTCCTC GCTGAATTATGGCTCGAAAGAGTGTGGACCAATTTGCTGCATCGGAGGATCCAAC AATGTGGCTCTTGGTACGACGAAGGACGCAATAATGGTGAAGTGGTGGGAG GAGCCGGCCATCTCGATGGATGTGAACGGTGAGAAGATTGTGTGGCGGCCAC TCGGAGATACAACAGGTCAACCTCAAGGCCATGCCGAGGGCTCGAAATCAAA GATGGCGAACGACTGCCGCTGCCGTTAAGGATATGGCAGCTGTGAATATAT CCGAGACCATCGCTCAATAATCCCAACGGCAGATTCTAGTGGTTGTGGAGATG GAGAGTACATAATTCACACATCAATGTTGCTAAGAAATAGCGCTTGGCTCGGC CCAAGAGTTCAATTTGGGACACAGTCTGTCGAGATGCTATCAGAGGAGGAACA TCCACTGTCAAAGTATTTCAAAAACITTCAAAGAAAAGAAATCATTTCAAGCCAGAATTT</p>

			GGTGTGAGAGCATATTCGGGGGCTACCTGCTGGGAGTTTGTTCGTTGCTGGAC TGGCGCTGTACGACTGGGAGACCCCTGGAGCTGGTGCCTGCGATCGCATCGAGATCCAAC CGAAACACGTGTACTGGTCGGAGAGTGGGAGCTGGTGGCGCTGGCCACTGAT GACTCCTACTTTGTGCTCCGCTACGACGACAGCGCTGCTCGCTGCACGCGAC GCCGGTGACGACGCTGTACCGCGGACGGCGTCGAGGATGCATTCCGAGGTCCTT GGTGAAGTGCACGAAACTGTAAAAACTGGATTG
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Table 8-CS

Target ID	Primers Forward 5' → 3'	Primers Reverse 5' → 3'	dsRNA DNA Sequence (sense strand) 5' → 3'
CS001	SEQ ID NO: 2041 TAAAGCATGGATGTT GGACAACTGGG SEQ ID NO: 2043 GCGTAATACGACTC ACTATAGGTAAAGC ATGGATGTTGGACA AACTGGG	SEQ ID NO: 2042 GCGTAATACGACTC ACTATAGGGGTGAG TCGCACGCCCTTGC C SEQ ID NO: 2044 GGTGAGTCGCACGC CCTTGCC	SEQ ID NO: 2040 TAAAGCATGGATGTTGGACAAACTGGGTGGCGTGTACGGCGCGGGCGCTCGAC CGCCCCCACAAGTTGCGCGAGTGCCCTGCCGTGGTGATCTTCTCAGGAACCG GCTCAAGTACGCGCTCACCGGAATGAAGTGCTTAAGATTGTAAGCAGCGACTT ATCAAAGTTGACGGCAAGTCAGACAGACCCACATATCCGCTGGATTATGG ATGTTGTTCCATTGAAAGACAAATGAGCTGTTCCGCTTATATATGATGTCAAAG GCAGATTTACTATTACCGTATTACTCCTGAGGAGGCTAAATACAGCTGTGCAAG GTGCGGCGGTGGCAGCGGCCCAAGACGTGCCCTTACCTGGTGACCCACGA CGACGCAACCGTGCATACCCGACCCCACTCATCAAGTCAACGACTCCATCCA GCTCGACATGCCACCTCCAAGATCATGACTTCAAGTTTGAATCTGGTAAC CTATGTATGATCAGGGAGGCGGTAACTTGGGCGCGTGGGCACCATCGTGTC CGGAGCGACATCCCGGGTCTTCGACATCGTGATATACGGGACTCCACCGGA CATACCTTCGCTACCGATTGAACAACGTGTTCAATCGGCAAGGGGCACGAAGG CGTACATCTCGCTGCCGCGCGCAAGGGCGTGCAGCTCACC
CS002	SEQ ID NO: 2046 CAAGAAGGAGGAGA AGGGTCCATCAAC SEQ ID NO: 2048 GCGTAATACGACTC ACTATAGGCAAGAA GGAGGAGAAGGGTC CATCAAC	SEQ ID NO: 2047 GCGTAATACGACTC ACTATAGGCTTGCT ACATCGATATCCTTG TGGGC SEQ ID NO: 2049 CTTGCTACATCGAT ATCCTTGTTGGC	SEQ ID NO: 2045 CAAGAAGGAGGAGGGTCCATCAACACACAGAGCTATACAGAAATTACGGAA ACGGAAGAGTTATTGCAAGAAACAAGAGTTTCTAGAGCGAAAGATCGACACTG AATTACAAACGGGAGAAAACATGGCACAAGATAAGAGAGCTGCCATTGCGGC ACTGAAGCGCAAGAGCGTTATGAAAAGCAGCTTACCCAGATTGATGGCAGCGTT ACCCAAATTGAGGCCCAAGGGAAGCGCTAGAAGGAGCTAACACCAATACACAG GTGCTTAACACTATGCGAGATGCTGCTACCGCTATGAGACTCGCCCCACAAGGATA TCGATGTAGACAAG

CS003	<p>SEQ ID NO: 2051 TGGTCTCCGCAACA AGCGTGAGG</p> <p>SEQ ID NO: 2053 GCGTAATACGACTC ACTATAGGTGGTCT CCGCAACAAGCGTG AGG</p>	<p>SEQ ID NO: 2052 GCGTAATACGACTC ACTATAGGCGAAGC GAGACTTCAGCGAG AAGTCA</p> <p>SEQ ID NO: 2054 CGAACGGAGACTTC AGCGAGAAGTCA</p>	<p>SEQ ID NO: 2050 TGGTCTCCGCAACAAGCGTGAGGTGTGGAGGGTGAAGTACACGCTGGCCAGGAT CCGTAAGGCTGCCCGTGAGCTGCTCACACTCGAGGAGAAAGACCCCTAAGAGGTT ATTGGAAGGTAATGCTCTCTTCGTCGTCGTGAGGATCGGTGTGTGGATGAG AAGCAGATGAAGCTCGATTATGTACTCGGTCTGAAGATTGAGGACTTCTTGGAAC GTGCTCTCCAGACTCAGGTGTCAAGGCTGGTCTAGCTAAGTCTATCCATCATGC CCGTATTCCTATCAGACAGAGGCACATCCGTGTCCGCAAGCAAGTTGTGAACATC CCTTCGTTTCATCGTGGGCTGGACTCTGGCAAGCACATTGACTTCTCGCTGAAGT CTCCGTTCCG</p>
CS006	<p>SEQ ID NO: 2056 GGATGATGATGGTA TAATTGCACCGGG</p> <p>SEQ ID NO: 2058 GCGTAATACGACTC ACTATAGGGGATGA TGATGGTATAATTGC ACCGGG</p>	<p>SEQ ID NO: 2057 GCGTAATACGACTC ACTATAGGCGTTAAA TGGTGTAGCATCAC CTATTTCAAC</p> <p>SEQ ID NO: 2059 CGTTAAATGGTGA GCATCACCTATTTCA CC</p>	<p>SEQ ID NO: 2055 GGATGATGATGGTATAATTGCACCGAGGATTCTGTATCTGTTGACGATGTAGTC ATTGGAAGAACTATAACTTTGCCAGAAACGATGATGAGCTGGAAAGGAACATCAA GACGTACAGTAAGAGAGATGCCCTACATTCTTCCGAAACAGTGAACCTGGTATT GTTGACCAAGTTATGCTTACACTTAACAGCGAAGGATACAAATTTTGTAAATACG TGTGAGATCTGTGAGAAATCCCAAAATTTGGAGACAAATTTGCTTCTCGTCATGGTC AAAAGGGACTTGTGGTATTCAATATAGCAAGAGATATGCCTTTCACTTGTGAA GGATTGACACCAAGATATTATCATCAATCCACATGCTATCCCTCTCGTATGACAA TGGTCACTTGATTGAATGATTCAAGGTAAAGGTCTCCTCAAAATAAAGGTGAAATAG GTGATGCTACACCATTTAAACG</p>
CS007	<p>SEQ ID NO: 2061 CTTGTTGAAACCCAG AGATTTTGAGGGC</p> <p>SEQ ID NO: 2063 GCGTAATACGACTC ACTATAGGCTTGTG AAACCAGAGATTTTG AGGGC</p>	<p>SEQ ID NO: 2062 GCGTAATACGACTC ACTATAGGCGGCAT GTCATAATTGAAGAC TATGTTGACTC</p> <p>SEQ ID NO: 2064 CGGCATGTCATAATT GAAGACTATGTTGA CTC</p>	<p>SEQ ID NO: 2060 CTTGTTGAAACCCAGAGATTTTGAGGGCTATCGTCGATTGCGGTTTCGAGCACCCCT TCAGAAGTTCAACATGAATGTAATCCCAAGCTGTTTTGGGAATGGATATTCCTTG TCAAAGCTAAATCCGGAATGGGAAACCCGCCGTATTTGTTTAGCAACACTGCAA CAGCTAGAACCCTTCAGAAAACCATGTTTACGTATTAGTAATGTCCCATACAAGGGA ACTCGCTTCCAAATAAGCAAGGAATATGAGAGGTTCTCTAAATATATGGCTGGTG TTAGAGTATCTGTATTCCTTGGTGGGATGCCAATTCAGAAAGATGAAGAAGTATTG AAGACAGCCTGCCCGCACATCGTTGTTGGTACTCTCCGAGAAATATTAGCATTTGG TTAAACAACAAGAAATGAATTTAAACACCTGAACACATTCATCCTCGGATGAATGT GACAAATGCTTGAATCTCTAGACATGAGACGTGATGTCAGGAAATATTACAGGA ACACCCCTCACGTAAGCAGGTCATGATGTTTCTGCAACATTTAGTAAGGAGAT CAGACCAGTCTGTAAGAAATTTATGCAAGATCCTATGGAAGTTTATGTGGATGATG AAGCTAAACTTACATTGCACGGTTTGCAGCAACATTTATGTTAACTCAAGGAAAT GAAAAGAAATAAGAAAGTTATTGAACCTTTTGGATGTTGCTGAGTTCAACCAAGTTGT CATATTTGTAAAGTCAGTGCAGCGCTGCATAGCTCTCGCACAGCTGCTGACAGAC</p>

CS009	<p>SEQ ID NO: 2066 ACGTTTCTGCAGCG GCTGGACTC</p> <p>SEQ ID NO: 2068 GCGTAATACGACTC ACTATAGGACGTTTC TGCAGCGGCTGGAC TC</p>	<p>SEQ ID NO: 2067 GCGTAATACGACTC ACTATAGGATAATT CTTATCGTACGCTGT CATATTCTCTG</p> <p>SEQ ID NO: 2069 GATAATTCATTATCGT ACGCTGTATATTCG TG</p>	<p>CAAACCTCCAGCTATTGGTATACACCGAAATATGACTCAAGATGAGCGTCTCTC CCGCTATCAGCAGTTCAAAGATTTCCAGAAGAGGATCCTTGTTCGACAAATCTTT TTGGACGGGTATGGACATTGAAAGAGTCAACATAGT GACATGCCG</p>
CS011	<p>SEQ ID NO: 2071 CGACACTTGACTGG AGAGTTCGAGA</p> <p>SEQ ID NO: 2073 GCGTAATACGACTC ACTATAGGCGACAC TTGACTGGAGAGTT CGAGA</p>	<p>SEQ ID NO: 2072 GCGTAATACGACTC ACTATAGGCTCTAG GTTACCATCACCGA TCAACT</p> <p>SEQ ID NO: 2074 CTCTAGGTTACCATC ACCGATCAACT</p>	<p>SEQ ID NO: 2070 CGACACTTGACTGGAGATTTCGAGAAAGATATGTGCCACATTAGGTGTCGAGG TGATCCCTTAGTATTCACACAAATAGAGGCCCTATAAGTTTAAATGATGGAT ACTGCTGCCAAGAAAGTTTGGTGTCTCCGAGATGGTTACTATATCCAAAGTCTC AATGTGCATCATCATGTTTCGATGTAACTCTGTCGTCACTACAAAATGTACCC AACTGGCACAGAGATTAGTGCAGTCTGTGAAGGCATTCCAAATTGTTCTTTGTG GCAACAAAGTAGATATCAAGGACAGAAAGTCAAGCAAAACTATTGTTTCCAC AGAAAAAGAACCTTCAGTATTATGACATCTCTGCCAAGTCAAACTACAATTTTCCA GAAACCTTCTCTCTGTTAGCGAGAAAGTTGATCGGTGATGGTAACCTAGAG</p>
CS013	<p>SEQ ID NO: 2076 TGCCGAACAGGTAT ACATCTCGTCTTTGG</p> <p>SEQ ID NO: 2078 GCGTAATACGACTC ACTATAGGTGCCGA ACAGGTATACATCTC GTCCTTGG</p>	<p>SEQ ID NO: 2077 GCGTAATACGACTC ACTATAGGCCACTA CAGCTACAGCACGT TCAGAC</p> <p>SEQ ID NO: 2079 CCACTACAGCTACA GCAGTTCAGAC</p>	<p>SEQ ID NO: 2075 TGCCGAACAGGTATACATCTCGTCTTTGGCCCTGTTGAAGATGTTAAACACGGG CGCCCGGTGTTCCAAATGGAAGTTATGGACTTATGTTAGGTGAATTTGTTGATG ATTACACGGTGCCTGTCATAGACGTATTTGCCATGCCCTCAAACCTGGCACAGGAGT GTCGGTTGAAGCTGTAGATCCTGTCTTCCAAGCAAGATGTTGGATATGTTGAAG CAAACCTGGACGACCTGAGATGGTAGTGGGATGGTACCACTCGCATCCTGGCTTTG GATGTTGTTATCTGGAGTCGACATTAATACTCAGCAGTCTTTCCGAAGCTTTGTCT GAACGTGCTGTAGCTGTAGTGG</p>
CS014	<p>SEQ ID NO: 2081 CAGATCAAGCATAT GATGGCCTTCATCG</p>	<p>SEQ ID NO: 2082 GCGTAATACGACTC ACTATAGGGAACA</p>	<p>SEQ ID NO: 2080 AGATCAAGCATATGATGGCCTTCATCGAACAAAGAGGCTAATGAAAAAGGCCGAGGA</p>

	<p>A</p> <p>SEQ ID NO: 2083</p> <p>GCGTAATACGACTC</p> <p>ACTATAGGCAGATC</p> <p>AAGCATATGATGCG</p> <p>CTTCATCGA</p>	<p>TGCGGTACGTATTT</p> <p>CGGGC</p> <p>SEQ ID NO: 2084</p> <p>GAACAATGCGGTAC</p> <p>GTATTTGCGGC</p>	<p>AATCGATGCAAGGCCGAAGAGGAGTTCAACATTGAAAAAGGCCGCTGGTGCA</p> <p>GCAGCAGCGGCTCAAGATCATGGAATCTAGGAATCTAGCAAGAAAGAGAAACAAGTGGAA</p> <p>CTCAGAAAAAGATCCAATCTTGAACATGCTGAATCAAGCCGCTCTGAAGGTGC</p> <p>TCAAAGTCGCTGAGGACCACTACGCAACGTTCTCGACGAGCTCGCAAGCGCC</p> <p>TGGCTGAGTGGCCCAAGACGTGAACATTTACAGAGATCTGCTGTCACGCTCGT</p> <p>CGTACAAGCCCTATTTCCAGCTCATGGAACCCACAGTAACAGTTCCGCTTAGGCAG</p> <p>GCGGACGCTCCTTAGTACAGTCCATATTGGCAAGGCACAGCAGGATTACAAAG</p> <p>CAAAGATCAAGAGGACGTTCAATTGAAGATCGACACCGAGAATCCCTGCCCGC</p> <p>CGATACCTGTGGCGGAGTGAACCTTATTGCTGCTAGAGGGCGTATTAAAGATCAGC</p> <p>AACACTCTGGAGTCTGCTGAGCTGATAGCCCCAACAACTGTTGCCCGAAATAC</p> <p>GTACCGCATTTGTT</p>
CS015	<p>SEQ ID NO: 2086</p> <p>ATCGTGCTTTTCAGA</p> <p>CGATAACTGCCCC</p> <p>SEQ ID NO: 2088</p> <p>GCGTAATACGACTC</p> <p>ACTATAGGATCGTG</p> <p>CTTTCAGACGATAAC</p> <p>TGCCCC</p>	<p>SEQ ID NO: 2087</p> <p>GCGTAATACGACTC</p> <p>ACTATAGGCCATTAC</p> <p>GATCACGTGCGATG</p> <p>ACTTC</p> <p>SEQ ID NO: 2089</p> <p>CCATTACGATCAG</p> <p>TGCGATGACTTC</p>	<p>SEQ ID NO: 2085</p> <p>ATCGTGCTTTCAGACGATAACTGCCCGCATGAGAAGATCCGCATGAACCGCGTCG</p> <p>TGCGAAACAACCTGCGGTACGCCGTGCAGACATAGTCTCCATAGCGCCTTGTC</p> <p>ATCGGTCAAATATGGAAACGGGTACATATATTGCCATTGATGATTCTGTCGAG</p> <p>GGTTGACTGGAATTTTATTGGAAGTCTACTTGAACCATCTTCAAGGACCTTA</p> <p>TGGCCTATCCATCGCGATGACACATTCATGGTTCGCGGGGCATGAGGGCTGT</p> <p>TGAATTCAAAGTGTGGAGACTGATCCGTCGCCGTATTGATCGTCTGCCGAC</p> <p>ACAGTGATACACTGCGAAGGAGACCTTATCAACGAGAGGAAAGAAAGAGCC</p> <p>CTAACGCCGTAGGTACGACGACATCGTGGTGTGTAACAGCTCGCTCAG</p> <p>ATCAAAGAGATGTCGAGTTGCCCTAAGGCATCCGTCGCTGTTCAAGGCAATTG</p> <p>GTGTGAAGCCGCCACGTGGAATCCTCATGTATGGCCGCCCTGTTACCGGCAAAA</p> <p>CTCTCATTGCTCGGGCAGTGGTAAATGAACTGGTGCAATCTTCTTGATCAAC</p> <p>GGCCGGAGATCATGTCCAACTCGCGGCGAGTCCGAATCGAACTTCGCAAG</p> <p>GCATTCGAGGAAGCGGACAAGAACTCCCGGCTATAATCTTCATCGATGAACCTGG</p> <p>ATGCCATCGCACCAAGAGGGAGAAGACTCACCGTGAAGTGGAGCGTCGTATTG</p> <p>TGTCGCAACTACTTACTCTTATGGATGGAATGAAGAAGTCATCGCACGTGATCGTA</p> <p>ATGG</p>
CS016	<p>SEQ ID NO: 2091</p> <p>AGGATGGAAGCGGG</p> <p>GATACGTTTGAG</p> <p>SEQ ID NO: 2093</p> <p>GCGTAATACGACTC</p> <p>ACTATAGGAGGATG</p> <p>GAAGCGGGGATACG</p>	<p>SEQ ID NO: 2092</p> <p>GCGTAATACGACTC</p> <p>ACTATAGGGCACCC</p> <p>CTGTCTCCGAAGAC</p> <p>ATGTT</p> <p>SEQ ID NO: 2094</p> <p>GCACCCCTGTCTCC</p>	<p>SEQ ID NO: 2090</p> <p>AGGATGGAAGCGGGGATACGTTTGAGCATCTCCTTGGGGAAGATACGGAGCAGC</p> <p>TGCCAGCCGATGTCAGCGACTCGAATACTGTGCGGTTCTCGTAGTGGCCCTGTG</p> <p>TGATGAAGTTCTTCTGAACTTGGTGAGGAACTCGAGGTAGAGCAGATCGTCGGG</p> <p>TGTCAGGGCTTCTCACCGACAGACGCTTCAATGGCCTGCACGTCTTACCGATG</p> <p>GCGTAGCAGGCGTACAGCTGGTGGAAACATCAGAGTGTCTTGGGGGTCAAT</p> <p>CCCTCACCGGATGGCAGACTTCATGAGACGAGACAGGGAAGGCAGCAGCTTACA</p> <p>GGCGGGTAGATCTGTCTGTGTGGAGCTGACGGTCTACGTAGATCTGTCCCTCAG</p> <p>TGATGTAGCCCCGTTAAATCGGGAATAGGATGGGTGATGTCGTGTTGGGCATAGT</p>

	TTTGAG	GAAGACATGTT	CAAGATGGGGATCTGCGTGATGGATCCGTTTCTACCCCTCTACACGCCCGGCTCTCTC TCGTAGATGGTGGCCAAATCGGTGTACATGTAACTGGGAACCCACGTCGTCCG GGCACCTCCTACGGGCGGGACACTTACGCAGAGCTCCGCGTACGAAGA CATGTCAGTCAAGATTACCAGCACGTGTTTCTCAGACTGGTAGGCCAAGAACTCA GCAGCAGTCAAGGCCAAACGTGGTGTGATGATTTCTCTCAATAGTGGGATCGTTGG CCAGATTCAAGAACAGGCACACGTTCTCCATGGAGCCGTTCTCTCGAAGTCCCTG CTTGAAGAACCGGGCGTCTCCATGTTACACCCCATGGCGGGAACACGATGGC AAAGTTGTCCTCGTGTGTCGTCAGCACAGATTGGCGGGGATCTTTACAAGACCG GCTTGCCCTACAGATCTGGCGGCAATTTCTGTTGTGGCAGACCGGCGAGCCGAG AAAATGGGGATCTTTTGGCCCGGAGCAATGGAGTTTCATCAGTCGATAGCGGAGA TACCAGTCTGGATCATTTTCTCAGGGTAGATACGGGACAGGGGTTGATGGGCT GTCCCTGGATGTCCAAAAGTCTTCAGCAAGGATTGGGGACCTTTGTCAATGGG TTTTCCAGAGCCGTTGAATACCGGACCCCAACATGCTTCCGAGACAGGGGTGC
CS018	<p>SEQ ID NO: 2096 CGTCCCTGTACCTG CTCAGCAATCCCA</p> <p>SEQ ID NO: 2098 GCGTAATACGACTC ACTATAGGCGTCCC TGACCTGCTCAGC AATCCCA</p>	<p>SEQ ID NO: 2097 GCGTAATACGACTC ACTATAGGCGAGCT CGAGGCCCCACCTT</p> <p>SEQ ID NO: 2099 CAGCGTCGAGGCC CACCTT</p>	<p>SEQ ID NO: 2095 CGTCCCTGTACCTGCTCAGCAATCCC AACAGCAGCAGAGTTACCGCCACGTCAG CGAGAGCGTCGAACACAAATCCTACGGCACGCAAGGTACACCACCTTCGGAACA GACCAAGCAGACACAGAAGGTGGCGTACACCAACGGTCCGACTACTCTCCAC GGACGACTTTAAGGTGGATACGTTTGAATACAGACTCCTCCGAGAAGTTTCGTTT AGGGAATCCATCAGAACCGGTACATTGGCGAGACAGACATTCAAGTACGACAG GAGTTCGACAACTCTCTCGTGTGGTGACCCCTCCTAAGTAGCACAAAAGCCTA GGAATCCAAAGCTGCAGGAGGGAGCCGACGTCAGTTTCAAGTGCAGCTGTCCG GTAACCCGCGGCCACGGGTGTCATGGTTCAAGAACGGGCGAGAGGATAGTCAACT CGAACAAACACGAAATCGTCACGACACATAATCAAAACAATCTTAGGGTAAGAAAC ACACAAAAGTCTGATACCTGGCACTACACGTTGTTGGCTGAAATCCTAACGGAT GCGTCGTACATCGGCATACCTGGCCGTGGAGTCCGCTCAAGAAACTTACGGCC AAGATCATAAATCACAATACATAATGGACAATCAGCAACAGCTGTAGAAGAAAGA GTAGAAGTTAATGAAAAGCTCTCGCTCCGCAATTCGTAAGAGTCTGCCAAGACC GCGATGTAACGGAGGGGAAAATGACGCGATTTCGATTGCCGCTACGGGCGAGAC CTTACCCAGAAGTCACGTGGTTCATTAAAGATAGACAAATTCGAGACGATTATWAT CATAAGATATTAGTAAACGAATCGTGTAAATCATGCACTTATGATTACAAACGTCGAT CTCAGTGTAGTGCGGTAGTATCATGTATAGCACGCAACAGACCGGCGGAAACTT CGTTTCAGTGTAGGCTGAACGTGATAGAGAAGGAGCAAGTGGTGGCTCCCAAT CGTGGAGCGGTTCAGCACGCTCAACGTGCGCGAGGCGGAGCCCGTGCAGCTGC ACGCGCGCGCCGTGGCAGCGCTACGCCACGCTACATGCATGCGAGGAGCGGC GTTCAAGTTATACCCCAATCCAGAGCTACGAATAAATACCGAAGGTGGGGCCTCGA CGCTG</p>

Table 8-PX

Target ID	Primers Forward 5' → 3'	Primers Reverse 5' → 3'	dsRNA DNA Sequence (sense strand) 5' → 3'
PX001	SEQ ID NO: 2340 GCGTAATACGACTC ACTATAGGCGAGGT GCTGAAGATCGTGA AG SEQ ID NO: 2342 CGAGGTGCTGAAGA TCGTGAAG	SEQ ID NO: 2341 CTTGCCGATGATGA ACACGTTG SEQ ID NO: 2343 GCGTAATACGACTC ACTATAGGCTTGCC GATGATGAACACGT TG	SEQ ID NO: 2339 CGAGGTGCTGAAGATCGTGAAGCAGCGCCTCATCAAGGTGGACGGCAAGGTCCG CACGACCCACCTACCGGCTGATGATGATGTTGTGTCGATTGAAAGACC AATGAGCTGTTCCGTTGATCTACGATGTGAAGGTGAAGCGCGTGGCGACG TCACTCCCGAGGAGGCCAAGTACAAGCTGTGCAAGGTGAAGCGCGTGGCGTAG GGCCCAAGAACGTCGCTACATCGTGACGACACACGGCGCACGCTGCGCTAG CCGACCCGCTCATCAAGGTCAACGACTCCATCCAGCTCGACATCGCCACCTGC AAGATCATGGACATCATCAAGTTCGACTCAGTAACCTGTGCAATGATCACGGGAG GGCGTAACCTGGGGCGAGTGGGCACCATCGTGTCCCGGAGAGGACACCCCGGG AGCTTCGACATCGTCCACATCAAGGACACCCAGCGACACACCTTCGCCACCAAGGT TGAACAACGTTTCATCATCGGCAAG
PX009	SEQ ID NO: 2345 GCGTAATACGACTC ACTATAGGCGAGCTA CAAGTATTGGGAGA ACCAG SEQ ID NO: 2347 CAGCTACAAGTATT GGGAGAACCAG	SEQ ID NO: 2346 TGTTGATCACTATGC CGGTCCCT SEQ ID NO: 2348 GCGTAATACGACTC ACTATAGGTTGTGAT CACTATGCCGGTCC T	SEQ ID NO: 2344 CAGCTACAAGTATTGGGAGAACCAGCTCATTTGACTTTTTGTGAGTATACAAGAAGA AGGGTCAGACACGCGGTGCTGGTCAGAACATCTTCAACTGTGACTTCGCAACC CGCCCCACACGGCAAGGTGCGACGTGGACATCCGCGCTGGGAGCCCTGC ATTGATGAGAACCACCTCTCTTCCACAAGTCTTCGCTTGACATCTTCTTGAAGCT GAATAAGATCTACGGCTGGCTCCAGAGTCTACAACGACACCGCTAACCTGCCT GAAGCCATGCCCGTGGACTTGCAGACCCACATTCGTAACATTACTGCCCTCAACA GAGACTATGCGAACATGGTGTGGTGTGCTGCCACGGCGAGACGCCGGCGGAC AAGGAGAACATCGGGCCGTGCGCTACCTGCCCTACCCGGGCTTCCCGGGGTAC TTCTACCCGTACGAGAACGCCGAGGGGTATCTGAGCCCGCTGGTCCGCCGTGCAT TTGGAGAGGCCGAGGACCGGCATAGTGATCAACA
PX010	SEQ ID NO: 2350 GCGTAATACGACTC ACTATAGGACCAGC ACTCTAGTGGACAA CGTC SEQ ID NO: 2352 ACCAGCACTCTAGT GGACAACGTC	SEQ ID NO: 2351 CTGTATCAATGTACC GCGGCAC SEQ ID NO: 2353 GCGTAATACGACTC ACTATAGGCTGTATC AATGTACCCGCGGCA C	SEQ ID NO: 2349 ACCAGCACTCTAGTGGACAACGTCGCGTTCCGGTCACCACTGTGCGCGCAATT GGGGCAGCAGCAGCCGCCAATTACACCACATATCGGCGGGCTTCGACCAGGAG GCGCGCGCGGTGTTGATGGCGCGGTGTTGGTGTACCGCGCGGAGCAGGAGG ACGGCCCGGACGTGCTGCGTGGCTCGACCGCATGCTCATACGCTGTGCCAGA AGTTCCGGCAGTACGCGAAGGACGACCCGAACAGCTTCGCTGTGCGGAGAAT CTAGCCTGTACCCGAGTTCATGTACCACCTGCCCGCTCGAGTTCCTGCAGGT CTTCAACAACCTGCCCGACGAGACCACTTCTACAGACACATGCTGATGCGCGAA GACCTGACCCCAATCCCTCATCATGATCCAGCCGATCCCTACTACTCGTACAGCTTCG GAGGCGCGCCCGAACCCGCTGCTGTAGACACCAAGCTCCATCCAGCCCGACCGCA

PX015	<p>SEQ ID NO: 2355 GCGTAATACGACTC ACTATAGGACGAG AAGATCCGCATGAA CC</p> <p>SEQ ID NO: 2357 GACGAGAAGATCCG CATGAACC</p>	<p>SEQ ID NO: 2356 GATGATGGCCGGAG AGTTCTTG</p> <p>SEQ ID NO: 2358 GCGTAATACGACTC ACTATAGGATGAT GGCCGGAGAGTTCT TG</p>	<p>TCCTGCTCATGGACACCTTCTCCAGATCCTCATCTACCATGGAGAGACAATGGC GCAATGGCGCGCTCTCCGCTACCAAGACATGGCTGAGTACGAGAACTTCAAGCA GCTGCTGCGAGCGCCCGTGGACGACGCGCAGGAGATCCTGCAGACCAGGTTCC CCGTGCCGCGGTACATTGATACAG</p> <p>SEQ ID NO: 2354 GACGAGAAGATCCGCATGAACCCGCTCGTCCGGAACAACCTGCGAGTGCGCCTG TCAGACATTGTCCATCGCTCTTGCCTGAGTGAAGTACGGCAAGAGAGTTG ATATTCTGCCATTGATGACTCTGTGAGGGTTTGAAGTGAACCTGTTGAAAGTC TACCTGAAGCCGTACTTCATGGAGGCGTACCGGCCATCCACCCGACGACACG TTCATGGTGGCGCGGCATGCGGCCGTCGAGTTCAGGTTGAGGAGACCGA CCCCCGCCTACTGATCGTGGCCCCGACACGGTCAATTGAGGGAGA GCCGATTAAACGGAGGAAAGAGAGGCTCTCAACGCCGCTCGGTACGACGA CATCGCGGGTCCGCAAGCAGCTGGCGCAGATCAAGGAGATGGTGGAGCTGC CGTGGCCACCCCTCGCTGTTCAAGGCCATCGGGTCAAGCCGCCCGGGGG ATACTGATGTACGGCCCCCGGACGGGAAGACCTTGATCGCTAGGGCTGTC GCTAATGAGACGGCGCATTTCTTCTCATCAACGGCCCCGAGATCATGTGGA AACTCGCCGGTGAATCCGAGTCGAACCTGCGCAAGGCGTTCCGAGGAGCGGACA AGAACTCTCCGGCCATCATC</p>
PX016	<p>SEQ ID NO: 2360 GCGTAATACGACTC ACTATAGGCTGGT CGTATTTTCAACGG CTC</p> <p>SEQ ID NO: 2362 CTGGTCTGATTTTC AACGGCTC</p>	<p>SEQ ID NO: 2361 AGTGATGTACCCGG TCAAGTCG</p> <p>SEQ ID NO: 2363 GCGTAATACGACTC ACTATAGGATGAT GTACCCGGTCAAGT CG</p>	<p>CTGGGTGTAATTTTCAACGGCTCCGGCAAGCCCATCGACAAGGGCCCCCGATC CTGGCCGAGGAGTACCTGGACATCCAGGGCAGCCCCATCAACCCGTGGTCCCGT ATCTACCCGGAGGAGATGATCCAGACTGGTATCTCCGCTATCGACGTGATGAAT CCATCGCCCGTGGTCAGAAAGATCCCATCTTCTCCGCCGCGGTCTGCCCCACA ACGAGATTGCTGCTCAGATCTGTAGGCAGGCTGGTCTTGTCAAGTCCCCGGAAA ATCCGTGTTGGACGACCAAGAACAACTTCCCATCGTGTTCGCCGCCATGGG AGTCAACATGGAGACCGCCAGGTTCTTCAAGCAGGACTTCGAGGAGAACGGTTC CATGGAGAACGTCGTCTGTTCTTGAACTTGGCCAATGACCCGACCATTGAGAGG ATTATACGCCGAGGTTGGCGTCTGACTGCTGCCGAGTTCTTGGCTACCAAGTGC GAGAAACACGTTGGTAATCTTGACCGACATGTCTTCAACGCGGAGGCTCTTC GTGAAGTGCAGCCGCCGTGAGGAGGTGCCGGGACGACGTGGTTCCAGGTT ACATGTACACGGATTGGCCACAATCTACGAGCGCGCGGCGGAGTCGAGGGCC GCAACGGCTCCATCACGCAGATCCCCATCTCTGACCATGCCCAACGACGACATCA CCACCCCATCCCGACTTGACCCGGGTACATCACT</p>

Table 8-AD

Target ID	Primers Forward 5' → 3'	Primers Reverse 5' → 3'	dsRNA DNA Sequence (sense strand) 5' → 3'
AD001	SEQ ID NO: 2462 GCGTAATACGACTC ACTATAGGGCTCCT AAAGCATGGATGTT GG SEQ ID NO: 2464 GCTCCTAAAGCATG GATGTTGG	SEQ ID NO: 2463 CAATATCAAACGAG CCTGGTG SEQ ID NO: 2465 GCGTAATACGACTC ACTATAGGCAATATC AAACGAGCCTGGGT G	SEQ ID NO: 2461 GCTCCTAAAGCATGGATGTTGGACAACTCGGAGGAGTATTCGCTCCTCGCCCCAG TACTGGCCCCACAAATTGCGTGAATGTTTACCTTTGGTGATTTTCTCGCAATCG GCTCAAGTATGCTCTGACGAATGTGAAGTAAACGAAGATTGTTATGCAGCGACTTAT CAAAGTTGACGGCAAGGTGCGAACCGATCCGAATTTATCCCGTGGTTTCATGGATG TTGTCACCAATTGAGAAGACTGGAGAGTTCTTCAGGCTGGTGTATGATGTGAAGGC CGTTTCACAAATTCACAGAATTAGTGCAGAAGAACCCAAAGTACAAGCTCTGCAAGGTC AGGAGAGTTCAAACTGGGCCAAAGGTATCCATTTCTGGGACCCATGATGGCCG TACTATCCGTTATCCTGACCCAGTCATTAAAGTTAATGACTCAATCCAATTGGATATT GCCACTTGTAATATCATGGACCACATCAGATTTGAATCTGGCAACCTGTGTATGATT ACTGGTGACGTAACTTGGGTGAGTGGGACTGTTGTGAGTCGAGAACGTCACCC CAGGCTCGTTTGATATTG
AD002	SEQ ID NO: 2467 GCGTAATACGACTC ACTATAGGGAAGAA AGATGGAAAGGCTC CGAC SEQ ID NO: 2469 GAAGAAAGATGGAA AGGCTCCGAC	SEQ ID NO: 2468 CATCCATGTGCTGA TGAGCTGC SEQ ID NO: 2470 GCGTAATACGACTC ACTATAGGCATCCAT GTGCTGATGAGCTG C	SEQ ID NO: 2466 GAAGAAAGATGGAAAGGCTCCGACCACCTGGTGAGGCCATTTCAGAACTCAGAGAAA CAGAAGAAATGTTAATCAAAAGCAGGAATTTTAGAGAAGAAAATCGAACAAAGAAA TCAATGTTGCAAAGAAAATGGAACGAAAATAAGCGAGCTGCTATTTCAGGCTCTGA AAAGGAAAAGAGGTATGAAAACAAATTCAGCAAAATTTGATGGCACCTTATCCACAA TTGAAATGCAAAGAGAAAGCTTTGGAGGGTGCTAATACTAATACAGCTGTATTACAAA CAATGAAATCAGCAGCAGATGCCCTTAAAGCAGCTCATCAGCACATGGATG
AD009	SEQ ID NO: 2472 GCGTAATACGACTC ACTATAGGGTCTTCT TCCAGACACTGGAT CCTC SEQ ID NO: 2474 GTCCTTCCAGACA CTGGATCCTC	SEQ ID NO: 2473 CGTGTTTCATCTCCCT CGAGTTG SEQ ID NO: 2475 GCGTAATACGACTC ACTATAGGCGTGT CATCTCCCTCGAGT TG	SEQ ID NO: 2471 GTCCTTCCAGACACTGGATCCTCGTATTTCCACACCTGGCAGTTAGATTCTTCTATC ATTGGCACATCACCTGGCCTAGGTTTCCGGCCAATGCCAGAAGATAGCAATGTAGA GTCAACTCTCATCTGTACCGTGAACAGATCGTGATGACTTCGTCAGTGGACAG ACACCTTGATGAAATTTCTTGCTGTGTAAGACTCCTGGTCTGACCCCTGGTCGAG GTCAGAACATCCACAACTGTGACTATGATAAGCCGCCAAAGAAAGGCCAAGTTTGC AATGTGGACATCAAGAAATGGCATCCCTGCTCAATCAAGAGAACTCACTACAACCTACCAC AAGAGCTCTCCATGCATATTCATCAAGCTCAACAAGATCTACAAATTTGGATCCCTGAA TACTACAATGAGAGTACGAAATTTGCCTGAGCAGATGCCAGAAGACCTGAAGCAGTA CATCCACAACCTGGAGAGTAAACAACCTCGAGGAGATGAACACG
AD015	SEQ ID NO: 2477 GCGTAATACGACTC	SEQ ID NO: 2478 AGAAATTCAGGCG	SEQ ID NO: 2476

AD016	<p>ACTATAGGGTTGAA GGACTAACCGGAA TTTG</p> <p>SEQ ID NO: 2479 GTTGAAGGACTAAC CGGGAATTTG</p>	<p>ACCAAGTGG</p> <p>SEQ ID NO: 2480 GCGTAATACGACTC ACTATAGGAGAAATTT CAAGCGACCAAGTGG</p>	<p>GTTGAAGGACTAACCGGGAATTTGTTTGAGGTGACTTAAACCCGTACTTTCTCGAA GCATACCGACCCATTACAAAGATGATCGGTTATTGTTCTGGTGTATCGGAGCA GTAGAATTCAAAGTAGTGGAAACAGATCTTACCATAATTGATTGTTGCTCTGATA CTGTTATCACTGTGAAGTGATCCAATAAACGTGAAGAGGAAGAAGCATTA ATGCTGTTGGTTATGATGACATTTGGGGTTCGGAACACAGCTAGCACAGATCAAG GAAATGTTGGAATTGCCATTACGGCACCCAGTCTCTTTAAGGCTATTGGTGTAAAG CCACCGAGGGGAATCTGCTGATGGACCCCTCGAAGTGGTAAACCCCTCATTTGC CAGGCTGTGGCTAATGAACTGGTGCACTCTCTTTTAAATAATGGTCTCGAAATTT ATGAGCAAGCTTGCTGGTGAATCTGAAAGCAACTTACGTAAGGCATTTGAAGAAAGCT GATAAGAAATGCTCCGGCAATTAATTTATGATGAACATAGATGCAATTCGCCCTAAAA GAGAAAAAATCATGGAGAGGTGGAACGTGCATAGTTTCACAACTACTAACTTTAA TGGATGGTCTGAAGCAAGTTCAATGTTATTGTTATGGCTGCCACAAATAGACCCA ACTCTATTGATGTGCCCTTGCGCCGCTTTGGCAGATTTGATAGGGAAATTGATATTG GTATACCAGATGCCACTGGTGCCTTGAAATTC</p> <p>SEQ ID NO: 2481</p> <p>ACCCGGAAGAAATGATCCAGACGGGGATCTCGACCATCGACGTGATGACGTCCATC CGCGAGGGCAGAGAATCCCCATCTCTCGGGCGAGGGCTGCCACACAACGAGA TCGCTGCGCAGATCTGCCAGACGGCGGGCTGGTGACGACAAAGGAGAACAAAGGA CGACTTCGCCATCGTTCGCGGCGATGGCGTCAACATGGAGACGGCGCGCTTC TTCAAGCCGAGTTCGCGAGACGGCGCGTGCAACGTGGTGTCTCTCAACC TGGCCAAACGACCCCAACCATGAGCGCATCATCACCCCGCCCTCGCGCTCAACCGT GGCCGAGTTCTTGGCTACCAAGTGAACAAGCAAGTGTCTGTCATCATGACCCGACA TGACCTCTACGCGGAGCGCTGCCGAGGTGAGCGCGCGCGGAGGAGGTTCT CTGGCGGAAGAGGCTTCCAGGGCTACAT</p>
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Table 9-LD

[illegible]

LD006	<p>TACAATGTTCAAGAAACAGTTGCATCTAAACCCCTATGGCCATCAAAATCAATGAACGCTAAGCTGATCCGGCGAGATTTTCAGGAG CTAAGGAAGCTAAATGGAGAAAAAATCACTGGATATACCACCGTTGATATATCCCAATGGCATCGTAAGAAACATTTTGAAGCATTT CAGTCAGTTGCTCAATGTACCTATAACCAGACCGTTGAGCTGGATATTACGGCTTTTAAAGACCGTAAGAAAAAATAGCACAAAGTT TTATCCGGCCCTTTATTCACATTTCTGCGCCCTGATGAATCTCATCCGGAATTCGTATGGCAATGAAGACGGTGAGCTGGTGATA TGGGATAGTGTTCACCCCTGTTACACCGTTTCCATGAGCAAACTGCTCATCGCTCTGGAGGAAATACCAACGAGATTTCC GGCAGTTTCTACACATATTCGCAAGATGTGGCGTGTACGGTGAACAACTGGCCATTTCCCTAAAGGGTTTATTGAGAAATATGTTT TTCCGCTCAGCCCAATCCCTGGGTGAGTTTACCAGTTTGTATTAACCGTGGCCATATGACAACTTCTCGCCCGCTTTTCACCAT GGGCAATATTATACGCAAGGCGACAAGGTGCTGATGCCGTGGGATTCAGGTTTCATCATGCCGTCTGTGATGGCTTCCATGTCCGG CAGAAATGCTTAATGAATTACAACAGTACTCGCATGAGTGGCAGGGGGCGTAACCGCTGGATCAGCTTAATATGACTCTCAATA AAGTCTCATACCAACAAGTCCACCTTATTCAACCATCAAGAAAAAGCCAAAATTTATGCTACTCTAAGGAAAACTTCACTAAAGAAG ACGATTTAGAGTGTTCACCAAGAAATTTCTGTCATCTTACTAAACAACCTAAAGATCGGTGTGATACAAAACTTAATCTCAATTAAGTTTA TGCTAAAATAAGCATAAATTTACCCACTAAGCGTGACCAGATAAACATACTCAGCACACGAGACATATATTTGGTGGCTCAAAATCA TAGAACTTACAGTGAAGACACAGAAAGCCGTAAAGAGAGGCAAGAGTATGAACCTTACCTCATCATTTCCATGAGGTGCTTCTGA TCCCGCGGGATATCACCACCTTTGTACAAGAAAGCTGGTGAATTCGCCCTTGGAGCGGCATGCAAGCGCTGAAGCGGAAGAGCG ATTAGAAAAAATCAGTTGCAAAATAGATGGCAGCTTAACTACTATTGAACCTTCAACGAGAAAGCTCTGGAGGGAGCTAGTACGAAACCC ACAGTATTGGAATCTATGAAAAATGCAGCTGAAGCTCTTAAGAAAGCCCATAAAACTTGGACGTGGACAATGTACACGACATGATGG ATGACATTGCAAGGGC</p>
LD006	<p>SEQIDNO: 241</p> <p>GCCCCTGGAGCGGAGACTACAACAACATATGGCTGGCAGGTGTTGGTTGCTTCTGGTGTGGTGAATACATCGACACTCTTGAAGAAGA AACTGTATGATTGCGATGAATCCTGAGGATCTCGGAGAGCAAAAGAAATATGCTTATTGTACGACCTACACCCACTGCGAAATCCAC CCGGCCATGATCTTGGCGTGTGGCGTCTATTATACCTTTCCCGCATCAACCAAGAGCCCAAGAAACACCTACCAAGAGCGCTATG GGTAAGCAAGCTATGGGGTCTACATTACGAATTTCCACGTGCGGATGGACACCCCTGGCCACGCTGCTATACTACCCGACCAAAACCT CTGGTCACTACCAGGTCTATGGAGTATCTGCGGTTCAAGAAATACCAAGCGGATCAACAGTATAGTTGCTATTGCTTGTATTAACCTG GTTAATCAAGAAGATCTGTTATTCTGAACGCGTCTGCTGTGGAAGAGGATTTTCCGATCCGTTTATCGTTTCTTATAAAGAT GCCGAATCGAAGCGAATTCGCGATCAAGAGAGCAGTTCGAGAAAGGCGAATTCACCAAGCTTTCTGTACAAAGTGGTATATCACTA GTGCGGCCGCTGCAGGTGACCATATGTCGACCTGCAGGCGGCCGACACTAGTATGCTGTTATGTTAGTGTCAAGCTGACCTG CAACACGTTAAATGCTAAGAAGTTAGAATATATGAGACACGTTAAGTGGTATATGAATGAAGCTGTAATAACCGAGTATAAACTCAAT AACTAATATCACCCTCTAGAGTATAATATAATCAAAATTCGACAATTTGACTTTCAAGAGTAGGCTAATGTAAATCTTTATATATTTCTACA ATGTTCAAGAAGAACAGTTGCATCTAAACCCCTATGGCCATCAAAATCAATGAACGCTAAGCTGATCCGGCGAGATTTTCAGGAGCTAA GGAAGCTAAATGGAGAAAAAATCACTGGATATACCACCGTTGATATATCCCAATGGCATCGTAAGAAACATTTTGAAGCATTTTCAGT CAGTTGCTCAATGTACCTATAACCAGACCGTTGAGTGGATATACGGCTTTTAAAGACCGTAAAGAAAAAATAGCACAAAGTTTAT CCGGCCCTTTATTCACATTTCTGCGCCCTGATGAATGCTCATCCGGAATTCGTTGCAATGAAGACGGTGAGCTGGTGATATGG GATAGTTTACACCTGTTACACCGTTCATGAGCAAACTGAAACGTTTTCATCGCTCTGGAAGTGAATACCAACGATTTTCGGC AGTTTCTACACATATATCGCAAGATGTGGCGTTTACGGTGAACCTGGCCATTTCCCTAAAGGGTTTATTGAGAAATATGTTTTTC GTCTCAGCCCAATCCCTGGGTGAGTTTACCAGTTTGTATTAACCTGGCCATATGGAACAATCTTCCGCCCCCTTTTACCATTG GCAATATTATACGCAAGGCGACAAGGTGCTGATGCCGCTGGCGATTGCAAGTTTCATCATGCCGCTCTGTGATGGCTTCCATGTCCGCA GAATGCTTAATGAATTACAACAGTACTGCGATGAGTGGCAGGGCGGTAACCGCTGAACGCTTAAATATGACTCTCAATAAA</p>

	<p>GTCTCATACCAAGTGGCCACCTTATTCAACCATCAAGAAAAAGCCAAAATTTATGCTACTCTAAGGAAAACTTCACTAAAGAAGAC GATTTAGAGTGTTTACCAAGAAATTTCTGTCATCTTACTAAACAACATAAGATCGGTGTGATACAAAACCTAATCTCATTAAGTTTATG CTAAATAGCATAAATTTTACCCACTAAGCGTGACGAGATAAACATAACTCAGCACACAGAGCATATATTTGGTGGCTCAAAATCATATA GAACTTACAGTGAAGACAGAGAAAGCCGTAAGAGAGCGTAGAGATGAAACTTACCTCATCATTTCCATGAGGTTGCTTCTGATC CCGGGATATACCCACTTTGTACAAGAAAGCTGGTGGCCCTTCTCGAACTGCTCTTCTGATCGCCAAATTCGCTCGATTCGGC ATCTTTATAGGAACGATAAACACCGGATCGGAAAAATCCTCTTTCCACAGCAGACGCGTTCAGAAATCAAGAAATCTTCTTGATTAAC CAGTATAACAAGCAATAGCAACTATACTGTTGATCCCGGCTGGTAATCTCTGAACCGCAGATACTCCATAGACCTGGTAGTGACCAG AGGTTTGTGGGTAGTATAGCACGTGGCCAGGTGTCATCCGACGTGGAATTCGTAATGTAGACCCCATAGCTTGCCTTACC CATAGCGCTCTGGTAGGTGTTCTTGGCTCTGGTTATGATCGGGGAAGGTATAATAGACGCGCAACGCCAAGATCATGGCCG GGTGGATTCGCAGTGGGTAGGTGCTACAATAAGCATATCTTTGCTCTGCCGAAGATCCTCAGGATTCATCGCAATCATGACAGT TCTCTTCAAGAGTGTGATGTATTCACCAACACAGCAAGCAACCAACACTGCCAGCCATAGTTGTTGTAGTCTCGCTCCAAGGGC</p>
LD007	<p>SEQIDNO: 242</p> <p>GCCCTCCGAAGGATGTGAAGGGTACTTACGTATCCATACACAGTTCAGGCTTCAGAGATTTTTTATTGAACCCAGAAAAATTTCTAA GAGCTATAGTTGACTGCGGTTTTGAACACCCCTTCAGAAGTTCAGCACGAATGTATCTCTAAGCTGTCAATGGCATGGACATTTTATGT CAAGCCAAATCTGGTATGGGCAAAACGGCAGTGTGTTCTGGCACACTGCAACAATTTGGAACCCAGCGACAATGTTGTTACGTTT TGGTATGTGTCACACTCGTGAACCTGGCTTTCCAAATCAGCAAGAGTACGAGAGTTTCCAGTAAATATATGCCAGTGTCAAGGTGG CGCTTTTTTGGAGGAATGCCTATTGCTAACGATGAAGAATTTGAAAACAAATGTCCACACATTTGTTGGGGACGCTTGGGC GTATTTTGGCGCTGTCAAGTCTAGGAAGTAGTCTCAAGAACCTGAAACACCTTCAATCTTGATGAGTGCATGATTAAGTAACTG TTGGATATGAGGAGAGACGTCCAGGAAATCTACAGAAACACCCCTCACACCAAGCAAGTGTGATGTTGATGTTCCACACTCAGCAAA GAAATCAGGCGGTTGTGCAAGAAATTCATGCAAGATCCAAATGGAGGTGTATGTAGACGATGAAGCCAAATGACGTTGCACGGATTA CAACAGCATACGTTAACTCAAGAAAAATGAAGAATAAAAAATTTTGAAGTGTGCTCGATGTTCTCGAAATTTAATCAGGTGGTCAAT TTTGTGAAGTCCGTTCAAGGTGTGGCTTTGGCACAGTTGCTGACTGAACAGAAATTTCCAGCCCATAGGAATTCACAGAGGAATG GACCAGAAAGAGAGGTTGCTCGGTATGAGCAGTTCAAAGATTTCCAGAAGAGAAATTTGGTAGCTACGAATCTCTTTGGCGGTGGC ATGGACATTTGAAGGGTCAACATTTGCTTCAACTATGATATGCCAGAGGACTCCGACACCTACTTGCATCGAAGGGCGAAATTCACCAG CTTTCTGTACAAAGTGGTATATCACTAGTGCAGGCGCCCTGCAGTGCACCATATGTCGACCTGCAGGCGGCCGCACTAGTGATGC TGTTATGTTCAAGTCAAGCTGACCTGCAACACAGGTTAAATGCTAAGAAGTTAGAATATATGAGACACGTTAACTGGTATATGAATAAG CTGTAATAACCGAGTATAAATCACTAATATCACCTCTAGAGTATAATAATCAAAATCGACAAATTTGACTTTCAAGAGTAGGC TAATGTAAATCTTTATATATTTTACAAATGTTCAAGAAACAGTTGTCATCTAAACCCCTATGGCCATCAATGAACGCTAAGCT GATCCGGCGAGATTTTCAGGAGCTAAGGAGCTAAATGGAGAAAAAATCACTGATATACCACCGTTGATATATCCCAATGGCATC GTAAAGAACAATTTGAGGCATTTTCAAGTCAAGTGTCAATGTACCTATAACCAAGACCGTTTCAGCTGGATATACGGCTTTTAAAGACC GTAAAGAAAAATAGCACAAAGTTTTATCCGGCTTTTATTCACATCTTGGCCGCTGATGAATGCTCATCCGGAATTCGATGGCAAT GAAAGACGGTGAGCTGGTATGGGATAGTGTACCCCTTTTACACCGTTTCCATGAGCAAACTGAAACGTTTTTCATCGCTCTGG AGTGAATACCAACGAGATTTCCGGCAGTTTTCACACATATATCGCAAGATGTGGCGTGTACGGTGAACACCTGGCCCTATTTCCCTTA AAGGTTTATGAGAAATGTTTTTCTGCTCAGCCCAATCCCTGGGTGAGTTTCAACAGTTTGAATTTAAACGTGGCCCAATATGGACAAC TTCTGCCCCCTTTTACCATTGGGCAATATATACGCAAGGCAAGGTCGTATGCCGCTGGCGATTGAGTTTCAAGTTTATCATGCCC GTCTGTGATGGCTTCCATGTCCGAGAGATGCTTAATGAATTAACAACAGTACTGCGATGAGTGGCAGCGGGGGGTAACCGCTGG ATCAGCTTAATATGACTCTCAATAAAGTCTCATACCAACAGTGCACCTTATTTCAACCATCAAGAAAAAAGCCAAAAATTTATGCTACTC</p>

	<p>TAAGGAAAACCTTCACTAAAGAAGACGATTAGAGTGTTTTACCAAGAAATTTCTGTCATCTTACTAAACAACAACTAAAGATCGGTGTGATAC AAAACCTAATCTCATTAAGTTTATGCTAAATAAGCATAAATTTACCCACATAAGCGTGACCGAGATAAACAATAACTCAGCACACACAGAG CATATATTGGTGGCTCAATAGAACTTACAGTGAAGACACAGAAAGCCGTAAAGAGGCAAGAGTATGAACCTTTACCTCA TCATTTCCATGAGGTCTCTGATCCCGGGGATATCGACCATTGTACAAGAAAGCTGGTGAAATTCGCCCTTCGATGCAAGTA GGTGCGGAGTCTCTGGCATATCATAGTTGAAGACAATGTTGACCCCTTCAATGCCATGCCACGCCCAAGAGATTCGTAGCTACC AATATTCTCTCTGGAATCTTTGAACCTGCTATACCGAGACAACCTCTCTTCTGTCCTTCTGTAATTCCTATGGCTGGAA ATTCTGTCAGTCAGCAACTGTGCCAAAGCCACACACCTTTGAACGGACTTCAAAAATGACCACCTGATTAAATTCGAGAACAATCG AGCAACTCAATAATTTTTATCTTTTCAATTTCTTTGAGTTTAACGTAATGCTGTGTAATCCGTGCAACGTCAATTTGGCTTCATCGT CTACATACACCTCCATTGGATCTTGCAATGAATTTCTTGACACCGGCCCTGATTTCTTTGCTGAGTGGCACTGAACATCACTTGC TTGGTGTGAGGGGTGTTTCTGTAGATTTCTGGAGCTCTCTCTCATATCCAACAGTTCTAACATTTTATCGCACTCATCAAGAATGAA GTGTTTCAGGTTCTTGAGGACTAGCTTCTAGACTTGACAAGCGCCAAATACGCCAGCGTCCCAACAACAAATGTGTGGACATTT GTTTTCAATACTTCTTCATCGTTAGCAATAGGCAATCTCCGAAAAGACGCCACCTTGACACTGGGCATATATTTACTGAACCTCT CGTACTCTTTGCTGATTTGGAAGCCAGTTCCAGGAGTGTACACATCACCAAAACGTAAACAACATTTGCCGTGGTCCAAATGTTG CAGTGTGCCGAGAACAAACACTGCCGTTTTGCCCATACCAATTTGGCTTGACATAAAATGTCATGCCATGCCAATGACAGCTTGAGGAATA CATTCGTGCTGAACCTCTGAAGGGTGTCAAACCGCAGTCAACTATAGCTCTTAGAAATTTCTGGTTTCAATAAAAAAATCTCTGAAGCC TGAACGTGTATGGATACGTAAGTACCTTCACATCCTTCTCGGAAGGGC</p>
LD010	<p>SEQIDNO: 243</p> <p>GCCCTTCGCCATTGGCGATGGTTTCGCCATGGAATATCAGAAATCTGGAAGAACGTGTCCATGAGCAGAAATCTATCGGGTTGGATG GAACTCGTATCCAAAAGCACAGTTCTGGTGCTCATTGAACTGTAGCTGTAGAGTATCGGCTGGATCATGATCAGCGACTGCGTG AGGTCTTCGCGCATAGCATGTGCTGTAGAGGACGTTCTGTCGGGAGAAATGTTAAACACCTGCAGGAACGTGACCTTCTCAAA TGGTACATGAACCTCGGGTAGAGGCTGAAGTTTTCGCCCAAGCGGGAACGAAATTCGGGTGCTCTGTTTATTCGCCGAAATTTCTGG CACAGACGTATCAACATCCTATCGACCCATCTCAAAACATCAGGGCTATCGTCTGATTCCGCTCTGTAACCTGCCATCCTCGCCATTA TCACTGCGCTGCCCTCGTATCGAATCCAGCACTGACATGATGATAGCGGAAGCATGGCCCAATTTCTAGCAACTGTGTTA CTCGGATCCTCTTCGGCCACTAGCATGCTGATATTGCGTGAATGAACCTGTATGAGCCCTTCCCTTGGGTATGGAGCGGAAT GTTGGTTGACGACCTCGAAGAACAAAGCCATGTTAGTACTTGGAGTTACCGTACACATTTCCACTGGACCGTGTACCCATTCCTAT TTCGGTGTCCGAAACCAAGGATTTCTCACATTCACGAAACACAAAGATCCAATACCGCTTGAATTTCAACTCCCTGGAAACACTTG ACCTCCAGAGTACCATTAAATGCCATCTTCAGCTCGTTTCTGATCTTTCGAAAATATCGCTGGAACGTTTGTCTGAACAGGGAA GAATTGAACGAGTCGCCATGACCATATGTCCCCCTGTTGAATTACAACACTGTTTCACTCCATCAATCCTGTCTGATCCAAAGCGC ATGAATATATGTCAGCGAGTGGCCATTGCTGCTCTCATCGCTAAATATCATAGTGTGATTGCTTTCTTCATGTATTGGCAT TGTCTTTTGGATGCTGGTGAGATCTGATAGTTGCTTCAGATCATCATTCAGACTTGACCAAGGCCCTTGAGAGCAAGTCTCTCC AACGAATAGCATGACCTTGGCACCAGTATTGGCGTATGTGCATCCAAACCCCAATGGCTATCGATAAAGCTGTCCCGTCCGATCT AAGGGCGCATTTGCCCTGGTGACAGGCCATGGGTCTCTTTGCAACTCTCCAATGAAGATCAGTGAGGTTTCATGCGCATTTGAGAT GGGTTGAAGGAACCTGCTTCTGGTGGCGTAGGAGCTTGCTCCAGGCCCTCATGGGTGTCCTGGTTGTTGAGAGCAG GTTGAGCACTTACTCGGCTCTGCCCACTTCCAACATCTCTTGAACCTGCTAGCTGTGAGGCTTTTCTGCTCCCTCGGAAACGTAAGA TTTGTGTCAGCCCTCGGTACCTAGTTCTGTGCACTTGACCCTCTCCCAAGGTAAATCAACCTTCAAGGCAATTCGGGGGCAACAA GCTCAAAGACATCTGCAACGAATCTTGAGAGAAAGGGCAATTCACAGCTTCTTGACAAAGTGGTATATCACTAGTGTGCGGCGC CTGCAGGTGACCATATGTCGACCTGCAGGCGCGGCACTAGTGTGCTGTTATGTTAGTGTCAAGCTGACCTGCAACACAGTTA</p>

	<p>AATGCTAAGAAGTTAGAAATATATGAGACACGTTAACTGGTATATGAATAAGCTGTAAATAACCGAGTATAAACTCATTAACTAATATAC CTCTAGAGTATAATATAATCAAAATTCGACAAATTTGACITTTCAAGAGTAGGCTAATGTAAATCTTTATATATTTCTACAATGTTCAAGAA ACAGTTGCATCTAAACCCCTATAGCCCATCAAAATCAATGAACGCTAAGCTAGCGGAGATTTTCAGGAGCTAAGGAAGCTAAAT GGAGAAAAAATCACTGGATATACCAACGTTGATATACCAATGGCATCGTAAGAACATTTTGAGGCAATTCAGTCAAGTGTCTCAAT GTACCTATAACCCAGACGTTGAGTATACGGCTTTTAAAGACCGTAAAGAAAAAATAGCACAAAGTTTTATCCGGCCCTTTAT CACATTTGCCCGCTGATGAATGCTCATCGGAATTCGATGGCAATGAAGACGGTGAGCTGGTGATGCGGAGATGTTTACACAT CCTGTTACACCGTTTCCATGAGCAAACTGAACGTTTTATCGCTCTGAGTGAATACCAACGAGATTTCCGGCAGTTTCTACACAT ATATTCGCAAGATGTGGCGTTACGGTGAAACCTGGCTATTTCCCTAAAGGTTTATGAGAATATGTTTTCGTCTCAGCCCAATC CCTGGGTGAGTTTACCAGTTTATTAACGTTGCCAATATGACAACTTCTTCGCCCCGTTTACCATGGGCAATATTATAC GCAAGGCGACAAGGTGCTGATGCCGCTGGGATTCAGTTTCAATCGCTGTGATGGCTTCCATGTCGGCAGATGCTTAATGA ATTACACAGTACTCGATGAGTGGCAGGGGCGTAAACGCTGATCAGCTTAAATATGACTCTCAATAAAGTCTCATACCAAC AAGTCCCACTTATTCAACCATCAAGAAAAAGCCAAATTTATGCTACTCTAAGGAAACTTCACTAAGAAAGACGATTAGAGTGTT TTACCAAGAAATTTCTGTCATCTACTAAACAACCTAAAGATCGGTGATACAAACCTAATCTCAATTAAGTTTATGCTAAATAGCAT AATTTACCCACTAAGCGTGACCAAGATTAACATAAATCAACGACAGCATATATGTTGGTCAATTTCTGATCCCGGGGATATC AAGACACAGAAAGCGTAAAGAGGCAAGATTAAGAACCTTACCTCATCATTTCCATGAGGTTGCTTCTGATCCCGGGGATATC GACCACCTTTGACAAAGAGCTGGTCAATTCGCCCTTCTCAAGGATCGTTGAGATCGTTGAGCTTTTGGCCCGGAAATGCC TTGATAGGGTTGATACCTTTGGGAAGATGGTCCAAGTGCAAGAACTAGTAGCCGAGGCGAGTAAAGTCTTCAAGGTTGCTTCTGATCCCGGGG ACGAAAGACCTCACAGCTAAGCAAGTTCAAGAGATGTTGGAAGTGGCAGAGCCGAGTAAAGTCTTCAAGGTTGCTTCTGATCCCGGGG GAACCCCATGAGCCCTGAGCACTCCAGCAAGCTCTACGCCACCAAGGAGGTTCCCTTCAACCCATCTCGAAATGCGACAT GAACCTCACTGATCTATTGGAGAGTTGCAAGAGACCCATGCTGCTCCACCAAGGCAATGCGCTTAGATCGACCGGGACAGC TTTATCGATAGCCATTGGTGTGGAGTGACATACGCCAATAGTGTGCCAGGTCATGCTATTGTTGAGGACCTTGTCTCTCAA GGCCCTGGTCAAGTCTTGAATGATGATCTGAAGCAACCTATCAGATCTCACCACGACATCCAAAAGACAAATGCGCTTTGGATCAGAC AAGCAATCAAGCACTATGATAATTTAGCGATGAGAGCAGCAACGAATGGCCACTGCGTTGACATATATTCATGCGCTTTGGATCAGAC AGGATTGATGGAGATGAACAGTGTGTAATTCAAAGGGGGACATATGGTCAATGGCGACTCGTTCAATTTCCCTGTTCAAGCAA ACGTTCCAGCGCATATTTTCAAGAGATCAGAAACAGAGCTGAAGATGGCATTAATGGTACTCTGGAGGGTCAAGTGTCCAGGGA GTTGAAATTCAGGCGGTATTGGATCTTGTTTTCGTTGAATGTAAGAACTCCTTTGGTTCCGACACCCGAAATAGGAATGGGTAAC ACGGTCCAGTGGAATGTTACGGTAACCTCAAGTACTACATGGCTTGTCTTGGAGGTCGTCAACCAACATTCGGCTCCCATAC CTCAAGGGGGAAGGGCTGCATACAGTTTCATCAGCAATATCAGCATGCTAGTGGCCAGAAGAGGATCCGAGTAACGACAGTTGCT AGAACTGGGCGGATGCTTCGGCTAATATACATCATGTGAGTTCGATCAGGAGGCGAGCCAGTGATAATGGCGAGGATG GCAGTTTACAGAGCGGAATCAGACGATAGCCCTGATGTTTGAAGTGGTGGATAGGATGTTGATACGCTGTGCCCAGAAATTCGGC GAATATAACAGGACGACCGAATTCGTTCCGCTTGGCGGAAACCTCAGCCCTCTACCCGAGTTTCATGTACCATTTGAGAAGGTCA CAGTTCTGCAGGTGTTTAACAATTCGCCGACGAAACGCTCTTACAGGCACATGCTTATGCGGAAAGACCTCAGCGAGTCCGTG ATCATGATCCAGCCGATCTACAGCTACAGTTTCAATGGACCCACCAAGACCTGTGCTTTTGATACGAGTTCCATCCAAACCCGATA GAATCTGCTCATGGACACGTTCTTCCAGATCTGATATTCATGGCGAAACCATCGCCCAATGGCGGAAGGGC</p>
LD011	<p>SEQIDNO: 244 GCCCTTGTGGAAGCAGGGCTGGCATGGCGACAAATTCATAGTTGGGATCACCAATAAGCTTCTAGCTAGCCATAGGAAAGGCTTCT CAAAGTTGTAGTTGGCAGAGATATCATAGTACTGCAAAATCTTCTTCTCTATGAAAGACAATACITTTTCGCTTTTACTTTCTGT</p>

	<p> CTTGATGTCAACCTTGTCCCGCAAGTACTATCGGGATATTTACAGACTCTGACAAGATCTCTGTGCCAATTTGGTACATTTCTG TATGTAACCTGTGAAGTTACATCAACATGATAATAGCACACTGTCCCTGAATGTAATATCCATCAGGAGACCACCAACTTCTCCTG ACCGCGAGTGCCCATACATTAACCGAATAGGCCCTGTGTGATGAAGACCAGAGGATGGACTTCAACTCCCAAGTAGCTAC ATCTCTTTTCAAAATCACCAGTCATATGAGCTTTACAAATTCGTTTCCAGTCCCTCCGACCAACACACACTTGAAGT GGAAGGGCGAATCGACCCAGCTTTCTGTACAAAGTGGTGATATCATCTAGTGGCGCCCTGCAGGTCGACCATATGGTCGACC TGCAGGCGGCCGCACTAGTGTCTGTATGTTCAAGTGTCAAGCTGACCTGCAAAACACGTTAAATGCTAAGAAGTTAGAATATAGAG ACACGTTAACTGGTATGATGAATAAGCTGTAATAACCGAGTATAAATCAATTAATCACTCTAGAGTATAATATAATCAAAATTC GACAAATTTGACTTCAAGAGTAGGCTAATGTAAATCTTTATATAATTTCTACAAATGTTCAAAGAAACAGTTGCACTAAACCCCTATGGC CATCAAAATCAATGAACGCTAAGCTGATCCGGCGAGATTTTCAGGAGCTAAGGAAGCTAAATGGAGAAAAAATCACTGGATATACC ACCGTTGATATATCCCAATGGCATCGTAAAGAACATTTTGAGGCAATTCAGTCAGTTGCTCAATGTACCTATAACCAAGACCGTTCAAGT GGATATTACGGCTTTTAAAGACCGTAAAGAAAAATAAGCACAAGTTTATCCGGCTTTTATTCACATTTCTGCCCGCTGATGAATG CTCATCCGGAATTCGATGGCAATGAAAGACGGTGAGCTGGTGATATGGGATAGTTTACCCCTTGTACACCGTTTTCATGAGCA AACTGAAACGTTTTCATCGCTCTGGAGTGAAATACCACGACGATTTCCGGCAGTTTCTACACATATATTCGCAAGATGTGGCGTTTAC GGTGAAAACCTGGCTATTTCCCTAAAGGTTTATGAGAAATATGTTTTCGCTCAGCCCAATCCCTGGTGAGTTTCAACGATTTTGA TTTAAACGTGGCCAATATGGACAACCTTCTCGCCCCGTTTTCACCATGGGCAATATATACGCAAGGCGACAAGGTGCTGATGCCG CTGGCGATTCAAGTTTCATCATGCCGCTGTGATGGCTTCCATGTGGCAGAAATGCTTAATGAATTAACAACAGTACTCGGATGAGTGG CAGGCGGGGGGTAAACCGGTGATCAGCTTAATATGACTCTCAATAAAGTCTCATACCAAGTCCACCTTATTTCAACCATCAAG AAAAAAGCCAAAATTTATGCTACTCTAAGGAAACTTCACTAAAGAAAGACGATTTAGAGTGTTTACCAAGAAATTTCTGTCTACTTA AACCACTAAAGATCGGTGTATACAAAACCTAATCTCAATTAAGTTTATGCTAAATAAGCATAATTTTACCCACTAAGCGTGACCAGAT AAACATAACTCAGCACACGAGCATATATATTGGTGGCTCAATATAGAACTTACAGTGAAGACACAGAAAGCCGTAAAGAAAGG CAAGATATGAACCTTACCTCATATTTCCATGAGGTGCTTCTGATCCCGCGGATATCGGACCACTTTGTACAAGAAAGCTGGGT CGAATTCGCCCTTCCCACTTCAAGTGTGTGGTGGTCGGAGATGGAGTACTGGAAACACGACATTTGTGAACGTCATATGACTGGT GAATTTGAAAAAAGATATGTAGCTACTTTGGGAGTTGAAGTCCATCCTCTGGCTTCCATACAAACAGGGGCCCTATTCCGTTCAATG TATGGACACTGCCGGTCAGGAGAAAGTTTGGTGGTCTCCGTGATGGATATACATTCAAGGACAGTGTGCTATTATCATGTTTGATGT AACTCCAGAGTTACATACAAGAAATGTACCAAAATTTGGCACAGAGATCTTGTCAAGTCTGTGAAAATATCCCGATAGTACTTTGCGGG AACAAAGTTGACATCAAGACAGAAAAAGTAAAGCGAAAAAGTATTGTCCTTCATAGGAAGAAATTTGCAGTACTATGATATCTCTGC CAAATCTAACTACAACCTTTGAGAAGCCCTTTCTATGGCTAGCTAGGAAGCTTATTGGTGATCCCAATCTAGAAATTTGTGCCCATGCCAG CCTGCTTCCACAAGGGC </p>
LD014	<p> SEQIDNO: 245 GCCCTTCGAGATCAAGCATATGATGGCTTTTCATTGAACAAGAGGGCAACGAAAAAGGCGAGAAATCGATGCCAAGGCCGAGGAAG AATTTAATATTGAAAAGGGCGCTTGTTCAGCAACAACGTCCTCAAGATTATGGAATATTATGAGAAGAAAGAGAAACAGGTCGAACT CCAGAAAAAATCCAATCGTCAACATGTTGAATCAGGCTCGATTGAAAGTATTGAAGTTAGGGAAGATCACGTTCTGACCGTACTA GAGGAGCGCGTAAACGACTTGGTCAGTGCACAAACGACAGGGAATAATTTCCAAATCTTGAAGAGCTCATTTTGCAGGGGATTA TATCAGCTTTTGTAGAAAGATGTTACCATTCAGTTCGGCCCCAGACGAGAACTGGTCAATCCATCTCCACCGTCAAGCAACA AGTATAAGATGCCACCGGTAAAGACATCCATCTGAAAATTTGATGACGAAATCCATCTGTCCCAAGAAACACCCGGGGAATCGACC TGCTGGCGCAGAAAAAATCAAGATCAGCAATCTATGGAGGCTCGTCTGGAGCTGATTTCGCAGCAACTTCTGCCCGGAGATCC GAAGGGCGAATTCACCAGCTTTCTTGTACAAAGTGGTATATCACTAGTGGCGCCGCTGCAGGTCGACCATATGGTCGACCTGCAGG </p>

[illegible]

	<p>CTGGTATGAAATGAAGCTGTAATACCGGAGTATAAAGCTCAATTAACCTATACCTCTAGAGTATAATCAATCAAAATTCGACAAATTTG ACTTTCAAGAGTAGGCTAATGTAATAATCTTTATATATTTTACAATGTTCAAGAAACAGTTGCATCTAAACCCCTATGGCCATCAAAAT CAATGAACGCTAAGCTGATCGGCGAGATTTTACGAGCTAAGGAGCTAAATGGAGAAAAAATCACTGGATATACCAACCGTTGAT ATATCCCAATGGCATCGTAAAGAACATTTTGAAGCAATTTAGTCACTGCTCAATGTACCTTAAACCAAGCCGTTAGCTGGATATAC GGCTTTTTAAAGACCGTAAAGAAAAAATAGCACAAAGTTTATCCGGCTTTATCCACCTTTTACACCTTTTACACCCGTTTCCATGAGCAAACTGAAAC AATTCGGTATGGCAATGAAGACCGTGAGCTGGTATGGATAGTGTTCACCTTTTACACCCGTTTACACCCGTTTCCATGAGCAAACTGAAAC GTTTTCATCGCTCTGAGTGAATACCCAGCAGATTTCCGGCAGTTTCTACACATATATCGCAAGATGTGGCGTTTACGGTGAAAC CTGGCTATTTCCCTAAAGGTTTATTGAGAAATATGTTTTCTGCTCAGCCAAATCCCTGGGTGAGTTTCAACAGTTTTCAGTTTAAACGT GGCCAATATGGACAACCTCTTCGCCCCGTTTCCACATGGGCAAAATATTATACGCAAGGCGACAAGGTGCTGATGCCGCTGGCGAT TCAGGTTTCATCATGCCGCTGTGATGGCTTCCATGTCCGACAGATGCTTAATGAATTACAACAGTACTCGCATGAGTGGCAGGGCGG GGCGTAAACGCGTGGATCAGCTTAATATGACTCTCAATAAAGTCTCATACCAACAGTGCACCTTATTCAACCATCAAGAAAAAAGC CAAATTTTATGCTACTCTAAGGAAACTTCACTAAAGAACGATTTAGAGTGTTTTACCAGAAATTTCTGTCTACTTACTAAACAATA AAGATCGGTGTGATACAAAACCTAATCTCATTAAGTTTATGCTAAATTAAGCATAAATTTTACCACCTAAGCGTGACCAAGATAAACATAA CTCAGCACACAGCATATATATTGGTGGCTCAATCATAGAACTTACAGTGAAGACACAGAAAGCCGTAAGAGAGGCAAGAGT ATGAAACCTTACCCTCATCTTCCATGAGGTGCTCTGATCCCGGGATATCACCATTTGTACAAGAAAGCTGGTCTGAAATTCGC CCTTGACTGTCTGGTGAACGGTCTCTGGTAATCTCGAAGATGTTAAGTTCCTCAAGTACAATGAAATCGTACAACCTCAAACT GGCTGATGGCACTATACGTTCCGGACAAGTTCTGGAAGTCAGTGGTCAAAAGCTGTGTTCAAGTGTTCGAGGGCACATCAAGGAAT CGACGCCAAAAACACCCGCTGTGAATTCACAGGAGATATTTGAGGACTCTCTTCTGAAGATATGTTGGGACGTGTTTCAATGGA TCAGGAAACCCATCGACAAAGGTCCCAATTTTGGCTGAAGACTTCTGGACATCCAGGTCAACCAATCAATCCGTGTCCTCCGT ATCTATCTGAGGAAATGATCCAGACGGTATTACAGTATTGACGTGATGAATCCATCCCTGCTGGTCAAGAGATCCCAATTTCT CTGACGTGCTGCTCCCTCACAATGAAATGCTGCCAGATCTGTAGACAGGCTGTTTGTAGTCAAGATCTCTGGTAAATCTGTACTTGA TGATCATGAAGATAACTTTGCTATTGTTTCTGCTGCTATGGTGTAAACATGGAACACAGCTAGGTTCTTCAACACAGGATTCGAAAGAGA ACGGTTCTATGGAGAAATGCTGCCCTGTTCTTGAATTTGGCCACGATCCTACCATGGAAGAAATATTACACCTCGTCTGGCTTTGACA GCTGCCGAAATCTTGGCTTACCAATGTGAGAACGACGCTTGGTCACTTTCAGAGATATGCTCTCGTATGCAGAAAGCTTTGCGTGAAG TATCTGCTGCCAGAGAGGTGCCTGGTCTGCTGGTTCCTGAGTTTCCAGGTTACATGTACACCGATTTAGCTACCATCTATGAACGTGCCG GCCGTGTTGAAGGACGTAAACGGATCCATCACCCAGATTCCTATATTGACTATGCCCAACGACGACATACCCATCCTTATCCAAAGGGC</p>
LD027	<p>SEQIDNO 2486</p> <p>GGGAGCAGACGATCGGTTGGTTAAATCTGGGACTATCAAAACAAAACGTTGTCTCAAAACCTTGGAGGACACGCCCCAAACGTAAC CGCGGTTTGTTCACCCCTGAACCTACCTGTGGCTCTCACAGGCGCAGGAAGATGGTACCGTTAGAGTTTGGCATACGAATACACACAG ATTAGAGAAATGTTGAATATGGTTTCGAGAGAGTGTGGACCATTTGTTGCTTGAAGGTTTGAATAATGTTTCTCGGGGTATGAC GAGGCGAGTATATTAGTGAAGTTGGAAGAGAGAAACCGGAGTATGATGGATGCCAGTGGCGGTAAATAATTTGGGCAAGGCAC TCGGAATTACAACAAGCTAATTTGAAGCGCTGCCAGAAAGTGGAGAAATGAAGAGATGGGAGCTTTTACCTGTCTGTGTAAGAGAT ATGGGAGCATGTGAAATATACCTCAACAAATCCAAACATAATCCGAATGGAAGATTCGTTGTAGTATGGGAGACGCGCAATATATCA TTTACACAGCGGATGGCTCTACGGAACAAGGCTTTTGAAGCGCTCAAGAGTTTGTCTGGGCTCAGGACTCCAGCGGATATGCCATTC GCGAGTCTGGTTCCACAATTCGGATATTCAAAACCTTCAAGAAAGAAAGAACCTTCAAGTCGGATTTTCAGCGCGGGAAGGAATCTACG GGGGTTTCTCTTGGGATTAATTCGGTGTACAGTGGGAAATAGTCTGCTCGCAACGGAGGACAGCTACTCTTCTTATGATTCGGGAG ACCGAGGGCGGTTATTGGTCTGACAGTGGAAATAGTCTGCTCGCAACGGAGGACAGCTACTCTTCTTATGATTCGGGAG</p>

CAAGTTCAAGAGCCAGGAGAACAAATCAAGTCGACAGGATGGCGTAGAGGCGCTTTCGATGTGTGGGGAAATGAACGAGTC
TGTCGGAACCCAGCTTCTTGACAAAGTGGTGATATCCCGCGGATCAGAAAGCAACCTCATGGAATGATGAGGTAAAGTTTCATAC
TCTTGGCTCTTCTACGGCTTCTGTGCTTCACTGTAAGTTCTATGATTTGAGCCACCAATATATGCTCTGGTGCTGAGTTATG
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GTTTAGAATGACAGAAATCTTGGTAAACACTCTAAATCGTCTTCTTAGTGAAGTTTCCCTAGAGTAGCATAAATTTTGGCTTT
TTCTTGATGGTTGAATAAGGTGGCACTTGGTATGAGACTTTATGAGAGTCATATTAAGCTGATCCACCGGTTTACGCCCCGCC
CTGCCACTCATCGCAGTACTGTTGTAATCATTAAGCATCTGCCGACATGGAAGCCATCACAGACGGCATGATGAACCTGAATCGCC
AGCGCATCAGCACCTTGTCGCTTGCGTATAATATTTGCCATGGTGAACGGGGGGAAGTGTGTCATATTGGCCACGTTT
AAATCAAACTGGTGAACCTCACCCAGGATGGCTGAGACGAAACATATTTCTCAATAAACCTTTAGGGAATAGGCCAGGTTTT
CACGGTAACACGCCACATCTTGGAAATATATGTAGAAACTGCCGGAATCGTCGTGTTTCACTCCAGACGGATGAACACGTTTC
AGTTGCTCATGGAAACGGGTGAACAAGGGTGAACACTATCCCATATCACCACTCACCGTCTTTCATTGCCATACGGAATTCGGA
TGAGCAATTCATCAGCGGGCAAGATGTGAATAAGCGCGGATAAACTTGTGCTTATTTCTTACGGTCTTTAAAAGGCCGTAAT
ATCCAGCTGAACGGTCTGGTTATAGGTACATTTAGCAACTGACTGAAATGCCCTCAAAATGTTCTTACGATGCCATTGGATATATCAA
CGTGGTATATCCAGTGATTTTCTCCATTTAGCTTCTTAGCTCCTGAAATCTCGCCGGATCAGCTTACGTTTCAATGAATTTG
ATGGCCATAGGGGTTAGATGCAACTGTTCTTTGAACATTTAGAAATATATAAGATTTTACATTAGCCTACTCTTGAAAGTCAAAAT
GTCGAATTTGATTATATTAATCTAGAGGTGATATTAGTTAATGAGTTTATCTCGGTTTATACAGCTTATTCATATACCACTTAACGT
GTCATATATTTCACTTCTAGCATTTAACGTGTTTGACGTGAGCTTGACACTGAACATAACAGCATCACTAGTGGCGCCGCTG
CAGTCGACCATATGGTCGACCTGCAGCGCGCCGCACTAGTGATATACCACITTTGACAAGAAAGCTGGTCGAAATTCGCCCTTTCGG
ACAGACTCGTTCAATTTCCCAACACATCGAAAGCGGCTCTACGCCATCTCTGCGACTTGAATTTCTCCCTGGCTTCTGAACCTT
GCTCCGAATCATAGAAGGATGAAGTAGCTGCTCCTCGTTGCGAGACAGACTAATTTTCCACTGTCAGACCAATAAACCGCCCTCG
GTTGTAATTTCAATCCGCTCTCACCAAGTCCAAATCGTAAACGTTAAACCGGACACCGGATTTATCCCAAGAGAAACCC
CCGTAGATTCTTCCGCGCTGAAATCCGACTTGAAGTTCTTCTTCTTGAAGTTTGAATATCCGAAATTTGGAACCCAGACTCGCG
AATGGCATACTCGCTGGAGTCTGAGCCAGACAACTCTTGAGCGCTTCCAAAGGCTTGTCCGTAGAGCCATCGCTGTGTAAT
GATATATTGCGGCTCTCCGCATACACGAACTCTCCATTGCGATTATGTTGAGGTTATTTACATGCTCTCCCATAT
CTTTACAGAGACAGGTAACGCTCCCATCTCTTATTTCTCCACTCTGCGAGCGCTTCAAAATAGCTTGTGTAATTCGAGTGC
CTTGCCCAATTTATTTACCGCCACTGGCATCCATACCTAAGTCCCGTCTTCTCTTCCAACTTTCACATAATATCTGCTCCTGTCATA
CCCCAGAGAAACATTTATCGAACCTTCAAGCAACAAATGGTCCACACTCTCTCGAACCCATAATTCAAACAAATCTCTAATCTGTGTG
TATTCGTATGCCAAACTCTAACGGTACCATCTTCGCTGCTGTGAGAGCCACAGGTAGTTCAAGGTGGAACAAACCGGGTTACGT
TTTGGCGGTGTCCTTCCAAAGGTTTGGACACACAGTTTTTTTGATAGTCCAGATTTTAAACCAACCGATCGTCTGCTCCC

Table 9-PC

Target ID	Hairpin Sequence 5' → 3'
PC001	<p>SEQ ID NO: 508</p> <p>AGATTCAAATTTGATGTAGTCAAGAAATTTAGATGTAGCAATTTCCATTTGAATTTGTGTCATTCACATTTTGATGTTGGGTCAGGGTAACGA ATGGTTCTGCCATCATGTGTTACCAAAAATGGGATTCCTTTGGACCAGTTTGGACTCTCTTACTTTACACAACCTTGATTTTGCCCTCT CAGCTGTAATACAGGTGCACAGCAATCTTCTTTAACATCATAGATCAGACGGGAAAATTCACACAGTCTTCTCAATAGTAATGACATCCA TGAACCCAGCAGGGTAATAGAAATCAGTCCCTCATTACCATCAACTTTGATCAACCTTTGCATGACAAATTTTAGTACTTCACTGTTTGT AAGGGCATACTTCAGCCTGTTACGAAGGAAAATCACTAAAGGCAGGGATTCCGCGCAACTTGTGAGGCCCGGTGATGACGAGGGGGC GAAGACACCCCCCAATTTGTCCAACATCCATGCAAGGGCGAAATTCGACCCAGCTTTCCTGTACAAAAGTGGTGATATCACTAGTGGCGGC GCCTGCAGGTCGACCATATGGTCGACCTGCAGGCGCGCACTAGTGATGCTGTTATGTTCAAGTCAAGCTGACCTGCAAAACACGTT AAATGCTAAGAAATTAGAAATATATGAGACACGTTAACTGGTATATGAATAAGCTGTAAATAACCGAGTAAACTCATTAACATAATCAC CTAGAGTATAATAATAATCGACAATTTGACTTTCAAGAGTAGGCTAATGTAAATCTTTATATATTTCTACAATGTTCAAAGAAA CAGTTGCATCTAAACCCCTATGGCCATCAAAATCAATGAACGCTAAGCTGATCCGCGAGATTTTCAGGAGCTAAGGAAGCTAAAATGG AGAAAAAATCACTGGATATACCCCGTTGATATATCCCAATGGCATGTAAGAACATTTTGAGGCAATTTTCACTCAGTTGCTCAATGTA CCTATAACCCAGACCGTTCAGCTGGATATTACGGCTTTTAAAGACCGTAAAGAAAATAAGCACAAGTTTTATCCGGCCTTTATTCCACA TTCTTCCCCCCTGATGAATGCTCATCCGGAATCCGTATGGCAATGAAGACGGTGAGCTGGTGATGGGATAGTGTTTACCCCTTGT TACACCGTTTTCCATGAGCAAACTGAAACGTTTTTCATCGCTCTGGAGTGAATACCACGACGATTTCCGGCAGTTTCTACACATATATTCCG CAAGATGTGGCGTTACGGTGAACCTGGCTATTCCCTAAAGGGTTTATTGAGAAATATGTTTTCTGCTCAGCCCAATCCCTGGGT GAGTTTCAACAGTTTGAATTAACGTGGCCAAATATGGACAACCTTCTCGCCCCGTTTTCAACATGGGCAAAATATTATACGCAAGGGGA CAAGGTGCTGATGCCGCTGGGATTCAAGTTTCATCATGCCGCTGTGATGGCTTCCATGTCCGCGAGAATGCTTAATGAATTACAACAGT ACTGCGATGAGTGGCAGGGCGGGCGTAAACGCGTGGATCAGCTTAATATGACTCTCAATAAAGTCTCATACCAACAAGTGCCACCTT ATTCAACCATCAAGAAAAAGCCAAAATTTATGCTACTTAAGGAAAACCTTCACTAAGAAGACGATTTAGAGTGTTTTACCAGAAATTTT TGTCATCTTACTAAACAATAAGATCGGTGTGATACAAAACCTAATCTCATTAAAGTTTATGCTAAAATAAGCATAAATTTTACCCACTAAG CGTGACCAGATAAACATAACTCAGCACACCCAGACATATATATTGGTGGCTCAAAATCATAGAACTTACAGTGAAGACACAGAAAGCCG TAAGAAGAGGCAAGAGTATGAACCTTACCTCATCATTTCCATGAGGTGCTTCTGATCCCGGGGATATCACCACCTTTGTACAAAGAAA GCTGGGTCGAATTCGCCCTTGCATGGATGTTGGACAAATTTGGGGGTGCTTTCGCCCTCGTCCATCCCGGCCCTCACAAAGTTGCG CGAATCCCTGCCCTTATGATTTTCTTCGTAACAGGCTGAAGTATGCCCTTACAACACAGTGAAGTCACTAAAATTGTCATGCAAAAGTT GATCAAAAGTTGATGGTAAAGTGAGGACTGATCTAATACCTGCTGGTTTCATGGATGTCATTACTATTGAGAAGACTGGTGAATTTT CCGCTGATCTATGATGTTAAAGGAAGATTGCTGTGCACCGTATTACAGCTGAAGAGGGCAAAATACAAGTTGTGTAAGTAAGGAGAG TCCAAACTGGTCCCAAGGAATCCCAATTTTGGTAACACATGATGGCAGAACCAATTCGTTACCCTTGACCCCAACATCAAAAGTGAATGAC ACAAATTCAAATGGAAATTTGCTACATCTAAAATTTCTTGACTACATCAAAATTTGAATCT</p>
PC010	<p>SEQ ID NO: 509</p> <p>CTCTCAAGGATTTTGCAGATGTGCTCAGCCTATTACCGCCCCAACCGGTTGATTGGATTGATCAGCTTCGGAAAAAATGGTCAAGTC CACGAAGTGGTACCGAAGGCTGCAGCAAGTCGTACGTTCTGTGGAACGAAAGATCTCACCGCCCAAGCAAGTCCAGGAGATGTTG GGCATTGGAAAAAGGGTCACCAAAATCCCAATCCCAACACAGCCAGGGCAACCTGGCGGGCCAGGCAAGATCCCCAAGCTGCCCCGTACCA</p>

CCGGGAGCAGATTCTTGACGCCGTGTCAAAATGCGACATGAACCTTGACAGATCTGATCGGGGAGTTGCAGAAAGACCCCTTGCCCC
GTACATCAGGGCAAAAGACCTCTTAGATCCACAGGCGCAGCATTTGTCATCGCTGCGCCCTCTTAGAATGCACCTATCCGAATACGG
GTGCAGAAATCATGATATCTTAGGAGGACCATGCTCTCAGGTCGCCGAGGTGTTGAACGACGATTTGAAGCAGCCCATCAGGTC
CCATCATGACATACAAAGACAATGCCAAATGAAGAGGCTATCAAACTACGATCTGGAATGCGAGCTGCCAACACA
GCCATGTCATCGACATTTACTCTGCGCCCTGGATCAGACGGGATGATGAGATGAAGCAGTCTGCAATTCACCCGAGGGCAT
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CGTTCAACGCCACCTTGGAGGTGAAGTGTCCAGGGAGTTAAAGTCCAAAGGGGCGATCGGCTGCTGCGTGTCTTGAACGTTAAAG
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AGCGGCAAAAGGAGATCAGAGTGACCGCATTTGCTAGAAATTTGGCGGACGCTACTGCCAACATCCACCATATTAGCGCTGGCTTC
GACCAAGAAAGCGCGCGAGTTGTGATGGCCCGAATGGCCGTTACAAGCGGGAATCGGACGAGACTCCCGACGTCTCAGATGGGT
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CTGATCCGCACTTACATGACATTTGAGACGGTGCAGTTCTGCAGGTGTTCAATAATTCCTCTGATGAACGTCGTTTTATAGGCAC
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GTTGTTGGACACAGCTCTATTACGCGGATAGATCTGCTCATGGACACTTTCTCCAGATACCTATTTCCATGGAGAGACCATTTGC
CCAATGGCAAGGGCGAATTCGACCCAGCTTTCTTGTAAGAGTGGTATACACTAGTGGCGCCCTGCAGGTGCAGGTGCAGCATATGGTC
GACCTGCAGGGCGCCGACCTAGTGCTGTTATGTTGAGTCAAGCTGACCTGCAACACGTTAAATGCTAAGAAAGTTAGAATATAT
GAGACACGTTAACTGGTATATGAATAAGCTGTAATAACCGAGTATAAATCACTTAATAATATCACCCTAGAGTATAATAATCAAA
TCGACAAATTTGACTTTCAAGAGTAGGCTAATGTAATAATCTTATATTTCTACAATGTTCAAGAAACAGTTGCATCTAAACCCCTATGG
CCATCAAAATCAATGAACGCTAAGCTGATCCGCGAGATTTTCAGGAGCTAAGAGCTAAATGGAGAAATACTCACTGGATATACC
ACGTTGATATATCCCAATGGCATCGTAAGAACATTTTGAGGCAATTCAGTCAGTTGCTCAATGTACCTATAACCGACCTTCAGCTG
GATATTACGGCTTTTAAAGACCGTAAAGAAATAAGCACAAAGTTTATCCGGCTTTTATTCACATCTTCCCGCTGATGAATGCT
CATCCGGAATTCGATGCGAATGAAAGACGCTGAGTGGTGTGATGGATGTTTACCCCTTGTACACCGTTTTCATGAGCAAAAC
TGAACGTTTTTCATCGCTCGGAGTGAATACACGACGATTTCCGGCAGTTTCTACACATATATTCGCAAGATGTGGCGTTACGGTG
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AAATTTATGCTACTCTAAGGAAACCTTCACTAAAGAACGATTTAGAGTGTTTTACCAGAAATTTCTGTCTACTTAACAACTAAAG
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GCACACGAGAGCATATATTTGGTGCTCAATCATAGAACTTACAGTGAAGACACAGAAAGCCGTAAAGAGAGGCAAGAGATGAAA
CCTTACCTCATCATTTCCATGAGGTGCTTCTGATCCCGGGATATCACCATTTGTACAAGAAAGCTGGGTGAAATTCGCCCTTCGC
CATTGGCAATGGTCTCTCCATGGAATGAGTATCTGGAAGAAAGTGTCCATGAGCAGGATTTCTATCCGGCTGAATAGAGCTTGTGTC
CAACAACAGAGCTGGCGGCCGCTTGAAGCTGAACGTACAAAATCGGCTGGATCATGATCAAAAGACTGAGTCAATCTCAGCGC
ATCAGCATGTGCTTAAACGACGTTTTCATCAGGAGAAATTTGAACACCTGCAGAACTCGGACCGCTCTCAATGGTACATGAACCTG
CGGATACAGACTGAAGTTCTCCCGCAACCTGAACGAAATTCGGATCGTCTTATTGACTCTCCGAACCTTCTGGCACAGCTGATCAACA
TCCTGTCCACCCATCTGAGCACGTCGGGAGTCTGTCGAGTCCGCTTGTAAACCGGCAATTCGGGCCATCACAACCTGCCCGCTTC
TTGGTCGAAGCCAGCGCTAATGTGGTGGATGTTGGCAGTAGCTCCGCCCAATTTCTAGCAATCGTGTGCTACTCTGATCCTCTTGCC

	<p>CGCTCGGTGCTGATACTGGGTGATGAGCTGGATGCGAGCCCTGCCTCCCTGCTGGTATGGCGCCGAATGCTGTTAACCCACCTCGA AGAACGCGCCACAGTAGAGCTCGCGCCAACGTGCAAGTTTCCACGTGCACAGTATCCCCATGCCCTAGTCCGATCGGAAACCCAG AGGGCTTTTAACTCAAGTCAAGCACGACGACGCGCTCCCTCGGACTTTTAACTCCCTGGAAACAGTTCACCTCCAAGGTGGCGTTG AACCCCTTTTGAAGTTCGCTTCGGGTCTTTGAGAACACTCGCTGGAAGTTTGTGTAAGAGAGGAATGAAAGGAATCGCCCAT GACCATGTGCCCTCCGGTGAATTCAGCACTGCTTCATCTCCATCAGTCCCGTCTGATCCAGGCGGAGGAGTAATGTCGATGCAAA TGGCTGTGGTGGCAGCTCGCATTCGCAAGTATCGTAATGTTGATAGCCTTCTTCATGTACTTGGCATTGCTTTGTGTATGTCATGA TGGACCTGATGGCTGCTTCAATCGTCTTCAACACCTGGCGGGACCTGAGAGCATGGTCTCTCTAAAGAAATCATGATTCTGC CACCCGTAATCGGATAGTGCAATCTAAGAGCGCCAGACGATGGACAATGCTGCGCTGTGGATCTAAGAGGTCTTTTGGCCCTGATG TACGGGCCAAGGCTTTCTGCAACTCCCGATCAGATCTGTCAAGTTTCTGCAATTTTACACGGGCTGCAAGAACTGCTCCCCG GTGGTACAGGGGCGAGCTTGGGATTTCTGCCCTGGCCGCCAGGTGGCTGGCTGTTGTTGGGATTTGGTGACCCCTTTTCCAATGC CCAACATCTCCTGGACTTGTCTGGCGGTGAGATCTTCTGTTCCACAGAACACGTACGACTTGTCTGAGCCCTTCGGTACCCAGTTCTGTG GACTTGCACCAATTTTCCGAACGTGATCAATCCAATCAACGCGTTGGCGGTAATAGGCTGAGCGACATCTGCAAGAAATCCTTGAGAG</p>
<p>PC014</p>	<p>SEQ ID NO: 510</p> <p>CGCAGATCAACATATGATGGCTTTTCATTGAACAAGAAGCCCAATGAGAAAGCAGAAGAAATCGATGCCAAGCGAGAGGAGGAATTC AAC ATTGAAAGGCGGTTAGTCCAGCAACAGAGACTCAAGATCATGTGAGTACTACGAGAAAAAGGAGAAAGCAAGTCGAACTTCAAAGAA AATTCAGTCTCTAATATGTTGAATCAGGCTCGTTTGAAGGTGCTGAAAGTGAGAGAGGACCAATGTCTAGAGCAGTCTCGAGGATGCTC GTAAAGTCTTGGTGAAGTAACCAAGACCAAGAAATACTCCAAATTTTGGAGAGCCCTAATCTTACAGGACTGTTCCAGCTGTTT GAGAAGGAGGTGACGCTCCGCTGAGACCGCAAGATAGGACTTGGTAGTCCCTGCCCCAACCTGCTGCCAAATACAAGGAC GCCACGGCAAGACATCCTACTCAAGGTGGACGATGAGTCGACCTGTCTCAGGAGATACCGGAGCGCTGATCTGCTCGCTCAG AAGAACAGATCAAGATCAGCAACACGATGAGGCTAGTGGATCTGATCGCTCAGCAATTTGGTCCCCGAGATCCGAAGGCGCAAT CGACCCAGCTTCTGTACAAGTGGTGATACACTAGTGGCGCCGCTGCAGGTCGACCATATGGTCGACCTGCAGGCGGCCGCACT AGTGATGCTGTTATGTTCAAGTCAAGCTGACCTGCAACACGTTAAATGCTAAGAGTTAGAATATATGAGACACGTTAACTGGTATAT GAATAAGCTGTAAATAACCGAGTAACTTAATCAATATCACCTCTAGAGTATAATATAATCAAAATTCGACAAATTTGACTTCAAGAG TAGGCTAATGTAAATCTTTATATATTTCTACAATGTTCAAGAAACAGTTGCTATCAACCCCTATGGCCATCAAAATTCATGAACGCTA AGCTGATCCGGCGAGATTTTCAGGAGCTAAGGAAGCTAAATGGAGAAAAAATCACTGGATATACCACTTGATATATATCCCAATGGC ATCGTAAAGAACATTTTGAAGCATTTAGTCAGTTGCTCAATGTACCTATAACCAAGACCGTTTCAGCTGGATATACGGCTTTTAAAGA CCGTAAAGAAAAATAAGCACAGTTTATCCGGCTTTATTCACATTTTCCCGCTGATGAATGCTCATCCGGAATTCGGTATGGCAA TGAAGACGGTGAGCTGGTGATGGGATAGTGTTCACCTTTGTTACACCGTTTCCATGAGCAAACTGAAACGTTTTCATCGCTCTGG AGTGAATACCAAGCAATTTCCGGCAGTTTCTACACATATATTCGCAAGATGTGGCGTGTACGGTGAACCTGGCCCTATTTCCCTAAA GGGTTTATTGAGAAATATGTTTTCTGCTCAGCCAAATCCCTGGTGAGTTTACCAGTTTTCAGTTTAAACGTGGCCAAATATGGACAATTC TTCGCCCCCGTTTTCACCATGGGCAATATTATACGCAAGGCGACAAAGTGTGATGCCGCTGGCGATTTCAGGTTTCATCATGCCGCTC GTGATGGCTTCCATGCGGAGAAATGCTTAATGAATTAACAACAGTACTGCGATGAGTGGCGGGCGGCTAAACCGGTGATCAGC TTAATGACTCTCAATAAGCTCTACCAACAGTGCACCTTATCAACCTCAAGAAAAAGCCAAAAATTTATGCTACTCTAAGGAA AACTTCACTAAAGAGCAGTTTAGAGTGTATTTTACCAAGAAATTTCTGCTCATCTTACTAAACAACTAAAGATCGGTGATACAAACCTAA TCTCATTAAGTTTATGCTAAAATAAGCATATTTTACCCCAATTAAGCGTGACCCAGATAAACATAACTCAGCACCCAGGACATATATTTG GTGGCTCAAAATCATAGAAACTTACAGTGAAGACACAGAAAGCGTAAAGAGAGGCAAGAGTATGAACCTTACCTCATCATTTCCATGA GGTTGCTTCTGATCCCGGGGATATCACCACTTTGTACAAGAAAGCTGGGTGCAATTCGCCCTTCGGATCTCGGGCACCAATTTGCTGA</p>

[illegible]

PC027	<p>GTGTGAGTTCACTGGAGATATTCTAAGAACTCCAGTATCAGAAAGATATGCTGGACGTGTCTTCAATGGATCAGGAAACCCATTGATA AAGTCCCCCGATCCTGGCTGAGGACTACCTCGACATCCAAGACAGCCGATCAACCCGTGGTCGGTATTTATCCCGAGGAAATGAT CCAGACTGGGATCAGGCCATCGACGTGATGAACCTCTATCGCCAGAGGCGAGAAGATCCGATCTTCCGCCGCTGGGCTGCCCCA CAATGAGATTGAGCCAGATTGTAGGCAGGCTGGCTTGGTCAAAAGTACCTGGCAAGTCTGTCTGGATGACCATGAAGACAACATTT GCTATTGTGTTGCTGCTATGGGTGTAACATGGAACCTGCCAGGTTCTCAAGCAGGACTTCGAAGAGAACGGCTCGATGGAGAACG TGCTGTGTTCTTGAACCTTGGCCAAACGATCCGACCATCGAACCCGCTTGGCTCTGACGGCCGCCGCAATCTCTGGC CTACCAGTCGGAAGACACGTGCTGGTCATCTTGACCCGACATGCTGTCGACGGGAGGCGTTGCGTGAGGTGCTGCCCCGCTCGAGA AGAACTGCCCGCGGTAGGGGTTTCCCGGTTACATGTACACCGATCTGGCCACCATTTACGAGCGCGCGGTCGTGTGGAGGGCGG CAACGGCTCCATCAGCGAGATCCCCATCTTGACTATGCCAA</p>
SEQ ID NO: 512	<p>GGGCCAAGCACAGCGAAATGCAGCAAGCTAACITGAAAGCACTACCAGAAGGAGCTGAAATCAGAGATGGAGAACGTTTGCCAGTCAC AGTAAAGGACATGGGAGCATGCGAGATTTACCCACAACAACTCAACACACACCCCAATGGCGGTTGTAGTGTTGTGGTGATGGA GAATACATAATATACACGGCTATGGCCCTTCGTAAACAAGCATTTGGTAGCGCTCAAGAATTTGTATGGCACAGGACTCCAGTGAATA TGCCATCCGCGAATCCGATCCACCATTCGAATCTTCAAGAATTTCAAAGAAAAGAAATTTCAAGTCCGACTTTGGTGCCGAAGGAAT CTATGGTGGTTTCTCTTGGGTGTGAATCAGTGTCTGGCTAGCTTTCTATGACTGGGAACGCTTGAGTTAGTAAGGCGCATTTGAAAT ACAGCCTAGAGCTATCTACTGTCAGATAGTGGCAAGTTGGTATGCCCTGCTACCGAAGATAGCTATTTTCATATTGTCTCTGACTCTGA CCAAGTCCAGAAAGCTAGAGATAACAACCAAGTTGCCAAGATGGAGTGGAGGCTGCCCTTGATGCTCTAGGTGAAATAAATGAATCC GTAAAGAACAGTCTTTGGGTAGGAGACTGCTTCATTTACACAACCGAGTCAACCGTATCAACTCTTGTGGTGGTGAATTTGGTAAC TATTGCACATCTGGACCGTCTCTATATGCTCGGCTATGTAACCTAGAGATGACAGGTTATCTTGTGTATAAGAGTTAGGAGTAGT CAGCTATCAATTTGCTATTATCTACTCGAATATCAGACTGCAGTATCGGACGAGACTTCCCAACGGCTGATCGAGTATGCTTCAAT TCCAAAAGAACACCGCACTAGGTGGCACAAAGGGCGAATTCGACCCAGCTTTCTGTACAAAGTGGTGATACACTAGTGCAGGCGCG CTGCAGTCCGACCATATGGTCGACCTGCAGCGCGCCGCACTAGTGTATGTTCAAGTGTCAAGCTGACCTGCAACACGTTAA ATGCTAAGAAAGTTAGAATATATGAGACACGTTAACTGGTATATGAATAAGCTGTAAATAACCGAGTAAACTCATTAACTAATATCACCT CTAGAGTATAATAATCAAAATTCGACAAATTTGACTTTCAAGAGTAGGCTAATGTAAATCTTTATATATTTCTACAATGTTCAAGAAACA GTTGCATCTAAACCCCTATGGCCATCAAAATTCGAATGACGCTAAGCTGATCCGGCGAGATTTTCAGGAGCTAAGGAAGCTAAAAATGGAG AAAAAATCACTGGATATACCCGTTGATATATCCCAATGGCATCGTAAAGAACATTTTGAGGCAATTTTCAGTCAGTTGCTCAATGTACC TATAACCAAGCGTTCAGCTGGATATTACGGCCCTTTTAAAGACCGTAAAGAAAATAAGCAAGTTTTATCCGGCTTTTATTCACATTCT TTGCCCGCCTGATGAATGCTATCCGGAATTCGATGGCAATGAAGACGGTGAGCTGGTGATGGGATAGTTTACCCCTTGTAC ACCGTTTTCCATGAGCAAACTGAAACGTTTTTCATCGCTCTGGAGTGAATACCCAGCAGATTTCCGGCAGTTTCTACACATATATTCGCA GATGTGGCGTGTACGGTGAAACCTGGCCATTTCCTAAAGGTTTATTGAGAAATATGTTTTCGTCTCAGCCCAATCCCTGGGTGAG TTTACCCAGTTTGTATTTAAACGTGGCCAAATATGGACAACCTTCTCGCCCCCGTTTTTACCCTATGGGCAATAATATACGCAAGGCGACAA GGTGTGATGCCGCTGGCGATTCAAGTTTCATCATGCCGCTGTGATGGCTTCCATGTGCGGCAAGTCTTAAATGAATACACAGTACT GCGATGAGTGGCAGGGGGCGTAAACCGGTGATCAGCTTAAATGACTCTCAATAAGTCTCATACCAACGAAGTCCACCTTATT CAACCATCAAGAAAAAGCCAAATTTATGCTACTTAAGGAAACCTTCACTAAAGAACGAGTATTAGAGTGTTTTACCAGAAATTTCTGT CATCTTACTAAACAACATAAGATCGGTGTGATACAAAACCTAATCTCAATAAGTTTATGCTAAATGAAGCAATAATTTACCCACATAAGCG TGACCAGATAAACATAACTCAGCACACCGAGAGCATATATTTGGTGGCTCAATCATAGAACTTACAGTGAAGACACAGAAAGCCGTAA GAAGAGGCAAGAGTATGAACCTTACCCTCATCATTTCCATGAGGTTGCTTCTGATCCCGGGGATATCACCACTTTGTACAAGAAAGCT</p>

	<p>ACCTTATTCAACCATCAAGAAAAAGCCAAAAATTTATGCTACTCTAAGGAAAACTTCACTAAAGAAGACGATTTAGAGTGTTTTACCAA GAATTTCTGTCACTTACTAAACAACATAAGATCGGTGTGATACAAAACCTAATCTCATTAAGTTTATGCTAAAAAAGCATAATTTTAC CCACTAAGCGTGACCAGATAAACATAACTCAGCACACAGAGCATATATTGGTGGCTCAATCATAGAACTTACAGTGAAGACAC AGAAAGCGTAAGAAGAGGCAAGAGATGAACCTTACCTCATATTCATGAGTTGCTTCGATCCCGGAGATATCACCATTT GTACAGAAAGCTGGTGGAAATTCGCCCTTCAATACCAACACGCCCTAAATTCGGAACCTCCAGTTATCATGCACAACTTTCCAGTTTC AAAACGGATATGATCCAAAATTTAGATGATGCAATATCGTATCTAATAGTGTCAATTAACCTTGATAGGGTCAGGGTAGCGAATAG TACGGCCATCATGAGTAGTTAAAAATGGCACACCTTTGGTCCAGTTGTACCCCTTTACCTTTACACAACCTTGATTTTGTCTTTCA GGAGTAATCTGTGGATGGTGAACGACCTTTCACATCATAGATCAATCTAAAGTGCTCACTGGTCTTTTGATAGATATAACATCCAT AAAACGGCTGGATAATTAGGGTCGGTACGGACTTTGCCATCAACCTTGATTAATCTTTGCATGACAATCTTTGGTACCTCGGCACCA GTAAGTGCATACCTCAACGATTACGCAAGAAGATCAATAACGGTAGTGAAATTCACGAAGTTTGTGTGACCCGGTGTGACCGTGA GCGAAGACACCCCCCGATTGTCCAACATCCATGCTTTGGTGCGTTTAAAC</p>
MP002	<p>SEQ ID NO: 1067</p> <p>GCTGATTTAAGTGCACTGCTGCAGTTTTTCATGGTAGTCAATACTGCTGTATTTGTGTGGCACCTTCTAATGCTCCCGCTGTGTTC AATAGTTAACATGGTACCATCAATTTGGGCTAATTTGTTGCTACCGTTTCTTACGCTTCAATGCTTGAATGCAGCTCGTTTATTAGT TGTACCAATTTTTTGGCTATCGCTACTTCTGTTCAATTTTTTTTTCTAAAAATCTGTTTCTTTATCAGCATCTCTTCCAGTGGATCGAA GCTTTGTATCGCATCTTCGGTTGATGGTCCCTCTCTCTCTTTTCCACCAAGGGCGAAATTCGACCAGCTTCTTGTACAAAAGTG GTGATATCACTAGTGCGCCCGCTGCAGGTGCAGCTATGTCGACCTGCAGCGGCCCGCAC TAGTGATGCTGTATGTTCAGTGT CAAGCTGACCTGCAAAACAGTTAAATGCTAAGAGTTAGAAATATAGACACAGTTAACTGGTATAGTAAGCTGTAATAACCGAG TATAAACTCATTAACTAATACCTCTAGAGTATAATAATAATCAAAATTCGACAATTTGACTTTCAAGAGTAGGCTAATGTAAATCTTTA TATATTCTACAATGTTCAAGAAACAGTTGCACTTAAACCCCTATGGCCATCAAAATCAATGAACGCTAAGCTGATCCGGCGAGATTT TCAGGAGCTAAGGAAGCTAAATGGAGAAAAAATCACTGGATATACCACCGTTGATATATCCCAATGGCATCGTAAAGAACAATTTTG AGGCAATTCAGTCAGTTGCTCAATGTACCTATACCAGACCGTTCACTGGATATTACGGCTTTTAAAGACCGTAAAGAATAAAG CACAAGTTTTATCCGGCTTTATTCACATTTCTTCCCGCTGATGAATGCTCATCCGGAATTCGATGCAATGCAATGAAGACGGTGAGC TGGTGATATGGGATAGTGTACCCCTTGTACACCGTTTTCATGAGCAAACTGAAACGTTTTTCATCGCTCTGGAGTGAATACCAAGA CGATTTCCGGCAGTTTCTACACATATATTCGAAGATGTGGCGTTTACGGTGAACCTTGCCCTATTTCCCTAAAGGTTTTATTGAG AATATGTTTTTCTGCTCAGCCAAATCCCCTGGGTGAGTTTCAACGATTTTGAATTAACGTGGCCCAATATGACAACTTCTTCGCCCGCT TTTCAACCATGGGCAATATTATACGCAAGGCGACAAGGTGCTGATGCCGCTGGCGATTCAAGTTCACTATCGCGTCTGTGATGGCTT CCATGTCGGCAGAAATGCTTAATGAATTAACACAGTACTGCGATGAGTGGCAGGGGGGCGTAAACGCGTGGATCAGCTTAAATGA CTCTCAATAAAGTCTCATACCAACAAGTGCCACCTTATTCAACCATCAAGAAAAAGCCAAAAATTTATGCTACTCTAAGGAAAACTTCA CTAAGAAGACGATTTAGAGTGTTTTACCAAGAAATTTCTGTCATCTTACTAAACAACATAAGATCGGTGTGATACAAAACCTAATCTCAT TAAAGTTTATGCTAAATAAGCATAAATTTACCCACTAAGCGTGACAGATAAACATAACTCAGCACACAGCATATATTTGGTGG CTCAAATCATAGAACTTACAGTGAAGACACAGAAAGCCGTAAGAAGAGGCAAGAGTATGAACCTTACCTCATCTTCCATCTTCCATGAGGT TGCTTCTGATCCCGGGATATCACCACTTTGTACAAGAAAGCTGGGTGAAATTCGCCCTTGGTGGCAAAAGGAAAGAGAGGGGACC ATCAACGGAAGATGCGATACAAAAGCTTCGATCCACTGAAGAGATCTGTGATAAAGAAACAGAAATTTTGAAGAAAAAATTTGAACAAG AAGTAGCGGATAGCCAAAAAATTTGTTACAACTAAATAACGAGCTGCAATGCAAGCATTAAGCGTTAAGAAACGGTACGAACAACAATT AGCCCAAAATTGATGTACCATGTTAACTATTGAACAACACAGCGGGAGGCAATTAGAAGGTGCCAACACAAATACAGCAGTATTGACTACC ATGAAAACTGCAGCAGATGCACTTAAATCAGC</p>

TTTTAAGACCGTAAAGAAAAAATAGCACAAAGTTTTATCCGGCCCTTTATTACACATTTCTGCCCCCTGATGAATGCTCATCCGGAATTC
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CATCGCTCTGGAGTGAATACCACGACGATTTCCGGCAGTTTTCTACACATATATTCGCAAGATGTGGCGTGTACGGTGAAAAACCTGG
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GCACACCAGAGCATATATATTGGTGGCTCAAATCATAGAACTTACAGTGAAGACACAGAAAGCCGTAAAGAGAGGCAAGAGTATGA
AACCTTACCTCATCTTCCATGAGGTGCTTCTGATCCCGCGGATATCACCCACTTTGTACAAGAAAGCTGGTCCGAATTCGCCCTT
GCTCGTTTGTTCATCCAGAACCTCCCATCGTGTAACTGGCTCAGAAAGATGGTACCGTCAAGAAATTTGGCATTTCTGGTACTTATCGAT
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GAAATTCACAAGCTAACCTTAAAGCGATGCTTCAAGCAGAAGGAGCCGAAATCAAGATGGTGAACGTTTACCAATACAAGTTAAAG
ACATGGGTAGCTGTGAAATTTATCCACAGTCAATATCTCATAATCCGAATGGTAGATTTTGTAGTAGTATGTTGGTATGGAGAGTATATT
ATATATACATCAATGGCTTTGCGTAAATAAAGCAATTTGGCTCCGCTCAGGAATTTGTATGGTCTTCTGATTTCTGAGTATGCCATTAGAGA
AAATCTTCTACAATCAAAGTTTTTAAAAATTTTAAAGAAAAAAGTCTTTTAAACCAGAAGGTGGAGCAGATGGTATTTTTTGG

Tables 10-NL (a)

RNAi	Mean % survival (days post start)									Survival analysis ¹
	0	1	2	3	4	5	6	7	8	
gfp	100	98	90	82	68	60	44	32	20	-
diet only	100	98	96	86	74	68	58	54	38	-
NL002	100	98	90	76	68	34	6	0	0	+
NL003	100	98	74	48	36	22	12	2	0	+
NL005	100	100	74	56	40	20	16	6	4	+
NL010	100	96	74	56	48	30	18	12	8	+

¹ = Data were analysed using Kaplan-Meier survival curve analysis

	Chi squared	P value	Sig. Dif. ²
diet versus:			
NL002	29.06	<0.0001	Yes
NL003	39.59	<0.0001	Yes
NL005	29.55	<0.0001	Yes
NL010	21.04	<0.0001	Yes
gfp dsRNA versus:			
NL002	15.09	0.0001	Yes
NL003	22.87	<0.0001	Yes
NL005	15.12	<0.0001	Yes
NL010	8.838	0.0029	Yes
diet versus GFP dsRNA	4.030	0.0447 (~0.05)	No

² alpha < 0.05

Tables 10-NL (b)

RNAi	Mean % survival (days post start)									Survival analysis ¹
	0	1	2	3	4	5	6	7	8	
gfp	100	96	84	82	76	70	54	50	44	-
diet only	100	96	88	82	76	70	54	50	44	-
NL009	100	94	75	63	42	30	24	22	14	+
NL016	100	94	84	78	54	44	36	18	14	+

¹ = Data were analysed using Kaplan-Meier survival curve analysis

	Chi squared	P value	Sig. Dif. ²
diet versus:			
NL009	11.98	0.0005	Yes
NL016	8.98	0.0027	Yes
gfp dsRNA versus:			
NL009	13.69	0.0002	Yes
NL016	11.37	0.0007	Yes
diet versus GFP dsRNA	0.03317	0.8555	No

² alpha < 0.05

Tables 10-NL (c)

RNAi	Mean % survival (days post start)									Survival analysis ¹
	0	1	2	3	4	5	6	7	8	
gfp	100	92	84	78	72	62	58	56	48	-
diet only	100	84	72	68	64	58	52	42	42	-
NL014	100	86	68	60	46	32	24	18	14	+
NL018	100	82	70	54	40	30	18	14	12	+

¹ = Data were analysed using Kaplan-Meier survival curve analysis

	Chi squared	P value	Sig. Dif. ²
diet versus:			
NL014	8.088	0.0045	Yes
NL018	10.47	0.0012	Yes
gfp dsRNA versus:			
NL014	14.55	0.0001	Yes
NL018	17.64	<0.0001	Yes
diet versus GFP dsRNA	0.6548	0.4184	No

² alpha < 0.05

Tables 10-NL (d)

RNAi	Mean % survival (days post start)										Survival analysis ¹
	0	1	2	3	4	5	6	7	8	9	
gfp	100	96	84	84	72	68	68	66	66	62	-
diet only	100	96	86	82	74	72	70	70	66	58	-
NL013	100	94	82	68	50	40	30	28	20	20	+
NL015	100	100	72	30	18	12	8	6	6	6	+
NL021	100	100	84	58	50	44	40	34	34	22	+

¹ = Data were analysed using Kaplan-Meier survival curve analysis

	Chi squared	P value	Sig. Dif. ²
diet versus:			
NL013	15.73	<0.0001	Yes
NL015	39.44	<0.0001	Yes
NL021	12.75	0.0004	Yes
GFP dsRNA versus:			
NL013	16.42	<0.0001	Yes
NL015	39.15	<0.0001	Yes
NL021	14.1	0.0002	Yes
diet versus GFP dsRNA	0.1031	0.7481	No

² alpha < 0.05

Table 11-NL

NL002 RNAi	Mean % survival (days post start)								Survival analysis ¹
	0	1	2	3	4	5	6	7	
diet only	100	100	96	90	86	78	78	78	-
1 µg/µl	100	84	80	44	26	8	6	6	+
0.2 µg/µl	100	84	60	12	8	4	2	2	+
0.08 µg/µl	100	84	62	18	14	6	6	6	+
0.04 µg/µl	100	84	48	24	22	22	22	22	+

¹ = Data were analysed using Kaplan-Meier survival curve analysis

	Chi squared	P value	Sig. Dif. ²
diet versus:			
NL002 1 µg/µl	57.53	<0.0001	Yes
NL002 0.2 µg/µl	74.54	<0.0001	Yes
NL002 0.08 µg/µl	64	<0.0001	Yes
NL002 0.04 µg/µl	39.49	<0.0001	Yes

² alpha < 0.05

Claims

1. An isolated nucleotide sequence comprising a nucleic acid sequence selected from the group comprising:

(i) sequences represented by any of SEQ ID NOs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 49 to 158, 159, 160-163, 168, 173, 178, 183, 188, 193, 198, 203, 208, 215, 220, 225, 230, 240 to 247, 249, 251, 253, 255, 257, 259, 275 to 472, 473, 478, 483, 488, 493, 498, 503, 508 to 513, 515, 517, 519, 521, 533 to 575, 576, 581, 586, 591, 596, 601, 603, 605, 607, 609, 621 to 767, 768, 773, 778, 783, 788, 793, 795, 797, 799, 801, 813 to 862, 863, 868, 873, 878, 883, 888, 890, 892, 894, 896, 908 to 1040, 1041, 1046, 1051, 1056, 1061, 1066 to 1071, 1073, 1075, 1077, 1079, 1081, 1083, 1085, 1087, 1089, 1091, 1093, 1095, 1097, 1099, 1101, 1103, 1105, 1107, 1109, 1111, 1113, 1161 to 1571, 1572, 1577, 1582, 1587, 1592, 1597, 1602, 1607, 1612, 1617, 1622, 1627, 1632, 1637, 1642, 1647, 1652, 1657, 1662, 1667, 1672, 1677, 1682, 1684, 1686, 1688, 1690, 1692, 1694, 1696, 1698, 1700, 1702, 1704, 1730 to 2039, 2040, 2045, 2050, 2055, 2060, 2065, 2070, 2075, 2080, 2085, 2090, 2095, 2100, 2102, 2104, 2106, 2108, 2120 to 2338, 2339, 2344, 2349, 2354, 2359, 2364, 2366, 2368, 2370, 2372, 2384 to 2460, 2461, 2466, 2471, 2476, 2481 or 2486, or the complement thereof,

(ii) sequences which are at least 70 %, preferably at least 75%, 80%, 85%, 90%, more preferably at least 95%, 96%, 97%, 98% or 99% identical to a sequence represented by any of SEQ ID NOs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 49 to 158, 159, 160-163, 168, 173, 178, 183, 188, 193, 198, 203, 208, 215, 220, 225, 230, 240 to 247, 249, 251, 253, 255, 257, 259, 275 to 472, 473, 478, 483, 488, 493, 498, 503, 508 to 513, 515, 517, 519, 521, 533 to 575, 576, 581, 586, 591, 596, 601, 603, 605, 607, 609, 621 to 767, 768, 773, 778, 783, 788, 793, 795, 797, 799, 801, 813 to 862, 863, 868, 873, 878, 883, 888, 890, 892, 894, 896, 908 to 1040, 1041, 1046, 1051, 1056, 1061, 1066 to 1071, 1073, 1075, 1077, 1079, 1081, 1083, 1085, 1087, 1089, 1091, 1093, 1095, 1097, 1099, 1101, 1103, 1105, 1107, 1109, 1111, 1113, 1161 to 1571, 1572, 1577, 1582, 1587, 1592, 1597, 1602, 1607, 1612, 1617, 1622, 1627, 1632, 1637, 1642, 1647, 1652, 1657, 1662, 1667, 1672, 1677, 1682, 1684, 1686, 1688, 1690, 1692, 1694, 1696, 1698, 1700, 1702, 1704, 1730 to 2039, 2040, 2045, 2050, 2055, 2060, 2065, 2070, 2075, 2080, 2085, 2090, 2095, 2100, 2102, 2104, 2106, 2108, 2120 to 2338, 2339, 2344, 2349, 2354, 2359, 2364, 2366, 2368, 2370, 2372, 2384 to 2460, 2461, 2466, 2471, 2476, 2481 or 2486, or the complement thereof, and

(iii) sequences comprising at least 17 contiguous nucleotides of any of the sequences represented by SEQ ID NOs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 49 to 158, 159, 160-163, 168, 173, 178, 183, 188, 193, 198, 203, 208, 215, 220, 225, 230, 240 to 247, 249, 251, 253, 255, 257, 259, 275 to 472, 473, 478, 483, 488, 493, 498, 503, 508 to 513, 515, 517, 519, 521, 533 to 575, 576, 581, 586, 591, 596, 601, 603, 605, 607, 609, 621 to 767, 768, 773, 778, 783, 788, 793, 795, 797, 799, 801, 813 to 862, 863, 868, 873, 878, 883, 888, 890, 892, 894, 896, 908 to 1040, 1041, 1046, 1051, 1056, 1061, 1066 to 1071, 1073, 1075, 1077, 1079, 1081, 1083, 1085, 1087, 1089, 1091, 1093, 1095, 1097, 1099, 1101, 1103, 1105, 1107, 1109, 1111, 1113, 1161 to 1571, 1572, 1577, 1582, 1587, 1592, 1597, 1602, 1607, 1612, 1617, 1622, 1627, 1632, 1637, 1642, 1647,

- 1652, 1657, 1662, 1667, 1672, 1677, 1682, 1684, 1686, 1688, 1690, 1692, 1694, 1696, 1698, 1700, 1702, 1704, 1730 to 2039, 2040, 2045, 2050, 2055, 2060, 2065, 2070, 2075, 2080, 2085, 2090, 2095, 2100, 2102, 2104, 2106, 2108, 2120 to 2338, 2339, 2344, 2349, 2354, 2359, 2364, 2366, 2368, 2370, 2372, 2384 to 2460, 2461, 2466, 2471, 2476, 2481 or 2486, or the complement thereof,
- 5 or wherein said nucleic acid sequence is an orthologue of a gene comprising at least 17 contiguous nucleotides of any of SEQ ID NOs 49 to 158, 275 to 472, 533 to 575, 621 to 767, 813 to 862, 908 to 1040, 1161 to 1571, 1730 to 2039, 2120 to 2338, 2384 to 2460, or a complement thereof.
- 10 2. A double stranded ribonucleotide sequence produced from the expression of a polynucleotide sequence of claims 1, wherein ingestion of said ribonucleotide sequence by a plant insect pest inhibits the growth of said insect pest.
3. The ribonucleotide sequence of claim 2, wherein ingestion of said sequence inhibits expression of a nucleotide sequence substantially complementary to said sequence.
- 15 4. A cell transformed with a polynucleotide comprising a nucleic acid sequence as defined in claim 1, optionally operably linked to a regulatory sequence.
5. The cell of claim 4, wherein said cell is a plant cell.
6. A plant transformed with a polynucleotide having a nucleic acid sequence as defined in claim 1, said nucleic acid sequence optionally operably linked to a regulatory sequence.
- 20 7. The plant of claim 6, wherein said sequence inhibits a pest biological activity.
8. The plant of claim 6, wherein said sequence inhibits expression of a target sequence.
9. The plant of claim 8 wherein said target sequence is an insect, nematode or fungal sequence.
10. The plant of any of claims 6 to 9, wherein said plant is cytoplasmic male sterile.
- 25 11. The plant of any of claims 6 to 10, wherein said plant further comprises or expresses a pesticidal agent selected from the group consisting of a patatin, a *Bacillus thuringiensis* insecticidal protein, a *Xenorhabdus* insecticidal protein, a *Photorhabdus* insecticidal protein, a *Bacillus laterosporous* insecticidal protein, and a *Bacillus sphearicus* insecticidal protein.
12. The plant of claim 11 wherein said *Bacillus thuringiensis* insecticidal protein is selected from the group consisting of a Cry1, a Cry3, a TIC851, a CryET170, a Cry22, a binary insecticidal protein CryET33 and CryET34, a binary insecticidal protein CryET80 and CryET76, a binary insecticidal protein TIC100 and TIC101, and a binary insecticidal protein PS149B1.
- 30 13. The plant of any of claims 6 to 12, wherein said plant is chosen from the group comprising alfalfa, apple, apricot, artichoke, asparagus, avocado, banana, barley, beans, beet, blackberry, blueberry, broccoli, brussel sprouts, cabbage, canola, carrot, cassava, cauliflower, a cereal, celery,
- 35

cherry, citrus, clemantine, coffee, corn, cotton, cucumber, eggplant, endive, eucalyptus, figes, grape, grapefruit, groundnuts, ground cherry, kiwifruit, lettuce, leek, lemon, lime, pine, maize, mango, melon, millet, mushroom, nut aot, okra, onion, orange, an ornamental plant or flower or tree, papaya,, parsley, pea, peach, peanut, peat, pepper, persimmon, pineapple, plantain, plum, pomegranate, potato, pumpkin, radicchio, radish, rapeseed, raspberry, rice, rye, sorghum, soy, soybean, spinach, strawberry, sugarbeet, sugarcane, sunflower, sweet potato, tangerine, tea, tobacco, tomato, a vine, waatermelon, wheat, yams and zucchini.

14. The plant of any of claims 6 to 13, wherein said plant is resistant against infestation by an insect chosen from the group comprising *Leptinotarsa* spp. (e.g. *L. decemlineata* (Colorado potato beetle), *L. juncta* (false potato beetle), or *L. texana* (Texan false potato beetle)); *Lema* spp. (e.g. *L. trilineata* (three-lined potato beetle)); *Epitrix* spp. (e.g. *E. cucumeris* (potato flea beetle), *E. hirtipennis* (flea beetle), or *E. tuberis* (tuber flea beetle)); *Epicauta* spp. (e.g. *E. vittata* (striped blister beetle)); *Epilachna* spp. (e.g. *E. varivertis* (mexican bean beetle)); *Phaedon* spp. (e.g. *P. cochleariae* (mustard leaf beetle)); *Nilaparvata* spp. (e.g. *N. lugens* (brown planthopper)); *Laodelphax* spp. (e.g. *L. striatellus* (small brown planthopper)); *Nephotettix* spp. (e.g. *N. virescens* or *N. cincticeps* (green leafhopper), or *N. nigropictus* (rice leafhopper)); *Sogatella* spp. (e.g. *S. furcifera* (white-backed planthopper)); *Acheta* spp. (e.g. *A. domesticus* (house cricket)); *Blissus* spp. (e.g. *B. leucopterus leucopterus* (chinch bug)); *Scotinophora* spp. (e.g. *S. vermidulate* (rice blackbug)); *Acrosternum* spp. (e.g. *A. hilare* (green stink bug)); *Parnara* spp. (e.g. *P. guttata* (rice skipper)); *Chilo* spp. (e.g. *C. suppressalis* (rice striped stem borer), *C. auricilius* (gold-fringed stem borer), or *C. polychrysus* (dark-headed stem borer)); *Chilothea* spp. (e.g. *C. polychrysa* (rice stalk borer)); *Sesamia* spp. (e.g. *S. inferens* (pink rice borer)); *Tryporyza* spp. (e.g. *T. innotata* (white rice borer), or *T. incertulas* (yellow rice borer)); *Cnaphalocrocis* spp. (e.g. *C. medinalis* (rice leafroller)); *Agromyza* spp. (e.g. *A. oryzae* (leafminer), or *A. parvicornis* (corn blot leafminer)); *Diatraea* spp. (e.g. *D. saccharalis* (sugarcane borer), or *D. grandiosella* (southwestern corn borer)); *Narnaga* spp. (e.g. *N. aenescens* (green rice caterpillar)); *Xanthodes* spp. (e.g. *X. transversa* (green caterpillar)); *Spodoptera* spp. (e.g. *S. frugiperda* (fall armyworm), *S. exigua* (beet armyworm), *S. littoralis* (climbing cutworm), or *S. praefica* (western yellowstriped armyworm)); *Mythimna* spp. (e.g. *Mythimna (Pseudaletia) seperata* (armyworm)); *Helicoverpa* spp. (e.g. *H. zea* (corn earworm)); *Colaspis* spp. (e.g. *C. brunnea* (grape colaspis)); *Lissorhoptrus* spp. (e.g. *L. oryzophilus* (rice water weevil)); *Echinocnemus* spp. (e.g. *E. squamos* (rice plant weevil)); *Diplotispa* spp. (e.g. *D. armigera* (rice hispa)); *Oulema* spp. (e.g. *O. oryzae* (leaf beetle)); *Sitophilus* spp. (e.g. *S. oryzae* (rice weevil)); *Pachydiplosis* spp. (e.g. *P. oryzae* (rice gall midge)); *Hydrellia* spp. (e.g. *H. griseola* (small rice leafminer), or *H. sasakii* (rice stem maggot)); *Chlorops* spp. (e.g. *C. oryzae* (stem maggot)); *Diabrotica* spp. (e.g. *D. virgifera virgifera* (western corn rootworm), *D. barberi* (northern corn rootworm), *D. undecimpunctata howardi* (southern corn rootworm), *D. virgifera zea* (Mexican corn rootworm); *D. balteata* (banded cucumber beetle)); *Ostrinia* spp. (e.g. *O. nubilalis* (European corn borer)); *Agrotis* spp. (e.g. *A. ipsilon* (black cutworm)); *Elasmopalpus* spp. (e.g. *E. lignosellus* (lesser cornstalk borer)); *Melanotus* spp. (wireworms); *Cyclocephala* spp.

- (e.g. *C. borealis* (northern masked chafer), or *C. immaculata* (southern masked chafer)); *Popillia* spp. (e.g. *P. japonica* (Japanese beetle)); *Chaetocnema* spp. (e.g. *C. pulicaria* (corn flea beetle)); *Sphenophorus* spp. (e.g. *S. maidis* (maize billbug)); *Rhopalosiphum* spp. (e.g. *R. maidis* (corn leaf aphid)); *Anuraphis* spp. (e.g. *A. maidiradicis* (corn root aphid)); *Melanoplus* spp. (e.g. *M. femurrubrum* (redlegged grasshopper) *M. differentialis* (differential grasshopper) or *M. sanguinipes* (migratory grasshopper)); *Hylemya* spp. (e.g. *H. platura* (seedcorn maggot)); *Anaphothrips* spp. (e.g. *A. obscurus* (grass thrips)); *Solenopsis* spp. (e.g. *S. milesta* (thief ant)); or spp. (e.g. *T. urticae* (twospotted spider mite), *T. cinnabarinus* (carmine spider mite); *Helicoverpa* spp. (e.g. *H. zea* (cotton bollworm), or *H. armigera* (American bollworm)); *Pectinophora* spp. (e.g. *P. gossypiella* (pink bollworm)); *Earias* spp. (e.g. *E. vittella* (spotted bollworm)); *Heliothis* spp. (e.g. *H. virescens* (tobacco budworm)); *Anthonomus* spp. (e.g. *A. grandis* (boll weevil)); *Pseudatomoscelis* spp. (e.g. *P. seriatus* (cotton fleahopper)); *Trialeurodes* spp. (e.g. *T. abutiloneus* (banded-winged whitefly) *T. vaporariorum* (greenhouse whitefly)); *Bemisia* spp. (e.g. *B. argentifolii* (silverleaf whitefly)); *Aphis* spp. (e.g. *A. gossypii* (cotton aphid)); *Lygus* spp. (e.g. *L. lineolaris* (tarnished plant bug) or *L. hesperus* (western tarnished plant bug)); *Euschistus* spp. (e.g. *E. conspersus* (conspere stink bug)); *Chlorochroa* spp. (e.g. *C. sayi* (Say stinkbug)); *Nezara* spp. (e.g. *N. viridula* (southern green stinkbug)); *Thrips* spp. (e.g. *T. tabaci* (onion thrips)); *Frankliniella* spp. (e.g. *F. fusca* (tobacco thrips), or *F. occidentalis* (western flower thrips)); *Empoasca* spp. (e.g. *E. fabae* (potato leafhopper)); *Myzus* spp. (e.g. *M. persicae* (green peach aphid)); *Paratrioza* spp. (e.g. *P. cockerelli* (psyllid)); *Conoderus* spp. (e.g. *C. falli* (southern potato wireworm), or *C. vespertinus* (tobacco wireworm)); *Phthorimaea* spp. (e.g. *P. operculella* (potato tuberworm)); *Macrosiphum* spp. (e.g. *M. euphorbiae* (potato aphid)); *Thyanta* spp. (e.g. *T. pallidovirens* (redshouldered stinkbug)); *Phthorimaea* spp. (e.g. *P. operculella* (potato tuberworm)); *Helicoverpa* spp. (e.g. *H. zea* (tomato fruitworm); *Keiferia* spp. (e.g. *K. lycopersicella* (tomato pinworm)); *Limonius* spp. (wireworms); *Manduca* spp. (e.g. *M. sexta* (tobacco hornworm), or *M. quinquemaculata* (tomato hornworm)); *Liriomyza* spp. (e.g. *L. sativae*, *L. trifolii* or *L. huidobrensis* (leafminer)); *Drosophilla* spp. (e.g. *D. melanogaster*, *D. yakuba*, *D. pseudoobscura* or *D. simulans*); *Carabus* spp. (e.g. *C. granulatus*); *Chironomus* spp. (e.g. *C. tentanus*); *Ctenocephalides* spp. (e.g. *C. felis* (cat flea)); *Diaprepes* spp. (e.g. *D. abbreviatus* (root weevil)); *Ips* spp. (e.g. *I. pini* (pine engraver)); *Tribolium* spp. (e.g. *T. castaneum* (red floor beetle)); *Glossina* spp. (e.g. *G. morsitans* (tsetse fly)); *Anopheles* spp. (e.g. *A. gambiae* (malaria mosquito)); *Helicoverpa* spp. (e.g. *H. armigera* (African Bollworm)); *Acyrtosiphon* spp. (e.g. *A. pisum* (pea aphid)); *Apis* spp. (e.g. *A. mellifera* (honey bee)); *Homalodisca* spp. (e.g. *H. coagulate* (glassy-winged sharpshooter)); *Aedes* spp. (e.g. *Ae. aegypti* (yellow fever mosquito)); *Bombyx* spp. (e.g. *B. mori* (silkworm)); *Locusta* spp. (e.g. *L. migratoria* (migratory locust)); *Boophilus* spp. (e.g. *B. microplus* (cattle tick)); *Acanthoscurria* spp. (e.g. *A. gomesiana* (red-haired chololate bird eater)); *Diploptera* spp. (e.g. *D. punctata* (pacific beetle cockroach)); *Heliconius* spp. (e.g. *H. erato* (red passion flower butterfly) or *H. melpomene* (postman butterfly)); *Curculio* spp. (e.g. *C. glandium* (acorn weevil)); *Plutella* spp. (e.g. *P. xylostella* (diamondback moth)); *Amblyomma* spp. (e.g. *A. variegatum* (cattle tick)); *Anteraea* spp. (e.g. *A. yamamai* (silkmoth)); and *Armigeres* spp. (e.g. *A. subalbus*).

15. A seed or reproductive or propagation material for a plant of any of claims 6 to 14, wherein said seed or reproductive or propagation material comprises a polynucleotide having a nucleic acid sequence as defined in claim 1 or wherein said seed comprises a double stranded ribonucleotide sequence produced from the expression of said polynucleotide.
- 5 16. A product produced from the plant of any of claims 6 to 14, or the seed or reproductive or propagation material of claim 15, wherein said product comprises a polynucleotide having a nucleic acid sequence as defined in claim 1 or wherein said seed comprises a double stranded ribonucleotide sequence produced from the expression of said polynucleotide.
- 10 17. The product of claim 16, wherein said product is selected from the group consisting of food, feed, fiber, paper, meal, protein, starch, flour, silage, coffee, tea, and oil.
18. A pesticide comprising a plant of any of claims 6 to 14, the seed or reproductive or propagation material of claim 15 or the product of claim 16 or 17; said plant, seed, reproductive or propagation material, or product expressing a nucleic acid sequence as defined in claim 1.
- 15 19. A method for controlling or preventing insect growth comprising providing an insect pest with plant material derived from the plant of any of claims 6 to 14, the seed or reproductive or propagation material of claim 15 or the product of claim 16 or 17, wherein said plant, seed, reproductive or propagation material, or product comprises a polynucleotide sequence that inhibits an insect biological activity.
- 20 20. The method of claim 19, wherein said polynucleotide comprises a nucleic acid sequence as defined in claim 1.
21. A method for producing a plant resistant against a plant pathogenic organism comprising:
- transforming a plant cell with a polynucleotide having a nucleic acid sequence as defined in claim 1, said nucleic acid sequence optionally operably linked to a regulatory sequence,
 - 25 - regenerating a plant from the transformed plant cell; and
 - growing the transformed plant under conditions suitable for the expression of an RNA molecule from said polynucleotide, said grown transformed plant resistant to said plant pathogenic organism compared to an untransformed plant.
22. A method for improving yield, comprising:
- 30 - transforming a plant cell with a polynucleotide having a nucleic acid sequence as defined in claim 1, said nucleic acid sequence optionally operably linked to a regulatory sequence,
 - regenerating a plant from the transformed plant cell; and
 - 35 - growing the transformed plant under conditions suitable for the expression of an RNA molecule from said polynucleotide, said expression inhibiting feeding by a plant pathogenic organism and loss of yield due to pest infestation.

23. The method according to any of claims 19 to 22, wherein polynucleotide expression produces an RNA molecule that suppresses a target gene in an insect pest that has ingested a portion of said crop plant, wherein said target gene performs at least one essential function selected from the group consisting of feeding by the pest, viability of the pest, pest cell apoptosis, differentiation and development of the pest or any pest cell, sexual reproduction by the pest, muscle formation, muscle twitching, muscle contraction, juvenile hormone formation and/or reduction, juvenile hormone regulation, ion regulation and transport, maintenance of cell membrane potential, amino acid biosynthesis, amino acid degradation, sperm formation, pheromone synthesis, pheromone sensing, antennae formation, wing formation, leg formation, egg formation, larval maturation, digestive enzyme formation, haemolymph synthesis, haemolymph maintenance, neurotransmission, larval stage transition, pupation, emergence from pupation, cell division, energy metabolism, respiration, cytoskeletal structure synthesis and maintenance, nucleotide metabolism, nitrogen metabolism, water use, water retention, and sensory perception

24. The method according to any of claims 19 to 22 wherein:

15 - the nucleic acid sequence is chosen from the group comprising:

(i) sequences represented by any of SEQ ID NOs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 49 to 158, 159, 160 to 163, 168, 173, 178, 183, 188, 193, 198, 203, 208, 215, 220, 225, 230, 240 to 246, or 2486, or the complement thereof,

(ii) sequences which are at least 70 %, preferably at least 75%, 80%, 85%, 90%, more preferably at least 95%, 96%, 97%, 98% or 99% identical to a sequence represented by any of SEQ ID NOs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 49 to 158, 159, 160 to 163, 168, 173, 178, 183, 188, 193, 198, 203, 208, 215, 220, 225, 230, 240 to 246, or 2486, or the complement thereof, and

(iii) sequences comprising at least 17 contiguous nucleotides of any of the sequences represented by SEQ ID NOs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 49 to 158, 159, 160 to 163, 168, 173, 178, 183, 188, 193, 198, 203, 208, 215, 220, 225, 230, 240 to 246, or 2486, or the complement thereof,

or wherein said nucleic acid sequence is an orthologue of a gene comprising at least 17 contiguous nucleotides of any of SEQ ID NOs 49 to 158, or the complement thereof,

30 and

- the insect is chosen from the group comprising *Leptinotarsa* spp. (e.g. *L. decemlineata* (Colorado potato beetle), *L. juncta* (false potato beetle), and *L. texana* (Texan false potato beetle)).

25. The method according to any of claims 19 to 22 wherein:

35 - the nucleic acid sequence is chosen from the group comprising:

(i) sequences represented by any of SEQ ID NOs 247, 249, 251, 253, 255, 257, 259, 275 to 472, 473, 478, 483, 488, 493, 498, 503, 508 to 512, or the complement thereof,

(ii) sequences which are at least 70 %, preferably at least 75%, 80%, 85%, 90%, more preferably at least 95%, 96%, 97%, 98% or 99% identical to a sequence represented by any of

SEQ ID NOs 247, 249, 251, 253, 255, 257, 259, 275 to 472, 473, 478, 483, 488, 493, 498, 503, 508 to 512, or the complement thereof, and

(iii) sequences comprising at least 17 contiguous nucleotides of any of the sequences represented by SEQ ID NOs 247, 249, 251, 253, 255, 257, 259, 275 to 472, 473, 478, 483, 488, 493, 498, 503, 508 to 512, or the complement thereof,

or wherein said nucleic acid sequence is an orthologue of a gene comprising at least 17 contiguous nucleotides of any of SEQ ID NOs 275 to 472, or the complement thereof,

and

- the insect is chosen from the group comprising *Phaedon* spp. (e.g. *P. cochleariae* (mustard leaf beetle)).

26. The method according to any of claims 19 to 22 wherein:

- the nucleic acid sequence is chosen from the group comprising:

(i) sequences represented by any of SEQ ID NOs 513, 515, 517, 519, 521, 533 to 575, 576, 581, 586, 591 or 596, or the complement thereof,

(ii) sequences which are at least 70 %, preferably at least 75%, 80%, 85%, 90%, more preferably at least 95%, 96%, 97%, 98% or 99% identical to a sequence represented by any of SEQ ID NOs 513, 515, 517, 519, 521, 533 to 575, 576, 581, 586, 591 or 596, or the complement thereof, and

(iii) sequences comprising at least 17 contiguous nucleotides of any of the sequences represented by SEQ ID NOs 513, 515, 517, 519, 521, 533 to 575, 576, 581, 586, 591 or 596, or the complement thereof,

or wherein said nucleic acid sequence is an orthologue of a gene comprising at least 17 contiguous nucleotides of any of SEQ ID NOs 533 to 575, or the complement thereof,

and

- the insect is chosen from the group comprising *Epilachna* spp. (e.g. *E. varivetis* (mexican bean beetle)).

27. The method according to any of claims 19 to 22 wherein:

- the nucleic acid sequence is chosen from the group comprising:

(i) sequences represented by any of SEQ ID NOs 601, 603, 605, 607, 609, 621 to 767, 768, 773, 778, 783 or 788, or the complement thereof,

(ii) sequences which are at least 70 %, preferably at least 75%, 80%, 85%, 90%, more preferably at least 95%, 96%, 97%, 98% or 99% identical to a sequence represented by any of SEQ ID NOs 601, 603, 605, 607, 609, 621 to 767, 768, 773, 778, 783 or 788, or the complement thereof, and

(iii) sequences comprising at least 17 contiguous nucleotides of any of the sequences represented by SEQ ID NOs 601, 603, 605, 607, 609, 621 to 767, 768, 773, 778, 783 or 788, or the complement thereof,

or wherein said nucleic acid sequence is an orthologue of a gene comprising at least 17 contiguous nucleotides of any of SEQ ID NOs 621 to 767, or the complement thereof,

and

- the insect is chosen from the group comprising *Anthonomus* spp. (e.g. *A. grandis* (boll weevil)).

28. The method according to any of claims 19 to 22 wherein:

- 5 - the nucleic acid sequence is chosen from the group comprising:

(i) sequences represented by any of SEQ ID NOs 793, 795, 797, 799, 801, 813 to 862, 863, 868, 873, 878 or 883, or the complement thereof,

(ii) sequences which are at least 70 %, preferably at least 75%, 80%, 85%, 90%, more preferably at least 95%, 96%, 97%, 98% or 99% identical to a sequence represented by any of
10 SEQ ID NOs 793, 795, 797, 799, 801, 813 to 862, 863, 868, 873, 878 or 883, or the complement thereof, and

(iii) sequences comprising at least 17 contiguous nucleotides of any of the sequences represented by SEQ ID NOs 793, 795, 797, 799, 801, 813 to 862, 863, 868, 873, 878 or 883, or the complement thereof,

- 15 or wherein said nucleic acid sequence is an orthologue of a gene comprising at least 17 contiguous nucleotides of any of SEQ ID NOs 813 to 862, or the complement thereof,

and

- the insect is chosen from the group comprising *Tribolium* spp. (e.g. *T. castaneum* (red floor beetle)).

20 29. The method according to any of claims 19 to 22 wherein:

- the nucleic acid sequence is chosen from the group comprising:

(i) sequences represented by any of SEQ ID NOs 888, 890, 892, 894, 896, 908 to 1040, 1041, 1046, 1051, 1056, 1061, or 1066 to 1070, or the complement thereof,

(ii) sequences which are at least 70 %, preferably at least 75%, 80%, 85%, 90%, more
25 preferably at least 95%, 96%, 97%, 98% or 99% identical to a sequence represented by any of
SEQ ID NOs 888, 890, 892, 894, 896, 908 to 1040, 1041, 1046, 1051, 1056, 1061, or 1066 to 1070, or the complement thereof, and

(iii) sequences comprising at least 17 contiguous nucleotides of any of the sequences represented by SEQ ID NOs 888, 890, 892, 894, 896, 908 to 1040, 1041, 1046, 1051, 1056, 1061,
30 or 1066 to 1070, or the complement thereof,

or wherein said nucleic acid sequence is an orthologue of a gene comprising at least 17 contiguous nucleotides of any of SEQ ID NOs 908 to 1040, or the complement thereof,

and

- the insect is chosen from the group comprising *Myzus* spp. (e.g. *M. persicae* (green peach aphid)).
- 35

30. The method according to any of claims 19 to 22 wherein:

- the nucleic acid sequence is chosen from the group comprising:

(i) sequences represented by any of SEQ ID NOs 1071, 1073, 1075, 1077, 1079, 1081, 1083, 1085, 1087, 1089, 1091, 1093, 1095, 1097, 1099, 1101, 1103, 1105, 1107, 1109, 1111,

1113, 1161 to 1571, 1572, 1577, 1582, 1587, 1592, 1597, 1602, 1607, 1612, 1617, 1622, 1627, 1632, 1637, 1642, 1647, 1652, 1657, 1662, 1667, 1672 or 1677, or the complement thereof,

(ii) sequences which are at least 70 %, preferably at least 75%, 80%, 85%, 90%, more preferably at least 95%, 96%, 97%, 98% or 99% identical to a sequence represented by any of
 5 SEQ ID NOs 1071, 1073, 1075, 1077, 1079, 1081, 1083, 1085, 1087, 1089, 1091, 1093, 1095, 1097, 1099, 1101, 1103, 1105, 1107, 1109, 1111, 1113, 1161 to 1571, 1572, 1577, 1582, 1587, 1592, 1597, 1602, 1607, 1612, 1617, 1622, 1627, 1632, 1637, 1642, 1647, 1652, 1657, 1662, 1667, 1672 or 1677, or the complement thereof, and

(iii) sequences comprising at least 17 contiguous nucleotides of any of the sequences
 10 represented by SEQ ID NOs 1071, 1073, 1075, 1077, 1079, 1081, 1083, 1085, 1087, 1089, 1091, 1093, 1095, 1097, 1099, 1101, 1103, 1105, 1107, 1109, 1111, 1113, 1161 to 1571, 1572, 1577, 1582, 1587, 1592, 1597, 1602, 1607, 1612, 1617, 1622, 1627, 1632, 1637, 1642, 1647, 1652, 1657, 1662, 1667, 1672 or 1677, or the complement thereof,

or wherein said nucleic acid sequence is an orthologue of a gene comprising at least 17
 15 contiguous nucleotides of any of SEQ ID NOs 1161 to 1571, or the complement thereof,

and

- the insect is chosen from the group comprising *Nilaparvata* spp. (e.g. *N. lugens* (brown planthopper)).

31. The method according to any of claims 19 to 22 wherein:

20 - the nucleic acid sequence is chosen from the group comprising:

(i) sequences represented by any of SEQ ID NOs 1682, 1684, 1686, 1688, 1690, 1692, 1694, 1696, 1698, 1700, 1702, 1704, 1730 to 2039, 2040, 2045, 2050, 2055, 2060, 2065, 2070, 2075, 2080, 2085, 2090 or 2095, or the complement thereof,

(ii) sequences which are at least 70 %, preferably at least 75%, 80%, 85%, 90%, more
 25 preferably at least 95%, 96%, 97%, 98% or 99% identical to a sequence represented by any of SEQ ID NOs 1682, 1684, 1686, 1688, 1690, 1692, 1694, 1696, 1698, 1700, 1702, 1704, 1730 to 2039, 2040, 2045, 2050, 2055, 2060, 2065, 2070, 2075, 2080, 2085, 2090 or 2095, or the complement thereof, and

(iii) sequences comprising at least 17 contiguous nucleotides of any of the sequences
 30 represented by SEQ ID NOs 1682, 1684, 1686, 1688, 1690, 1692, 1694, 1696, 1698, 1700, 1702, 1704, 1730 to 2039, 2040, 2045, 2050, 2055, 2060, 2065, 2070, 2075, 2080, 2085, 2090 or 2095, or the complement thereof,

or wherein said nucleic acid sequence is an orthologue of a gene comprising at least 17
 contiguous nucleotides of any of SEQ ID NOs 1730 to 2039, or the complement thereof,

35 and

- the insect is chosen from the group comprising *Chilo* spp. (e.g. *C. suppressalis* (rice striped stem borer), *C. auricilius* (gold-fringed stem borer), or *C. polychrysus* (dark-headed stem borer)).

32. The method according to any of claims 19 to 22 wherein:

- the nucleic acid sequence is chosen from the group comprising:

(i) sequences represented by any of SEQ ID NOs 2100, 2102, 2104, 2106, 2108, 2120 to 2338, 2339, 2344, 2349, 2354 or 2359, or the complement thereof,

(ii) sequences which are at least 70 %, preferably at least 75%, 80%, 85%, 90%, more preferably at least 95%, 96%, 97%, 98% or 99% identical to a sequence represented by any of SEQ ID NOs 2100, 2102, 2104, 2106, 2108, 2120 to 2338, 2339, 2344, 2349, 2354 or 2359, or the complement thereof, and

(iii) sequences comprising at least 17 contiguous nucleotides of any of the sequences represented by SEQ ID NOs 2100, 2102, 2104, 2106, 2108, 2120 to 2338, 2339, 2344, 2349, 2354 or 2359, or the complement thereof,

or wherein said nucleic acid sequence is an orthologue of a gene comprising at least 17 contiguous nucleotides of any of SEQ ID NOs 2120 to 2338, or the complement thereof,

and

- the insect is chosen from the group comprising *Plutella* spp. (e.g. *P. xylostella* (diamondback moth)).

33. The method according to any of claims 19 to 22 wherein:

- the nucleic acid sequence is chosen from the group comprising:

(i) sequences represented by any of SEQ ID NOs 2364, 2366, 2368, 2370, 2372, 2384 to 2460, 2461, 2466, 2471, 2476 or 2481, or the complement thereof,

(ii) sequences which are at least 70 %, preferably at least 75%, 80%, 85%, 90%, more preferably at least 95%, 96%, 97%, 98% or 99% identical to a sequence represented by any of SEQ ID NOs 2364, 2366, 2368, 2370, 2372, 2384 to 2460, 2461, 2466, 2471, 2476 or 2481, or the complement thereof, and

(iii) sequences comprising at least 17 contiguous nucleotides of any of the sequences represented by SEQ ID NOs 2364, 2366, 2368, 2370, 2372, 2384 to 2460, 2461, 2466, 2471, 2476 or 2481, or the complement thereof,

or wherein said nucleic acid sequence is an orthologue of a gene comprising at least 17 contiguous nucleotides of any of SEQ ID NOs 2384 to 2460, or the complement thereof,

and

- the insect is chosen from the group comprising *Acheta* spp. (e.g. *A. domesticus* (house cricket)).

34. A transgenic plant resistant to an insect pest comprising a polynucleotide comprising a nucleic acid sequence selected from the group comprising:

(i) sequences represented by any of SEQ ID NOs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 49 to 158, 159, 160-163, 168, 173, 178, 183, 188, 193, 198, 203, 208, 215, 220, 225, 230, 240 to 246, or 2486, or the complement thereof,

(ii) sequences which are at least 70 %, preferably at least 75%, 80%, 85%, 90%, more preferably at least 95%, 96%, 97%, 98% or 99% identical to a sequence represented by any of

SEQ ID NOs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 49 to 158, 159, 160-163, 168, 173, 178, 183, 188, 193, 198, 203, 208, 215, 220, 225, 230, 240 to 246, or 2486, or the complement thereof, and

(iii) sequences comprising at least 17 contiguous nucleotides of any of the sequences represented by SEQ ID NOs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 49 to 158, 159, 160-163, 168, 173, 178, 183, 188, 193, 198, 203, 208, 215, 220, 225, 230, 240 to 246, or 2486, or the complement thereof,

or wherein said nucleic acid sequence is an orthologue of a gene comprising at least 17 contiguous nucleotides of any of SEQ ID NOs 49 to 158, or the complement thereof.

35. A transgenic plant resistant to an insect pest comprising a polynucleotide comprising a nucleic acid sequence selected from the group comprising:

(i) sequences represented by any of SEQ ID NOs 247, 249, 251, 253, 255, 257, 259, 275 to 472, 473, 478, 483, 488, 493, 498, 503, 508 to 512, or the complement thereof,

(ii) sequences which are at least 70 %, preferably at least 75%, 80%, 85%, 90%, more preferably at least 95%, 96%, 97%, 98% or 99% identical to a sequence represented by any of SEQ ID NOs 247, 249, 251, 253, 255, 257, 259, 275 to 472, 473, 478, 483, 488, 493, 498, 503, 508 to 512, or the complement thereof, and

(iii) sequences comprising at least 17 contiguous nucleotides of any of the sequences represented by SEQ ID NOs 247, 249, 251, 253, 255, 257, 259, 275 to 472, 473, 478, 483, 488, 493, 498, 503, 508 to 512, or the complement thereof,

or wherein said nucleic acid sequence is an orthologue of a gene comprising at least 17 contiguous nucleotides of any of SEQ ID NOs 275 to 472, or the complement thereof.

36. A transgenic plant resistant to an insect pest comprising a polynucleotide comprising a nucleic acid sequence selected from the group comprising:

(i) sequences represented by any of SEQ ID NOs 513, 515, 517, 519, 521, 533 to 575, 576, 581, 586, 591 or 596, or the complement thereof,

(ii) sequences which are at least 70 %, preferably at least 75%, 80%, 85%, 90%, more preferably at least 95%, 96%, 97%, 98% or 99% identical to a sequence represented by any of SEQ ID NOs 513, 515, 517, 519, 521, 533 to 575, 576, 581, 586, 591 or 596, or the complement thereof, and

(iii) sequences comprising at least 17 contiguous nucleotides of any of the sequences represented by SEQ ID NOs 513, 515, 517, 519, 521, 533 to 575, 576, 581, 586, 591 or 596, or the complement thereof,

or wherein said nucleic acid sequence is an orthologue of a gene comprising at least 17 contiguous nucleotides of any of SEQ ID NOs 533 to 575, or the complement thereof.

37. A transgenic plant resistant to an insect pest comprising a polynucleotide comprising a nucleic acid sequence selected from the group comprising:

(i) sequences represented by any of SEQ ID NOs 601, 603, 605, 607, 609, 621 to 767, 768, 773, 778, 783 or 788, or the complement thereof,

(ii) sequences which are at least 70 %, preferably at least 75%, 80%, 85%, 90%, more preferably at least 95%, 96%, 97%, 98% or 99% identical to a sequence represented by any of SEQ ID NOs 601, 603, 605, 607, 609, 621 to 767, 768, 773, 778, 783 or 788, or the complement thereof, and

5 (iii) sequences comprising at least 17 contiguous nucleotides of any of the sequences represented by SEQ ID NOs 601, 603, 605, 607, 609, 621 to 767, 768, 773, 778, 783 or 788, or the complement thereof,

or wherein said nucleic acid sequence is an orthologue of a gene comprising at least 17 contiguous nucleotides of any of SEQ ID NOs 621 to 767, or the complement thereof.

10 38. A transgenic plant resistant to an insect pest comprising a polynucleotide comprising a nucleic acid sequence selected from the group comprising:

(i) sequences represented by any of SEQ ID NOs 793, 795, 797, 799, 801, 813 to 862, 863, 868, 873, 878 or 883, or the complement thereof,

15 (ii) sequences which are at least 70 %, preferably at least 75%, 80%, 85%, 90%, more preferably at least 95%, 96%, 97%, 98% or 99% identical to a sequence represented by any of SEQ ID NOs 793, 795, 797, 799, 801, 813 to 862, 863, 868, 873, 878 or 883, or the complement thereof, and

20 (iii) sequences comprising at least 17 contiguous nucleotides of any of the sequences represented by SEQ ID NOs 793, 795, 797, 799, 801, 813 to 862, 863, 868, 873, 878 or 883, or the complement thereof,

or wherein said nucleic acid sequence is an orthologue of a gene comprising at least 17 contiguous nucleotides of any of SEQ ID NOs 813 to 862, or the complement thereof.

39. A transgenic plant resistant to an insect pest comprising a polynucleotide comprising a nucleic acid sequence selected from the group comprising:

25 (i) sequences represented by any of SEQ ID NOs 888, 890, 892, 894, 896, 908 to 1040, 1041, 1046, 1051, 1056, 1061, or 1066 to 1071, or the complement thereof,

(ii) sequences which are at least 70 %, preferably at least 75%, 80%, 85%, 90%, more preferably at least 95%, 96%, 97%, 98% or 99% identical to a sequence represented by any of SEQ ID NOs 888, 890, 892, 894, 896, 908 to 1040, 1041, 1046, 1051, 1056, 1061, or 1066 to 1071, or the complement thereof, and

30 (iii) sequences comprising at least 17 contiguous nucleotides of any of the sequences represented by SEQ ID NOs 888, 890, 892, 894, 896, 908 to 1040, 1041, 1046, 1051, 1056, 1061, or 1066 to 1071, or the complement thereof,

or wherein said nucleic acid sequence is an orthologue of a gene comprising at least 17 contiguous nucleotides of any of SEQ ID NOs 908 to 1040, or the complement thereof.

40. A transgenic plant resistant to an insect pest comprising a polynucleotide comprising a nucleic acid sequence selected from the group comprising:

(i) sequences represented by any of SEQ ID NOs 1071, 1073, 1075, 1077, 1079, 1081, 1083, 1085, 1087, 1089, 1091, 1093, 1095, 1097, 1099, 1101, 1103, 1105, 1107, 1109, 1111,

1113, 1161 to 1571, 1572, 1577, 1582, 1587, 1592, 1597, 1602, 1607, 1612, 1617, 1622, 1627, 1632, 1637, 1642, 1647, 1652, 1657, 1662, 1667, 1672 or 1677, or the complement thereof,

(ii) sequences which are at least 70 %, preferably at least 75%, 80%, 85%, 90%, more preferably at least 95%, 96%, 97%, 98% or 99% identical to a sequence represented by any of
 5 SEQ ID NOs 1071, 1073, 1075, 1077, 1079, 1081, 1083, 1085, 1087, 1089, 1091, 1093, 1095, 1097, 1099, 1101, 1103, 1105, 1107, 1109, 1111, 1113, 1161 to 1571, 1572, 1577, 1582, 1587, 1592, 1597, 1602, 1607, 1612, 1617, 1622, 1627, 1632, 1637, 1642, 1647, 1652, 1657, 1662, 1667, 1672 or 1677, or the complement thereof, and

(iii) sequences comprising at least 17 contiguous nucleotides of any of the sequences
 10 represented by SEQ ID NOs 1071, 1073, 1075, 1077, 1079, 1081, 1083, 1085, 1087, 1089, 1091, 1093, 1095, 1097, 1099, 1101, 1103, 1105, 1107, 1109, 1111, 1113, 1161 to 1571, 1572, 1577, 1582, 1587, 1592, 1597, 1602, 1607, 1612, 1617, 1622, 1627, 1632, 1637, 1642, 1647, 1652, 1657, 1662, 1667, 1672 or 1677, or the complement thereof,

or wherein said nucleic acid sequence is an orthologue of a gene comprising at least 17
 15 contiguous nucleotides of any of SEQ ID NOs 1161 to 1571, or the complement thereof.

41. A transgenic plant resistant to an insect pest comprising a polynucleotide comprising a nucleic acid sequence selected from the group comprising:

(i) sequences represented by any of SEQ ID NOs 1682, 1684, 1686, 1688, 1690, 1692, 1694, 1696, 1698, 1700, 1702, 1704, 1730 to 2039, 2040, 2045, 2050, 2055, 2060, 2065, 2070,
 20 2075, 2080, 2085, 2090 or 2095, or the complement thereof,

(ii) sequences which are at least 70 %, preferably at least 75%, 80%, 85%, 90%, more preferably at least 95%, 96%, 97%, 98% or 99% identical to a sequence represented by any of
 SEQ ID NOs 1682, 1684, 1686, 1688, 1690, 1692, 1694, 1696, 1698, 1700, 1702, 1704, 1730 to 2039, 2040, 2045, 2050, 2055, 2060, 2065, 2070, 2075, 2080, 2085, 2090 or 2095, or the
 25 complement thereof, and

(iii) sequences comprising at least 17 contiguous nucleotides of any of the sequences
 represented by SEQ ID NOs 1682, 1684, 1686, 1688, 1690, 1692, 1694, 1696, 1698, 1700, 1702, 1704, 1730 to 2039, 2040, 2045, 2050, 2055, 2060, 2065, 2070, 2075, 2080, 2085, 2090 or 2095,
 or the complement thereof,

30 or wherein said nucleic acid sequence is an orthologue of a gene comprising at least 17 contiguous nucleotides of any of SEQ ID NOs 1730 to 2039, or the complement thereof.

42. A transgenic plant resistant to an insect pest comprising a polynucleotide comprising a nucleic acid sequence selected from the group comprising:

(i) sequences represented by any of SEQ ID NOs 2100, 2102, 2104, 2106, 2108, 2120 to
 35 2338, 2339, 2344, 2349, 2354 or 2359, or the complement thereof,

(ii) sequences which are at least 70 %, preferably at least 75%, 80%, 85%, 90%, more preferably at least 95%, 96%, 97%, 98% or 99% identical to a sequence represented by any of
 SEQ ID NOs 2100, 2102, 2104, 2106, 2108, 2120 to 2338, 2339, 2344, 2349, 2354 or 2359, or the
 complement thereof, and

(iii) sequences comprising at least 17 contiguous nucleotides of any of the sequences represented by SEQ ID NOs 2100, 2102, 2104, 2106, 2108, 2120 to 2338, 2339, 2344, 2349, 2354 or 2359, or the complement thereof,

5 or wherein said nucleic acid sequence is an orthologue of a gene comprising at least 17 contiguous nucleotides of any of SEQ ID NOs 2120 to 2338, or the complement thereof.

43. A transgenic plant resistant to an insect pest comprising a polynucleotide comprising a nucleic acid sequence selected from the group comprising:

(i) sequences represented by any of SEQ ID NOs 2364, 2366, 2368, 2370, 2372, 2384 to 2460, 2461, 2466, 2471, 2476 or 2481, or the complement thereof,

10 (ii) sequences which are at least 70 %, preferably at least 75%, 80%, 85%, 90%, more preferably at least 95%, 96%, 97%, 98% or 99% identical to a sequence represented by any of SEQ ID NOs 2364, 2366, 2368, 2370, 2372, 2384 to 2460, 2461, 2466, 2471, 2476 or 2481, or the complement thereof, and

15 (iii) sequences comprising at least 17 contiguous nucleotides of any of the sequences represented by SEQ ID NOs 2364, 2366, 2368, 2370, 2372, 2384 to 2460, 2461, 2466, 2471, 2476 or 2481, or the complement thereof,

or wherein said nucleic acid sequence is an orthologue of a gene comprising at least 17 contiguous nucleotides of any of SEQ ID NOs 2384 to 2460, or the complement thereof.

20 44. The transgenic plant according to any of claims 34 to 43 further comprising or expressing a pesticidal agent selected from the group consisting of a patatin, a *Bacillus thuringiensis* insecticidal protein, a *Xenorhabdus* insecticidal protein, a *Photorhabdus* insecticidal protein, a *Bacillus laterosporus* insecticidal protein, and a *Bacillus sphearicus* insecticidal protein.

25 45. The transgenic plant of claim 44 wherein said *Bacillus thuringiensis* insecticidal protein is selected from the group consisting of a Cry1, a Cry3, a TIC851, a CryET170, a Cry22, a binary insecticidal protein CryET33 and CryET34, a binary insecticidal protein CryET80 and CryET76, a binary insecticidal protein TIC100 and TIC101, and a binary insecticidal protein PS149B1.

30 46. Use of an isolated nucleic acid according to claim 1, a double stranded ribonucleotide sequence according to claim 2 or 3, a cell according to claim 4 or 5, a plant according to any of claims 6 to 14, a seed or reproductive or propagation material of claim 15, a product of claim 16 or 17, a transgenic plant of any of claims 34 to 45 for preventing insect growth on a plant.

47. Use of an isolated nucleic acid according to claim 1, a double stranded ribonucleotide sequence according to claim 2 or 3, a cell according to claim 4 or 5, a plant according to any of claims 6 to 14, a seed or reproductive or propagation material of claim 15, a product of claim 16 or 17, a transgenic plant of any of claims 34 to 45 for preventing insect infestation of a plant.

35 48. Use of an isolated nucleic acid according to claim 1, a double stranded ribonucleotide sequence according to claim 2 or 3, a cell according to claim 4 or 5, a plant according to any of claims 6 to 14, a seed or reproductive or propagation material of claim 15, a product of claim 16 or 17, a transgenic plant of any of claims 34 to 45 for improving yield.

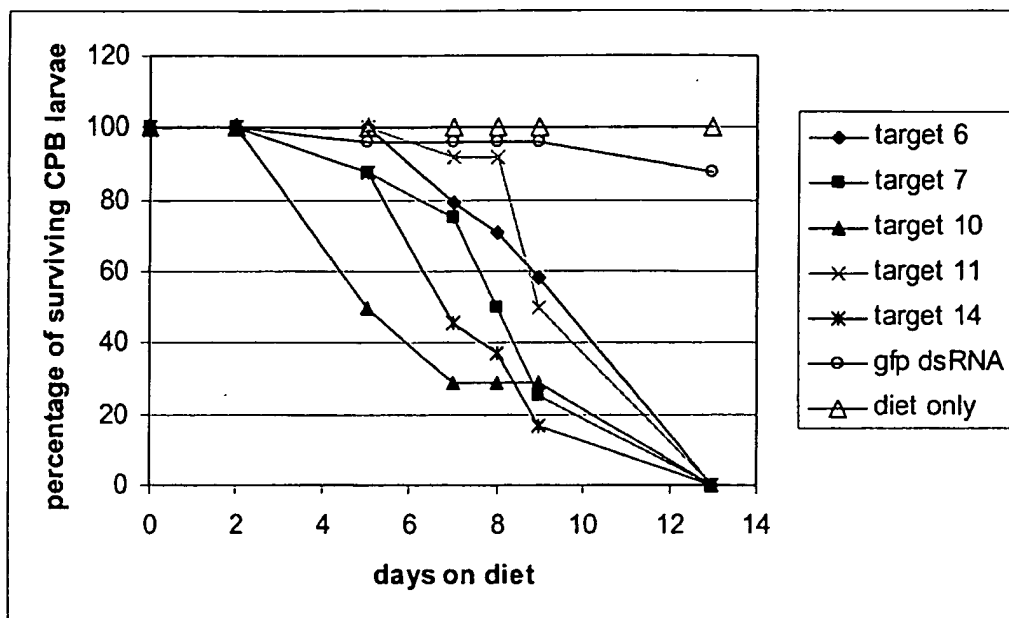


FIGURE 1-LD

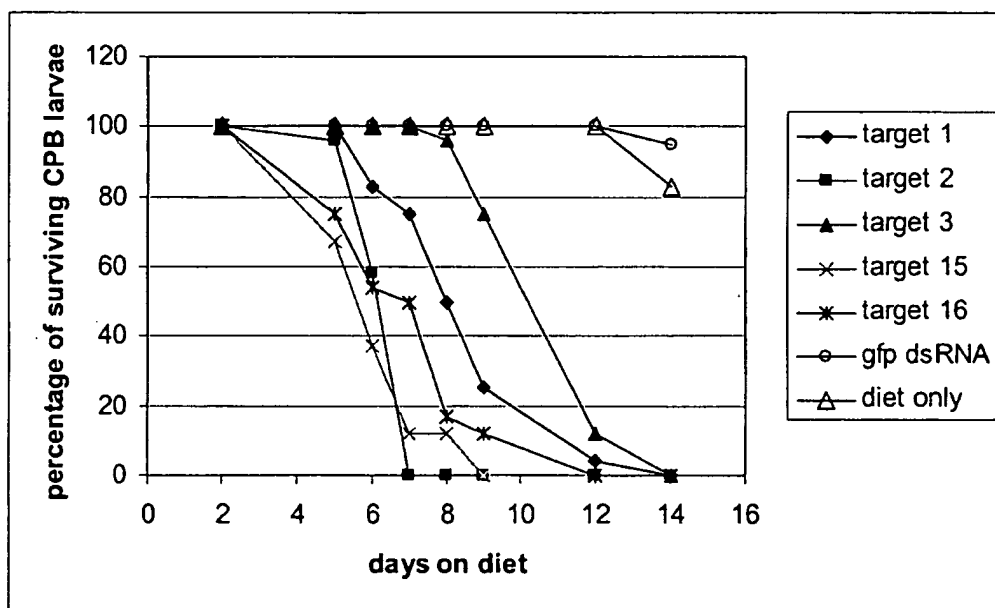


FIGURE 2-LD

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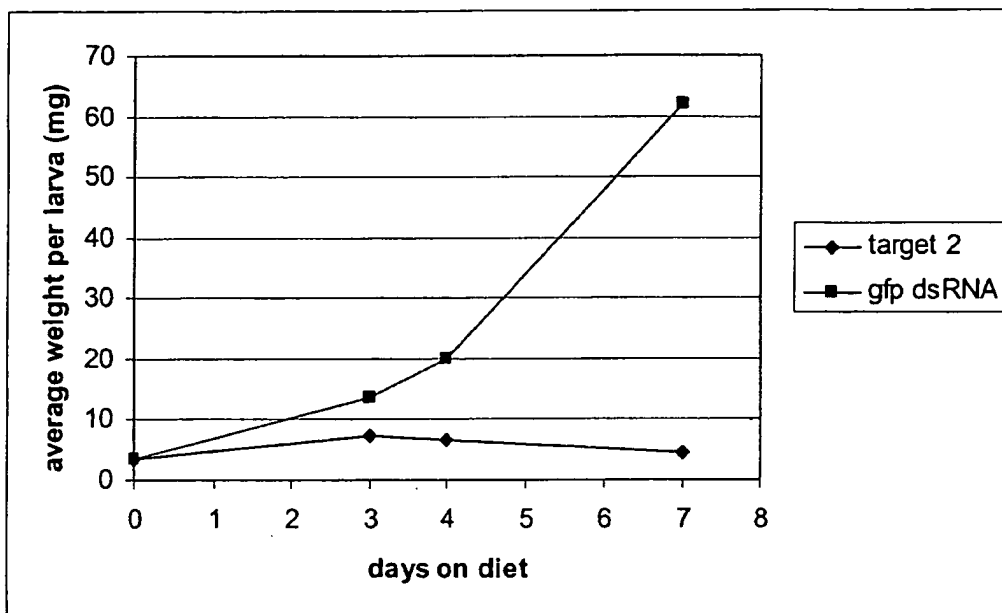


FIGURE 3-LD

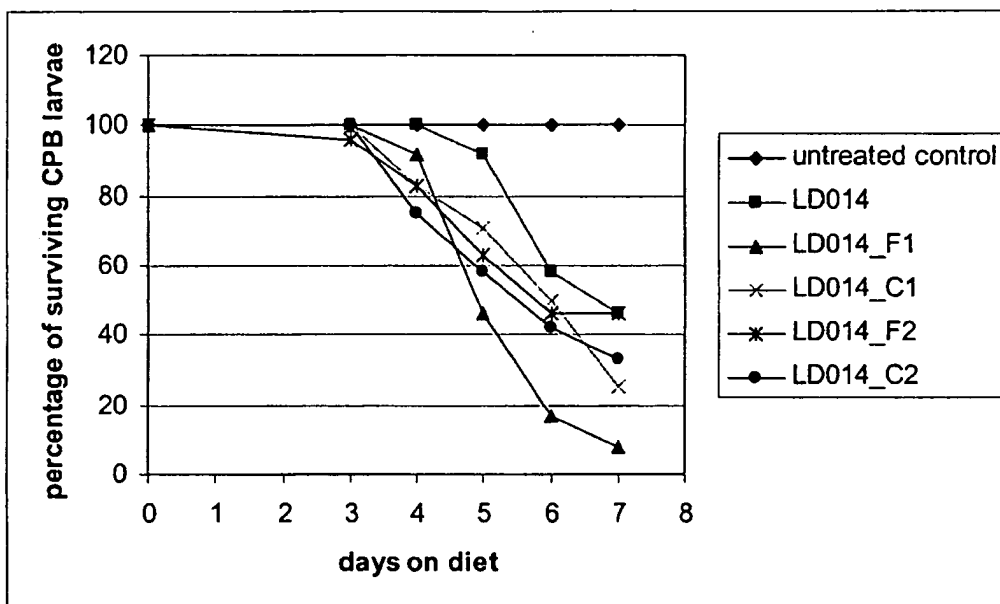


FIGURE 4-LD

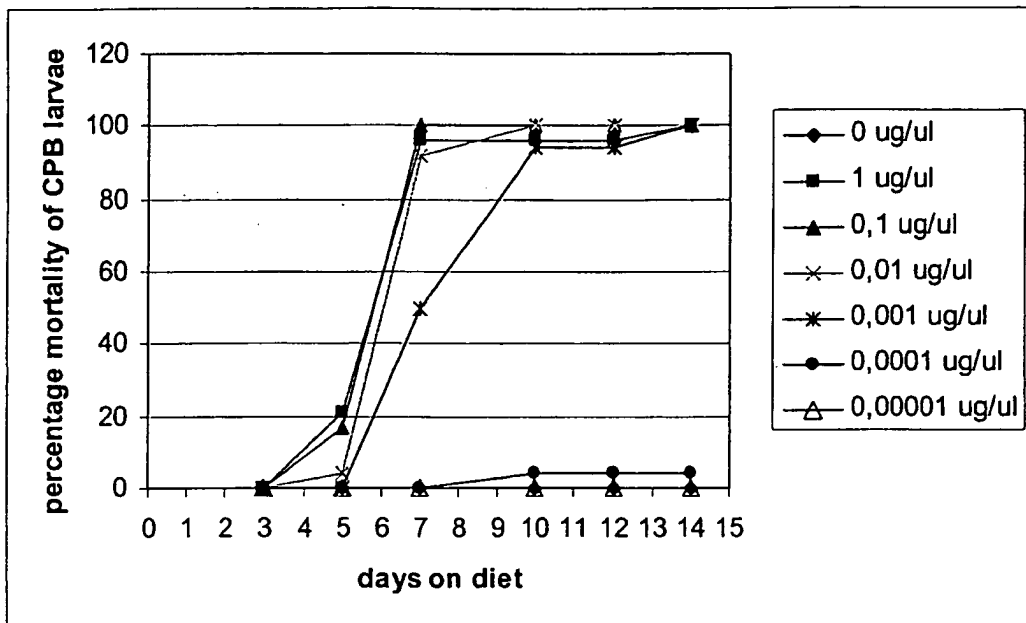


FIGURE 5-LD (a)

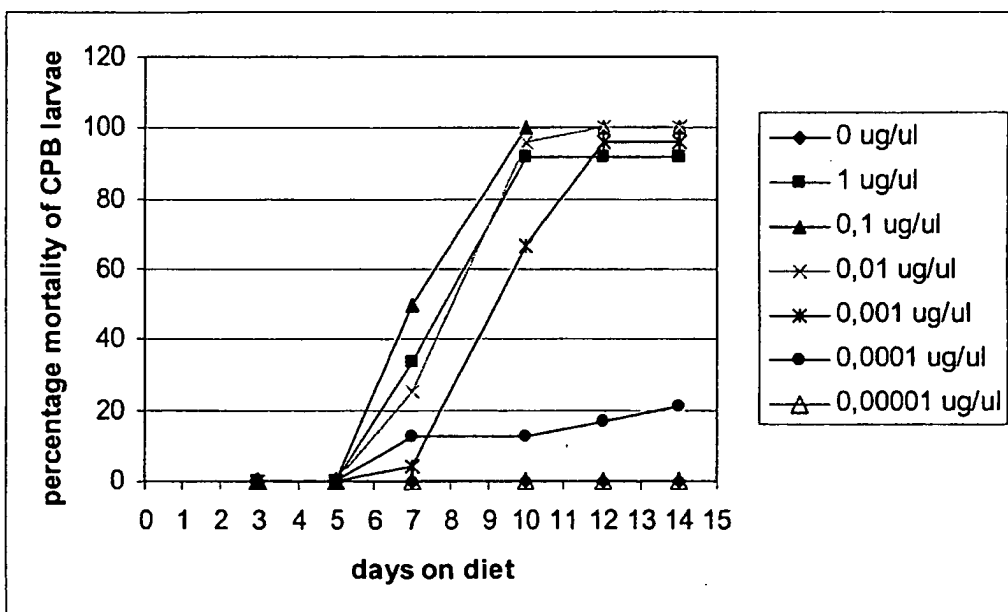


FIGURE 5-LD (b)

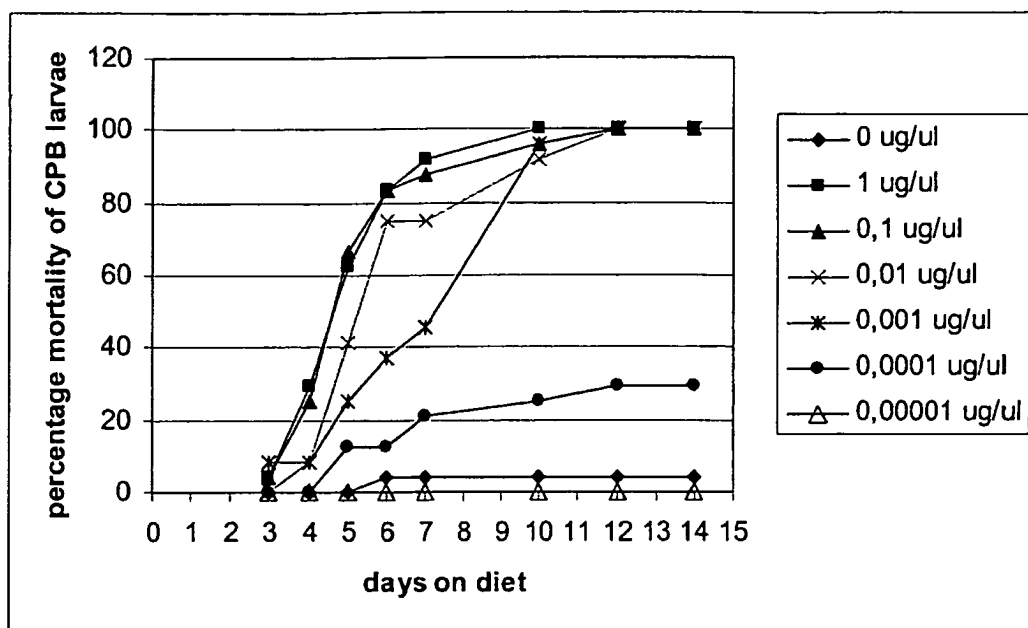


FIGURE 5-LD (c)

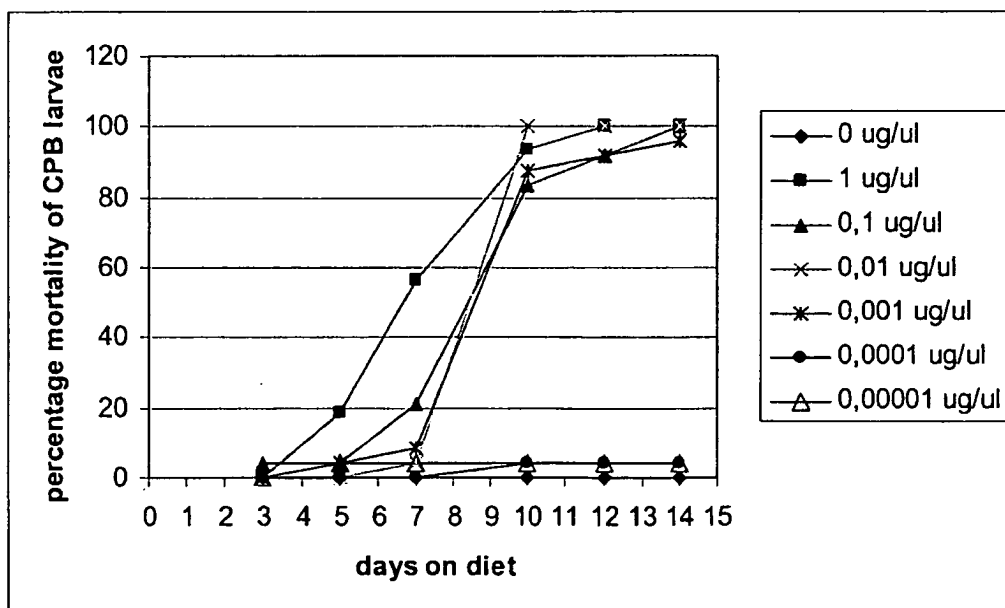


FIGURE 5-LD (d)

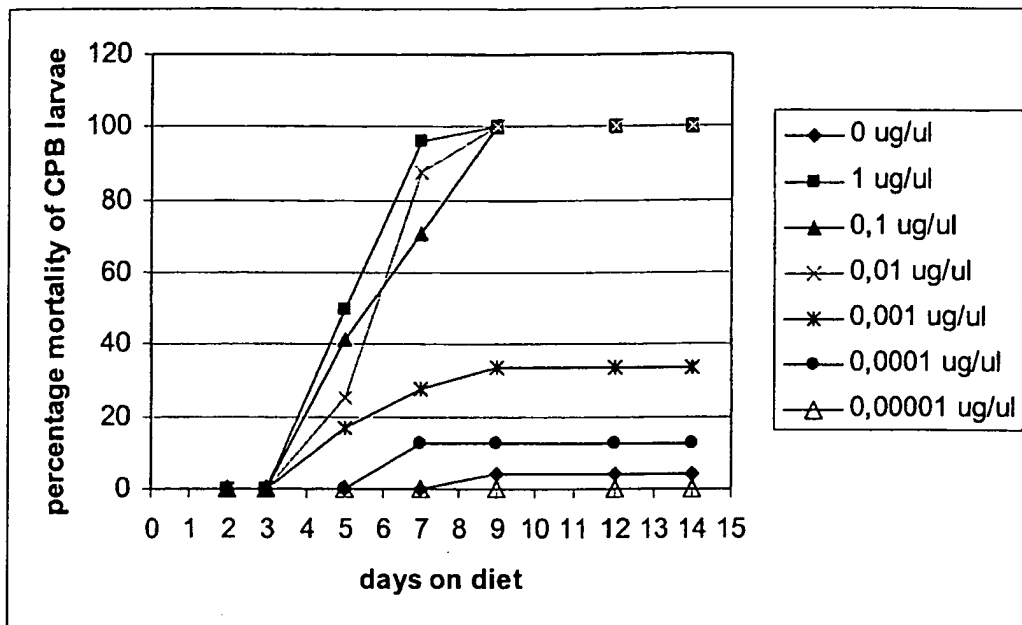


FIGURE 5-LD (e)

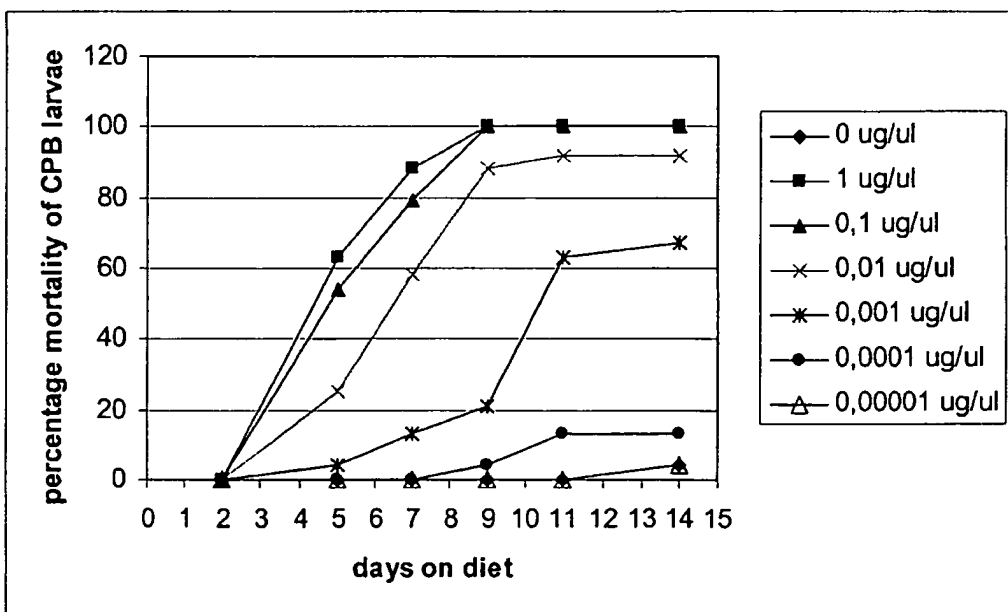


FIGURE 5-LD (f)

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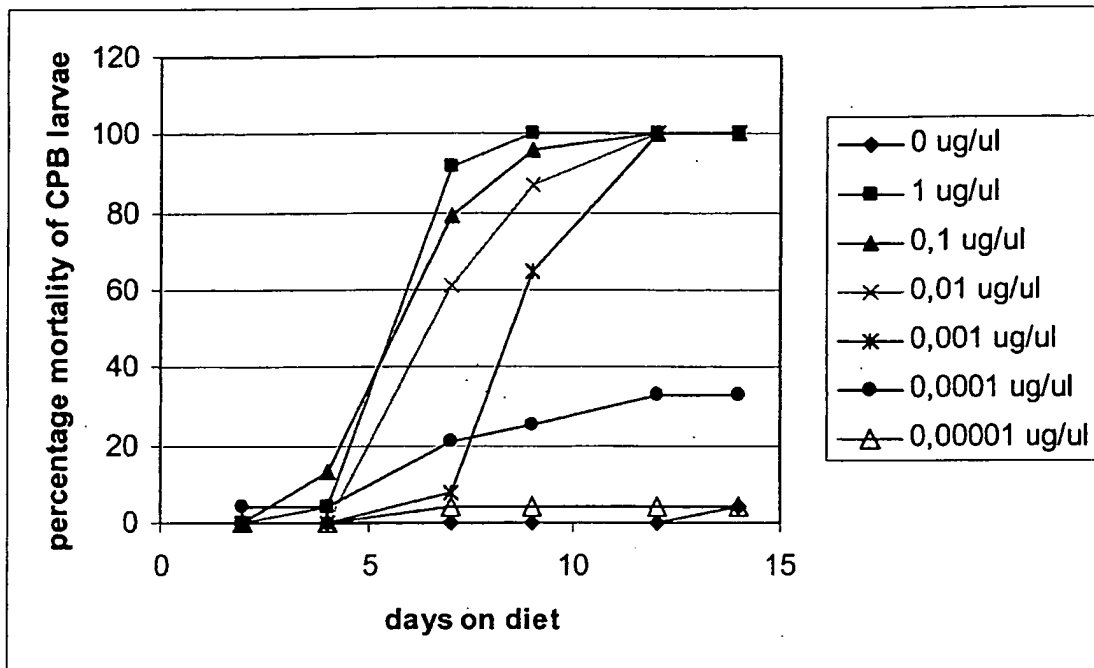


FIGURE 5-LD (g)

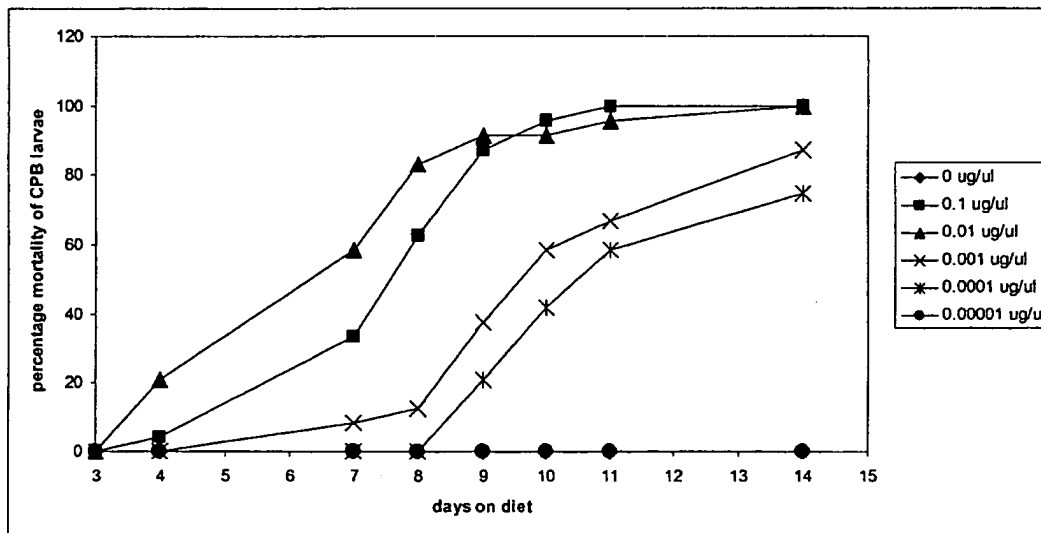


FIGURE 5-LD (h)

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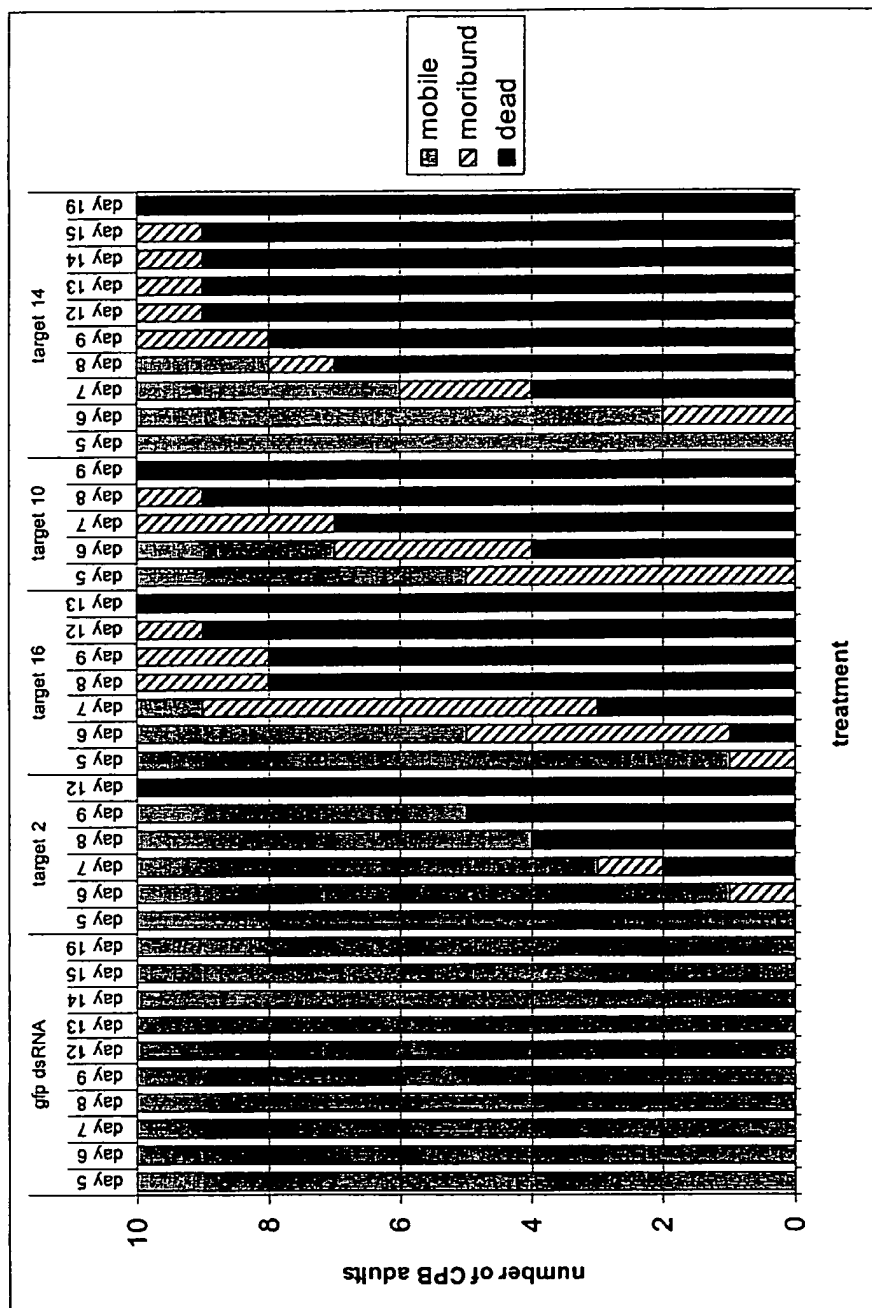


FIGURE 6-LD

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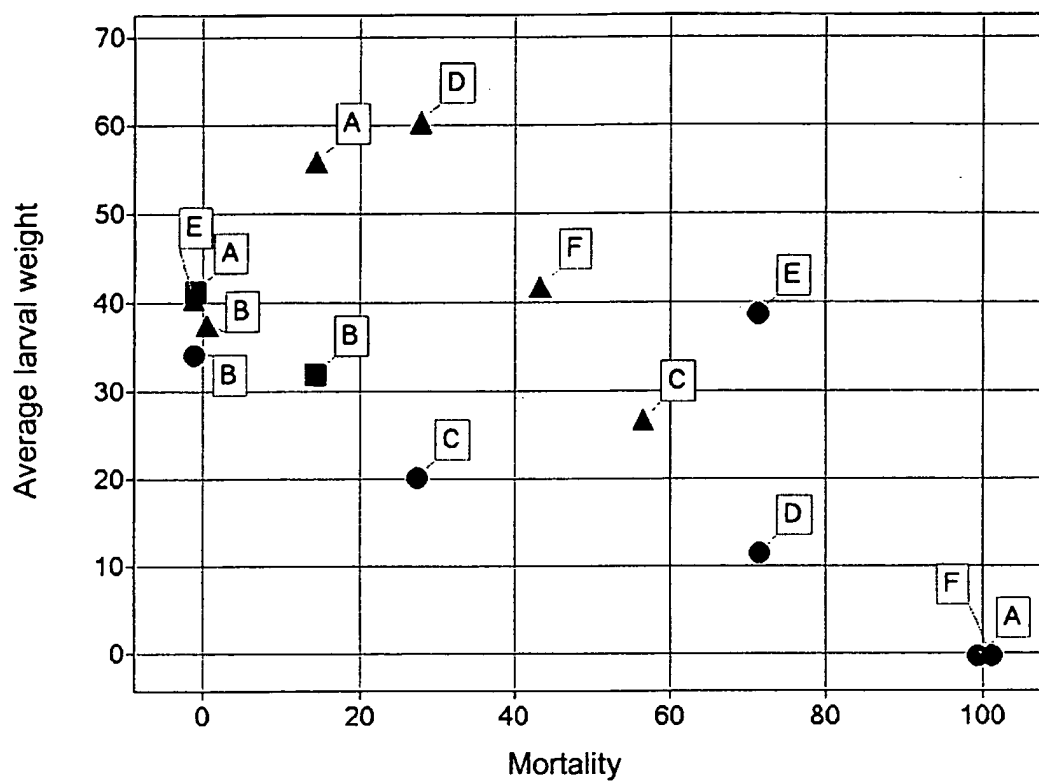


FIGURE 7-LD

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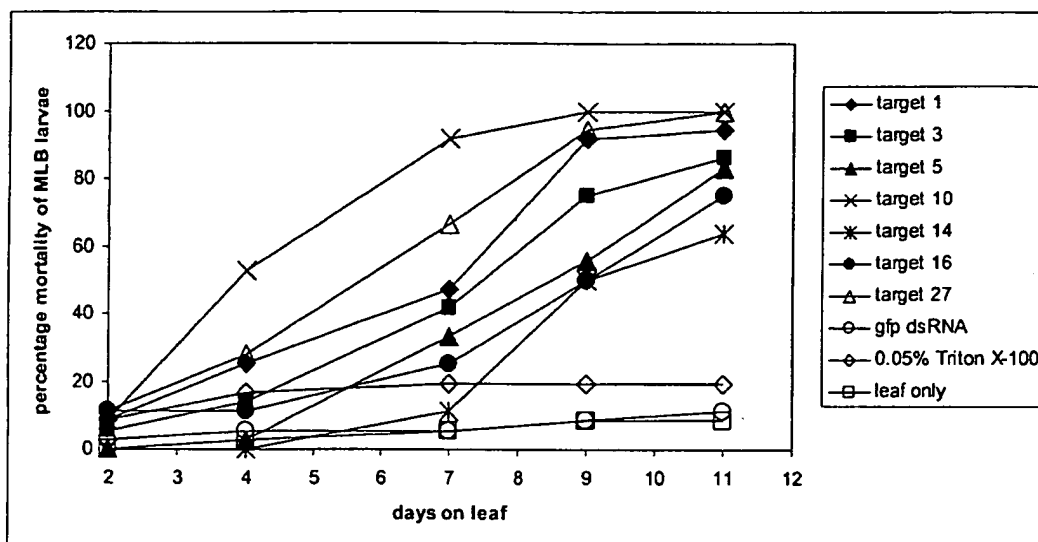


FIGURE 1-PC (a)

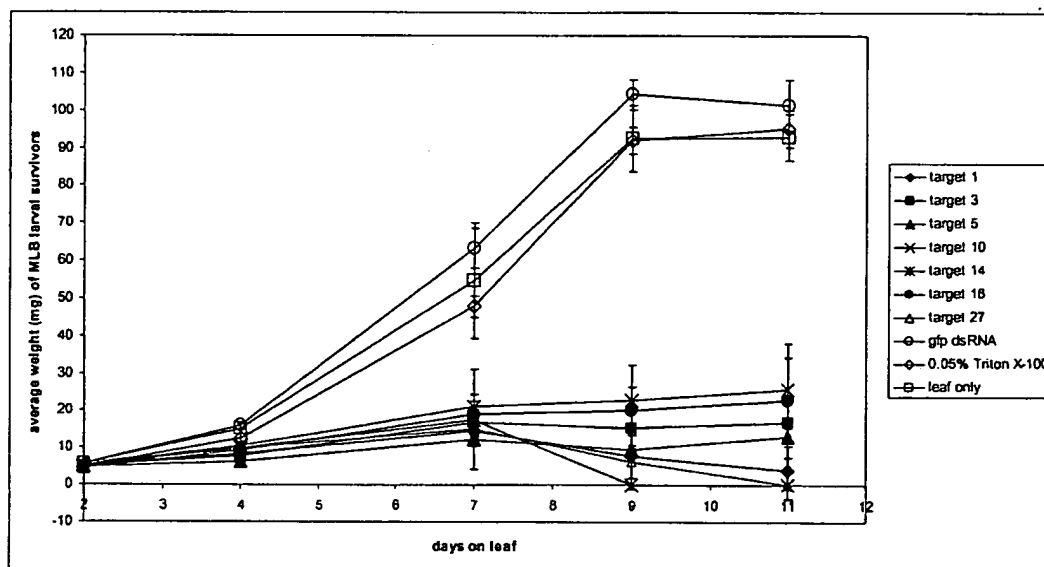


FIGURE 1-PC (b)

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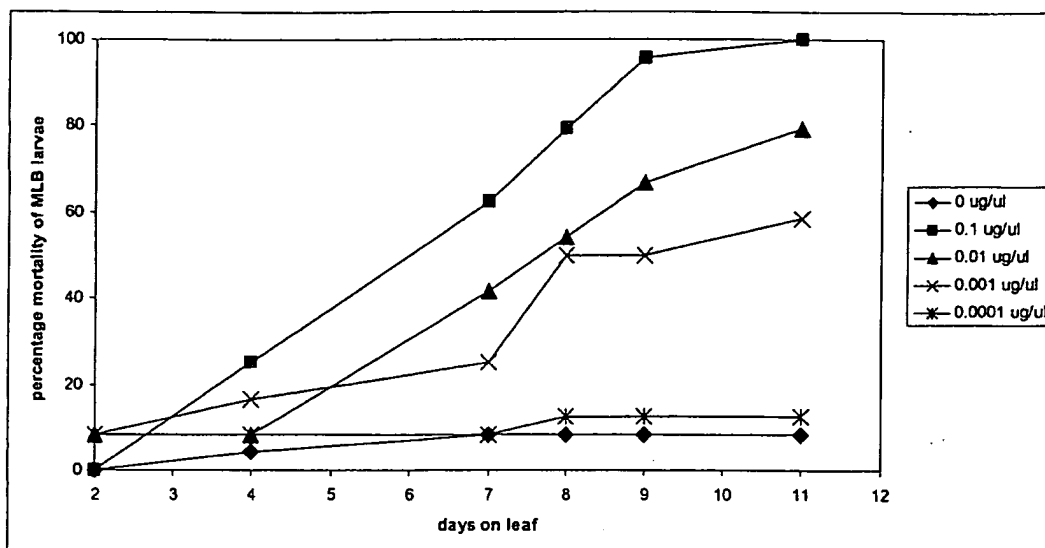


FIGURE 2-PC (a)

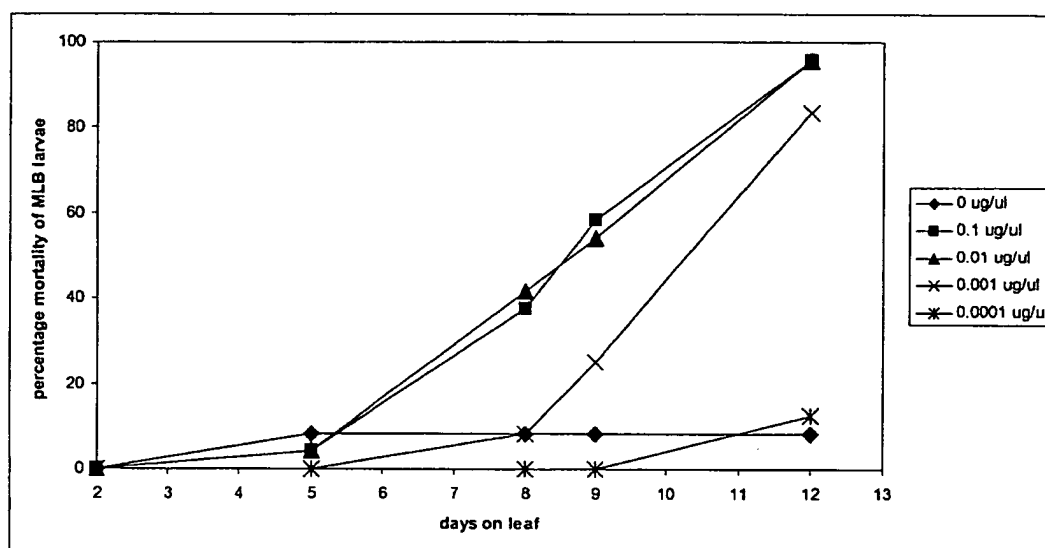


FIGURE 2-PC (b)

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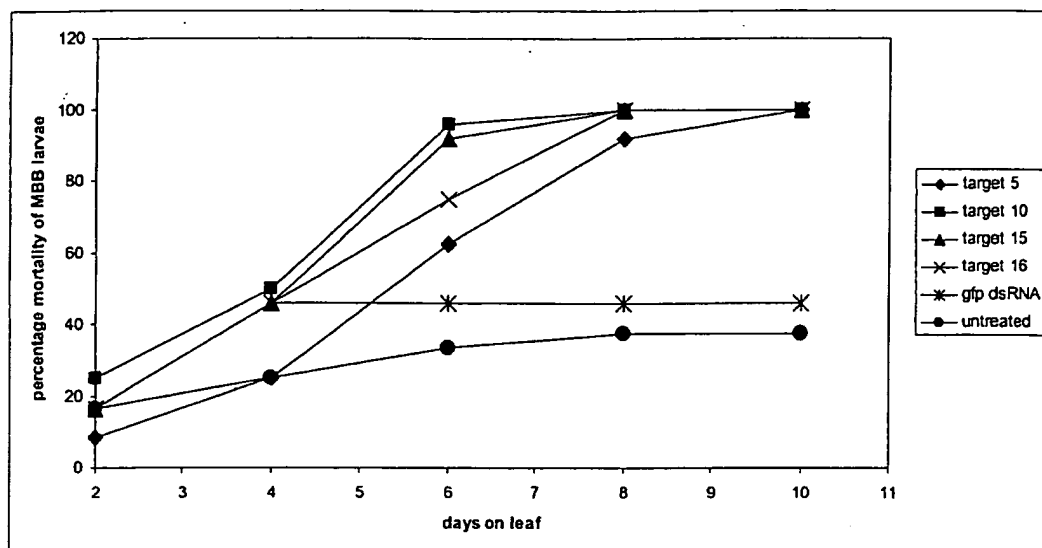


FIGURE 1-EV

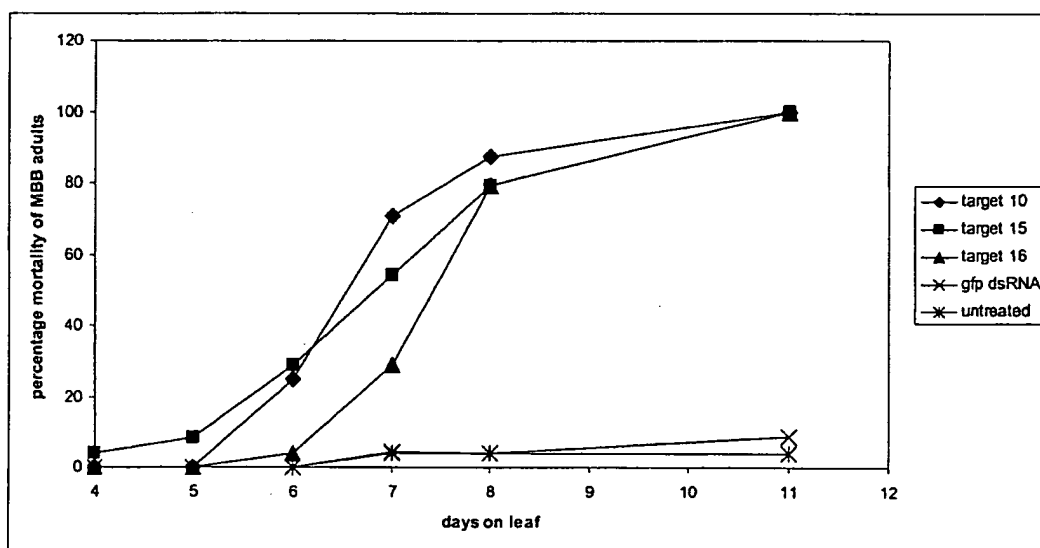


FIGURE 2-EV (a)

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(i)



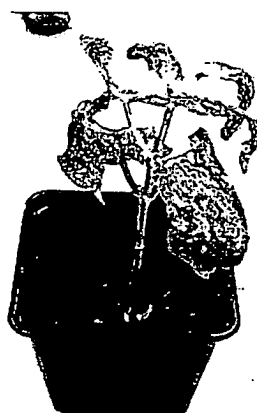
(ii)



(iii)



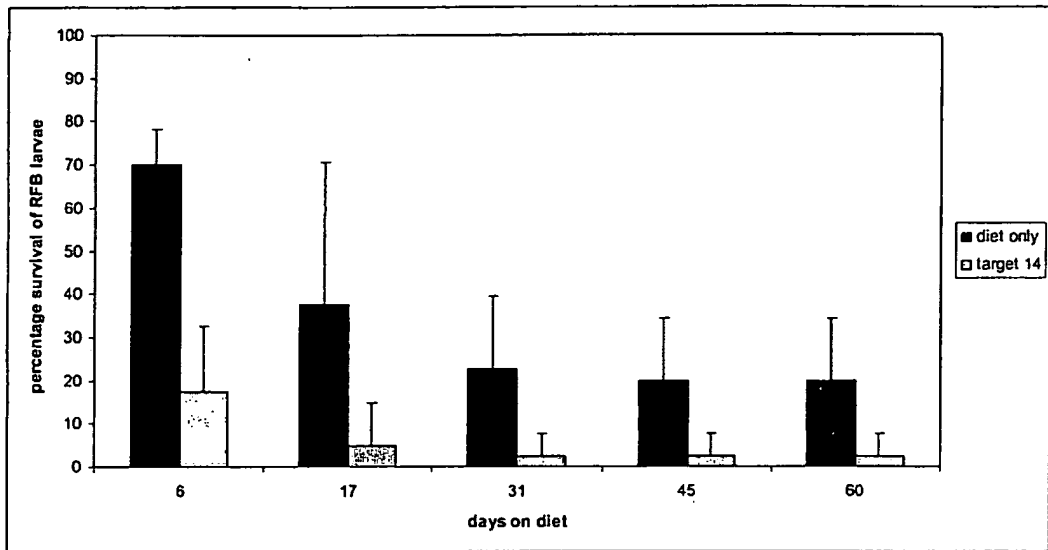
(iv)



(v)

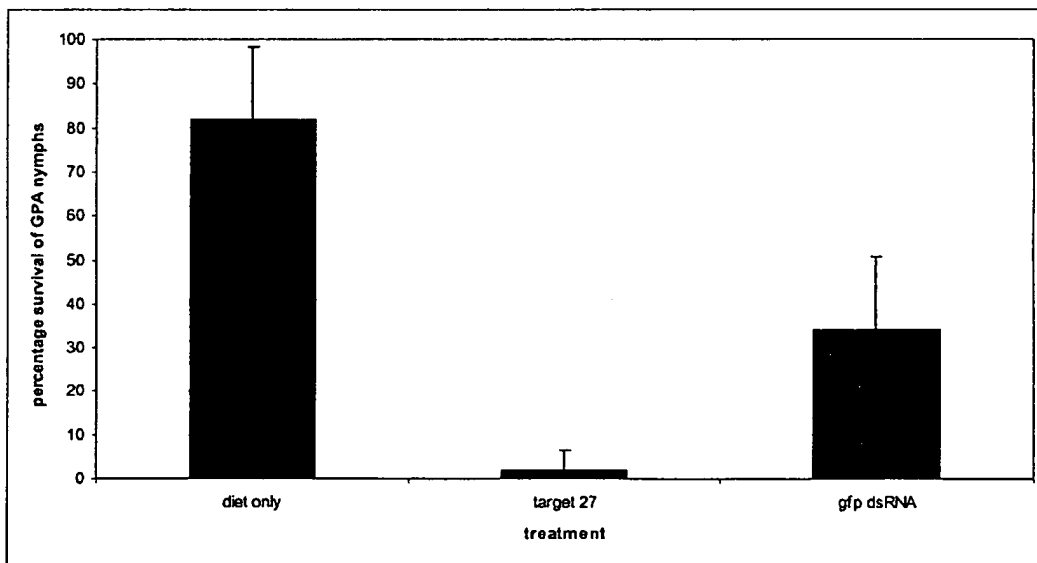
FIGURE 2-EV (b)

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FIGU

RE 1-TC



FIGU

RE 1-MP

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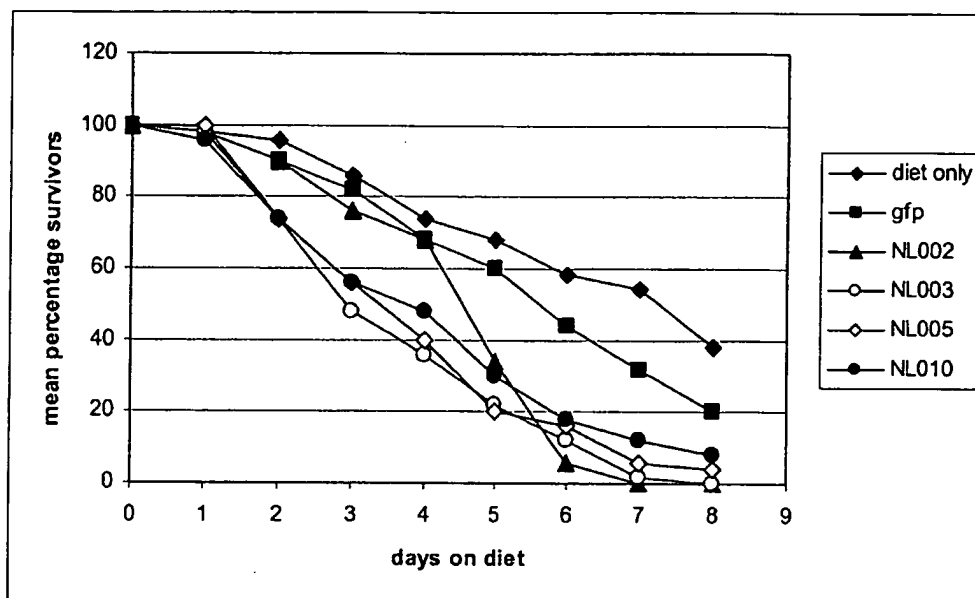


FIGURE 1-NL (a)

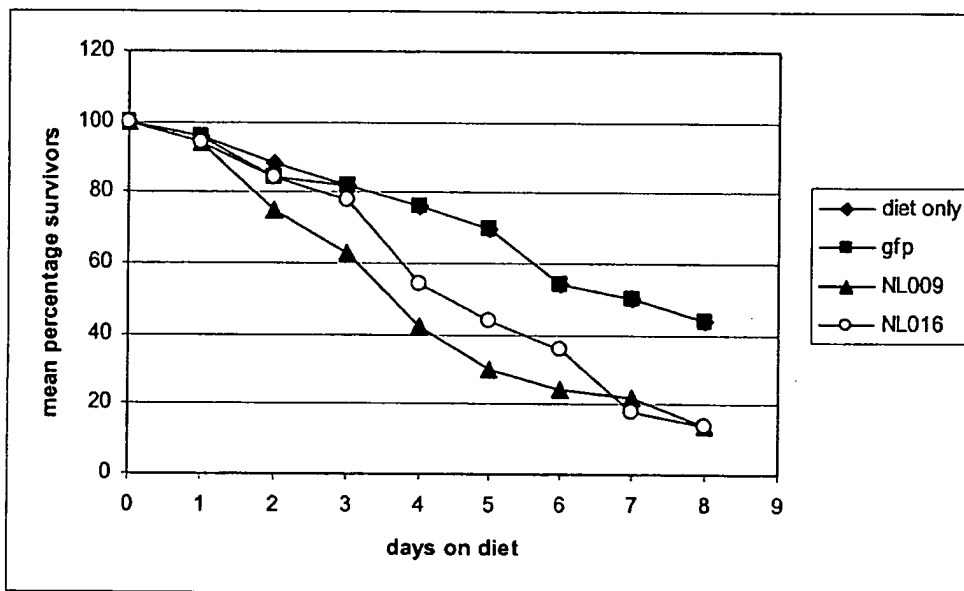


FIGURE 1-NL (b)

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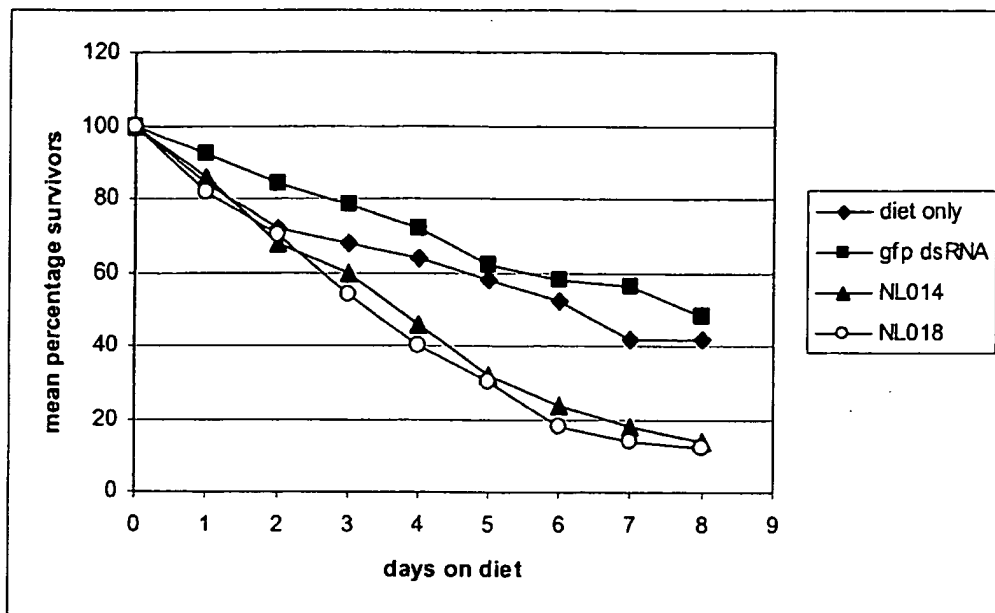


FIGURE 1-NL (c)

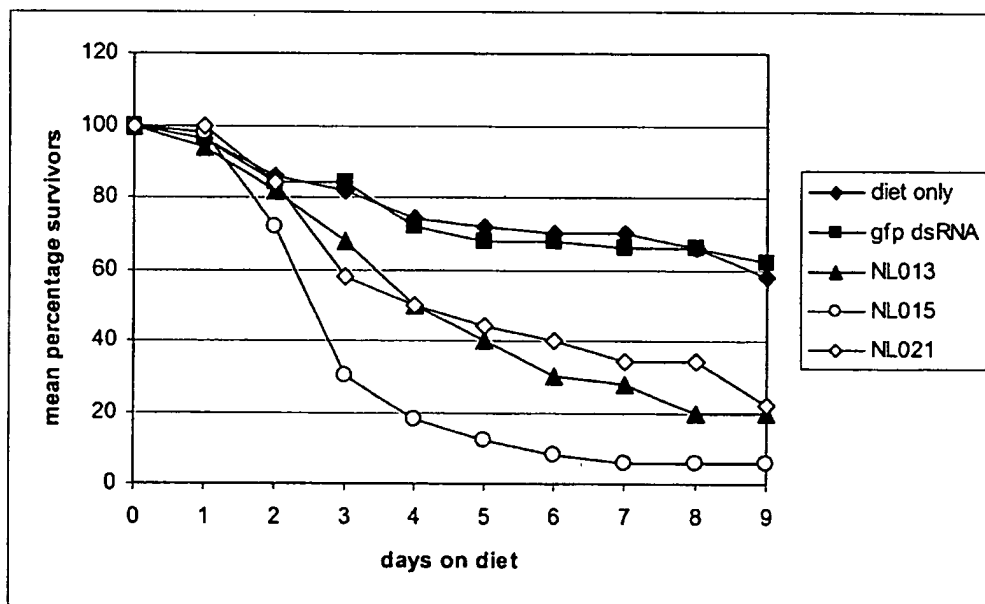


FIGURE 1-NL (d)

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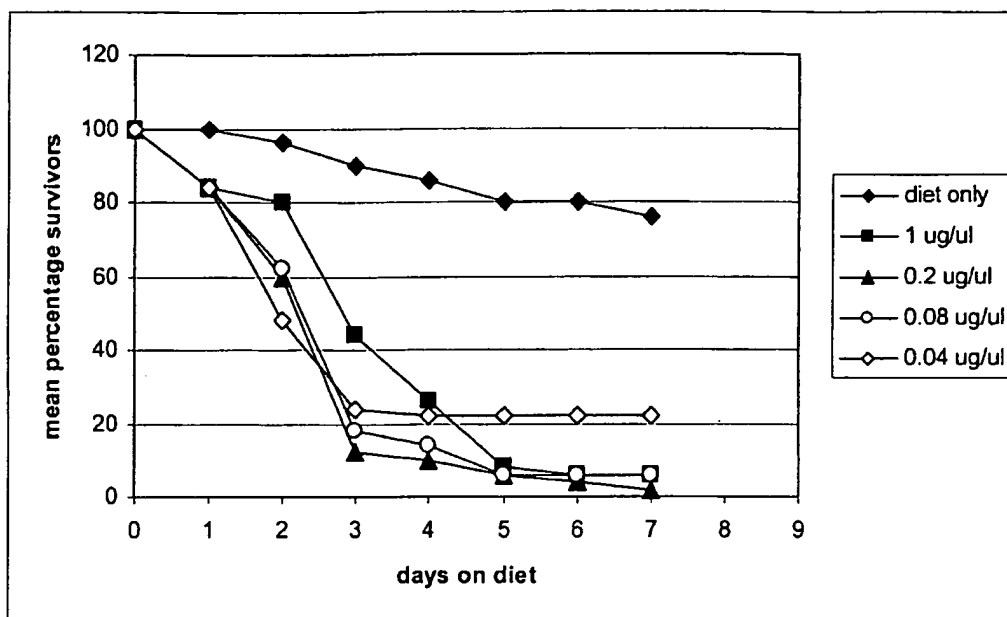


FIGURE 2-NL

INTERNATIONAL SEARCH REPORT

International application No
PCT/EP2007/000286

A. CLASSIFICATION OF SUBJECT MATTER

INV. C12N15/82 A01H5/00 C12N5/10 C12N15/12 C12N15/11

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

C12N A01H C07K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

EPO-Internal, PAJ, Sequence Search, WPI Data

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	<p>DATABASE UniProt [Online] 30 August 2005 (2005-08-30), "Ribosomal protein S4e." XP002432593 retrieved from EBI accession no. UNIPROT:Q4GXU7 Database accession no. Q4GXU7 abstract</p>	1-23, 34, 44-48
X	<p>& DATABASE EMBL SEQUENCE LIBRARY [Online] Ebi. hinxton; ribosomal protein S4e; rpS4e gene 16 July 2005 (2005-07-16), LONGHORN, S.J.: "Biphyllus lunatus mRNA for ribosomal protein S4e" retrieved from EBI. HINXTON accession no. www.ebi.co.uk Database accession no. AM048926 abstract</p>	1-23, 34, 44-48

☒ Further documents are listed in the continuation of Box C.

☒ See patent family annex.

* Special categories of cited documents:

- *A* document defining the general state of the art which is not considered to be of particular relevance
- *E* earlier document but published on or after the international filing date
- *L* document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
- *O* document referring to an oral disclosure, use, exhibition or other means
- *P* document published prior to the international filing date but later than the priority date claimed

- *T* later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
- *X* document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
- *Y* document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
- *Z* document member of the same patent family

Date of the actual completion of the international search

28 September 2007

Date of mailing of the international search report

12/02/2008

Name and mailing address of the ISA/

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Authorized officer

Holtorf, Sönke

INTERNATIONAL SEARCH REPORT

International application No

PCT/EP2007/000286

C(Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 2005/110068 A (MONSANTO TECHNOLOGY LLC; BAUM, JAMES, A; GILBERTSON, LARRY, A; KOVALIC) 24 November 2005 (2005-11-24) page 5, line 7 claim 39; example 6	1-23, 34, 44-48
X	WO 2005/019408 A (BAR ILAN UNIVERSITY; HAZERA GENETICS LTD; RAHAN MERISTEM LTD; MICHAEL) 3 March 2005 (2005-03-03) the whole document	1-23, 34, 44-48
X	WO 01/34815 A (CAMBRIA BIOSCIENCES, LLC) 17 May 2001 (2001-05-17) the whole document	1-23, 34, 44-48
A	WO 2005/049841 A (COMMONWEALTH SCIENTIFIC AND INDUSTRIAL RESEARCH ORGANISATION; BAYER BI) 2 June 2005 (2005-06-02) the whole document	
A	WO 01/37654 A (DNA PLANT TECHNOLOGY CORPORATION; TOBIAS, CHRISTIAN; SHAH, GOWRI; GUTT) 31 May 2001 (2001-05-31) the whole document	
A	WO 03/004644 A (COMMONWEALTH SCIENTIFIC AND INDUSTRIAL RESEARCH ORGANISATION; WHYARD,) 16 January 2003 (2003-01-16) the whole document claim 13 page 23 - page 24 page 20, line 21	
A	WO 02/46432 A (AVENTIS CROPS SCIENCE GMBH; GUNKEL, NIKOLAS) 13 June 2002 (2002-06-13) the whole document	

INTERNATIONAL SEARCH REPORT

International application No.
PCT/EP2007/000286

Box No. II Observations where certain claims were found unsearchable (Continuation of item 2 of first sheet)

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box No. III Observations where unity of invention is lacking (Continuation of item 3 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.

2. ☐ As all searchable claims could be searched without effort justifying an additional fees, this Authority did not invite payment of additional fees.

3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Invention 1: 1-23, 34, 44, 45, 46-48 partially

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest and, where applicable, the payment of a protest fee.
- ☐ The additional search fees were accompanied by the applicant's protest but the applicable protest fee was not paid within the time limit specified in the invitation.
- ☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

Invention1: 1-23,34,44,45, 46-48 partially

Isolated Leptinotarsa-specific nucleotide sequence as characterized by SEQID1; double stranded ribonucleotide sequence produced by expressing said SEQID1; cell or plant transformed by said sequence, said plant further expressing a pesticidal agent or insecticidal protein; a seed, reproductive or propagation material comprising said sequence, a product produced from said plant; a pesticide comprising said plant, a method for controlling or preventing insect growth comprising bringing into contact said insect pest with said seed, reproductive or propagation material which inhibits the insect's biological activity; a method for producing a plant resistant against a plant pathogenic organism, a method for improving yield by transforming said plant with said sequence which suppresses a Leptinotarsa-specific target gene, a transgenic plant resistant to an insect pest comprising said sequence; said transgenic plant further expressing another pesticidal agent or insecticidal protein; use of said sequence, double stranded ribonucleotide sequence, cell, plant, seed, reproductive or propagation material, product, transgenic plant for preventing either insect growth, insect infestation or for improving yield.

Inventions 2-149: claims 1-23,24,34,44,45, 46-48 partially

as invention 1, but limited to the Leptinotarsa-specific SEQIDs 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 49 to 158, 159, 160-163, 168, 173, 178, 183, 188, 193, 198, 203, 208, 215, 220, 225, 230, 240 to 246 and 2486.

Invention 150: claims 1-23,44,45, 46-48 partially, 25, 35 completely

as invention 1, but limited to the Phaendon-specific nucleotide sequences as characterized by SEQIDs 247, 249, 251, 253, 255, 257, 259, 275 to 472, 473, 478, 483, 488, 493, 498, 503, 508 to 512 and the use for Phaendon-specific infestation in plants.

Invention 151: claims 1-23,44,45, 46-48 partially, 26, 36 completely

as invention 1, but limited to the Epilachna-specific nucleotide sequences as characterized by SEQIDs 513, 515, 517, 519, 521, 533 to 575, 576, 581, 586, 591 or 596 and the use for Epilachna-specific infestation in plants.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

Invention 152: claims 1-23,44,45, 46-48 partially, 27, 37 completely

as invention 1, but limited to the Anthonomus-specific nucleotide sequences as characterized by SEQIDs 601, 603, 605, 607, 609, 621 to 767, 768, 773, 778, 783 or 788 and the use for Anthonomus-specific infestation in plants.

Invention 153: claims 1-23,44,45, 46-48 partially, 28, 38 completely

as invention 1, but limited to the Tribolium-specific nucleotide sequences as characterized by SEQIDs 793, 795, 797, 799, 801, 813 to 862, 863, 868, 873, 878 or 883 and the use for Tribolium-specific infestations.

Invention 154: claims 1-23,44,45, 46-48 partially, 29, 39 completely

as invention 1, but limited to the Myzus-specific nucleotide sequences as characterized by SEQIDs 888, 890, 892, 894, 896, 908 to 1040, 1041, 1046, 1051, 1056, 1061, or 1066 to 1070 and the use for Myzus-specific infestation in plants.

Invention 155: claims 1-23,44,45, 46-48 partially, 30, 40 completely

as invention 1, but limited to the Nilaparvata-specific nucleotide sequences as characterized by SEQIDs 1071, 1073, 1075, 1077, 1079, 1081, 1083, 1085, 1087, 1089, 1091, 1093, 1095, 1097, 1099, 1101, 1103, 1105, 1107, 1109, 1111, 1113, 1161 to 1571, 1572, 1577, 1582, 1587, 1592, 1597, 1602, 1607, 1612, 1617, 1622, 1627, 1632, 1637, 1642, 1647, 1652, 1657, 1662, 1667, 1672 or 1677 and the use for Nilaparvata-specific infestations in plants.

Invention 156: claims 1-23,44,45, 46-48 partially, 31, 41 completely

as invention 1, but limited to Chilo-specific nucleotide sequences as characterized by SEQIDs 1682, 1684, 1686, 1688, 1690, 1692, 1694, 1696, 1698, 1700, 1702, 1704, 1730 to 2039, 2040, 2045, 2050, 2055, 2060, 2065, 2070, 2075, 2080, 2085, 2090 or 2095 and the use for Chilo-specific infestation in plants.

Invention 157: claims 1-23,44,45, 46-48 partially, 32, 42 completely

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

as invention 1, but limited to Plutella-specific nucleotide sequences as characterized by SEQIDs 2100, 2102, 2104, 2106, 2108, 2120 to 2338, 2339, 2344, 2349, 2354, or 2359 and the use for Plutella-specific infestations in plants.

Invention 158: claims 1-23,44,45, 46-48 partially, 33, 43 completely

as invention 1, but limited to Acheta-specific nucleotide sequences as characterized by SEQIDs 2364, 2366, 2368, 2370, 2372, 2384 to 2460, 2461, 2466, 2471, 2476 or 2481 and the use for Acheta-specific infestations.

INTERNATIONAL SEARCH REPORT

Information on patent family members

International application No

PCT/EP2007/000286

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
WO 2005110068 A	24-11-2005	AU 2005244258 A1 BR PI0509743 A CA 2562022 A1 EP 1732379 A2	24-11-2005 25-09-2007 24-11-2005 20-12-2006
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